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BIOPHARMACEUTICAL REPORT

ASA BIOP Section Chairs : Ted Lystig(2024), Erik Bloomquist (2025), Steven Novick (2026)

Note from Editor:

As 2025 comes to a close, we hope this year has brought you meaningful connections and moments to celebrate. Recent gatherings such as JSM and RISW united statisticians, data scientists, and quantitative researchers, sparking dynamic conversations on emerging trends and innovations.

In this Winter issue, we continue the conversation about the role of statisticians in the biopharmaceutical industry, offering plenty of engaging reads. Among them are an insightful piece from Margaret Gamalo on Systems Biostatistics: Making Speed in Drug Development Safe, and thoughtful reflections from Haoda Fu and Amy Xia on the roots of our profession and its evolving impact. You'll also find practical guidance on leadership and career development, along with key takeaways from recent conferences.

As we wrap up, I want to extend heartfelt thanks to all our contributors, readers, and the editorial team. Your insights and passion drive progress in biostatistics and quantitative science, and we look forward to continuing this journey with you in the year ahead. Wishing you a peaceful, restorative, and joy-filled holiday season!

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SYSTEMS BIOSTATISTICS: MAKING SPEED IN DRUG DEVELOPMENT SAFE

Margaret Gamalo (Pfizer)

Highlights:

- While AI accelerates discovery and many drug development tasks, it also amplifies the interconnectedness of all stakeholders, requiring faster, more coordinated decisions. The challenge is not just speed but maintaining rigor and safety while managing and integrating complex data, all within a trust-driven pharmaceutical framework that adheres to clear standards and principles of transparency and fairness.
- Statisticians must adapt by using AI tools to manage infrastructure, automate non-critical tasks, and focus on high-value activities like decision-making, judgment, and ensuring the integrity of evidence. They must think broadly across systems, while also maintaining deep expertise in specific domains, to guide the drug development process safely in an increasingly fast-paced environment.

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Picture the trial lifecycle, where many of you already live, but now with AI quietly managing much of the plumbing. Before breakfast, a simulation engine has swept through thousands of design variants: sample sizes, accrual curves, interim looks, stopping rules, surfacing trade-offs we once uncovered only through repeated team meetings. By lunch, a drafting assistant proposes eligibility criteria with the pragmatism of a seasoned clinician, flags contradictions you would rather catch now than at site initiation, and highlights fairness or feasibility risks before they balloon into a screen failure bonanza. Three months later, a monitoring agent detects potential anomalies in the data, forwards them to clinicians and the trial manager for discussion, updates Bayesian posteriors in near real time for safety and early blinded efficacy, nudges you when pre-specified rules are close, and logs both the decision and the reasoning behind it. A year or two later, a reproducible pipeline runs exactly as pre-specified, checking results against a synthetic twin for accuracy. And when you finally open the draft clinical study report, the tables, listings, figures, and narrative read like one coherent story rather than twelve appendices colliding at the printer.

If AI can take care of all that, what does that leave for you? Keep that question in mind as we step back and consider the broader context in which we work. In the end, my goal is to let you reflect on your own role in this evolving landscape.

AI has not changed who is at the table -- sponsors, regulators, payers, healthcare professionals, and patients -- but it has tightened the clock and deepened the interdependence of every move. Drug development has always been cross-functional and buffeted by crosswinds; that has not changed. What has changed is the cadence. Discovery cycles compress, data volumes explode, and decisions cascade faster across CMC (Chemistry, Manufacturing, and Controls, which defines and proves the drug's composition, quality, and scalable GMP production), preclinical, clinical, biostatistics, safety, and market access. The challenge has never been only speed; it has always been trust, trust at scale. Over the past two decades, we have navigated a persistent arc of headwinds: waves of innovation that stretched capital and teams; shifting definitions of "value" across a broader set of stakeholders and debates over who defines it; regulatory complexity multiplied across regions; supply chain shocks that turned timing

into a moving target; and, with digitization, new data and AI risks, from patient privacy to model governance. What is new today is not these forces, but the speed with which we meet them. AI broadens the pipeline and accelerates discovery, amplifying both opportunity and interdependence, but the constraints remain. Faster is not automatically better; it just means that we collide with the same limits sooner. Our mission does not change: deliver breakthroughs people trust at costs health systems can sustain. To do that, we pair acceleration with rigor -- clear evidentiary standards, sound statistics, privacy- and quality-by-design principles, and transparent benefit-risk communication -- so that moving faster also means moving safer.

The momentum of AI in discovery is real. Analyst estimates vary, but many project that a substantial share—possibly up to ~30%—of new drug programs discovered this next few years will be AI-enabled in some way. Analysts project the global AI-in-drug-discovery market to grow ~25–30% annually from 2024–2029, fueled by cost/time pressures, broader AI adoption, exploding life-science data and compute, pharma–AI partnerships, looming patent cliffs, generative-AI–enabled design, and demand for personalized medicine [1]. Open any life-science feed (STAT, Endpoints, Pink Sheet, even LinkedIn) and you will see AI's fingerprints across the stack: Big Tech - Big Bio tie-ups, foundation models moving from structure prediction to de-novo design, and university-industry consortia accelerating target/chemistry workflows. However, as AI compresses discovery timelines, development must adapt in step [2].

There is no stop sign, but the playbook must evolve: modular, risk-tiered INDs; predictive and in-silico toxicology with auditable error bounds; manufacturing process acceleration and bridging; and adaptive designs that unify dose escalation, cohort expansion, and early proof of concept - especially outside oncology. Speed will no longer be exceptional; it will be expected. That means that the infrastructure surrounding it – pre-clinical, clinical, statistical, regulatory, and operational --must mature in parallel. In early development, modular INDs could open first-in-human studies with core pharmacokinetics and short-term toxicology, layering long-term studies and special populations as data mature. U.S. sponsors often face slower Phase I entry because FIH authorization can default to a one-size-fits-all process, while some regions allow faster starts for clearly lower-risk programs. A balanced fix is a formal, EMA-style risk-tiered FIH pathway—linking data package and protocol safeguards (e.g., MABEL-based starts, sentinel/staggered dosing, exposure caps, real-time stopping rules)—so low-risk assets move faster while high-risk, first-in-class agents remain under enhanced protection. This is in line with the commentary by Scott Gottlieb [3]. Predictive or in-silico toxicology can complement animal studies, provided that their models are transparently validated and bounded by measurable error [4]. Risk-tier frameworks may also emerge, where lower-risk or well-characterized modalities qualify for streamlined INDs, while first-in-class or high-uncertainty compounds maintain full preclinical requirements. As more candidates reach first-in-human, adaptive designs that merge dose escalation, cohort expansion, and early proof-of-concept will become essential, particularly in chronic, non-oncology settings. Statistics provide the guardrails that keep this speed trustworthy, defining operating characteristics, quantifying uncertainty, and preventing repeats of "rush-to-clinic" failures like TGN1412[5]. Acceleration is only progress if it remains safe, auditable, and scientifically sound.

Payers and HTA bodies have also moved upstream. In the EU, the Joint Clinical Assessment forces early alignment on PICO and comparators. PICO forces a decision-relevant question (Population, Intervention, Comparator, Outcomes) that matches real clinical practice, and the comparator is essential to estimate relative effectiveness and cost-effectiveness rather than absolute performance. Without an appropriate, justified comparator, HTA results risk bias, poor transferability, and conclusions that are not actionable for payers or guideline bodies. In the US, the Medicare TCET pathway enables earlier, conditional coverage tied to post-market evidence plans; and in the UK, the NICE Early Value Assessment offers provisional adoption with explicit evidence commitments. For statisticians, that means designing for access early: payer-relevant estimands must sit alongside primary endpoints, and measures such as time to next treatment, hospital-free days, treatment-free intervals, and resource use must be built in -- not bolted on. When access is conditional, real-world evidence programs, such as registries, burden, and utilization studies, must be established early as target trial emulations with preanalysis protocols and transportability controls.

Patients are changing as well. Many now arrive as informed consumers: AI and natural language processing quietly prescreen eligibility; "blue button" tools surface nearby trials [6]; and patient portals reveal

travel and time costs, as well as remote visit options. In this emerging marketplace of trial choice, ranking must be fair, explainable, and resistant to gaming, and the trial burden must be explicitly modeled, or feasibility projections will fail. The statistical toolkit expands accordingly: uplift modeling to estimate incremental recruitment benefit; constrained bandits to allocate patients fairly under burden and capacity limits; conjoint analysis to quantify real-world trade-offs; heterogeneous-treatment-effect modeling to identify who truly benefits; and target-trial emulation to ensure resulting claims remain grounded in clinical reality.

Together, these strands create a new equilibrium. Sponsors win through global pipeline partnerships and randomized evidence packaged with AI-informed post-market loops that continuously earn trust. Regulators converge on flexible, risk-tiered INDs, keep randomized trials as anchors of truth, and use AI with RCT–RWE embedding to extend generalizability, ideally harmonized through ICH guidance. Payers press for conditional reimbursement paired with AI-enabled real-world monitoring, while patients increasingly act as informed consumers. In this ecosystem, systems biostatistics become the connective tissue of evidence: aligning estimands with regulatory and payer decisions, architecting adaptive designs and simulations, and synthesizing RCT and real-world evidence under explicit assumptions and sensitivity analyses. We do not eliminate bias; we expose, mitigate, and quantify it so that every choice about benefit, risk, and access remains fair, transparent, and auditable.

As the scientific and regulatory landscape becomes more complex, with integrated data streams, divergent global frameworks, and accelerating decision cycles, the role of statisticians becomes more vital than ever. Our discipline anchors evidence amid volatility and complexity. First, signal versus noise: the convergence of omics, clinical, electronic health record, and claims data generates a torrent of patterns; statisticians discern truth from coincidence. Second, regulatory credibility: If a model is not interpretable, validated, and auditable, it is not deployable. Third, integration complexity: Without causal structure, multimodal data degenerates into a decorative quilt of bias; we establish the weights and guardrails that preserve inferential integrity. Fourth, decision risk: as fragmentation increases, so does the cost of error; we quantify trade-offs so that leadership can decide with clarity and confidence. Fifth, ethics and fairness: When an algorithm systematically underserves a subgroup, it is not a technical flaw but an ethical failure, and the responsibility to detect and correct it lies with us.

Statistical stewardship requires embedding statistical principles within AI systems rather than treating AI as an opaque instrument. Causal inference must reside within predictive pipelines; bias correction must occur where it alters actions; and transportability must be made explicit rather than assumed. We construct operating-characteristic frameworks that stress test trial designs and portfolios against population shifts, supply disruptions, enrollment volatility, and patient nonadherence. We translate the models into evidence that satisfies ICH, FDA, EMA, NMPA and regional regulatory expectations. And we insist on explainability that can be interrogated and replayed: What drove the decision, what alternatives were considered, and how conclusions evolve when assumptions change. The distinction between tooling and stewardship lies in judgment, in knowing when the right answer is a better model and when it is a better question.

Used well, large language models are accelerators, not autopilots. In a systems-biostatistics workflow, they manage the infrastructure—the drafts, retrieval, and code scaffolds—so that human time is spent on judgment and decision-making rather than operational assembly. They can outline derivations and simulations, propose eligibility criteria that we re-rank for coverage and fairness, and generate draft protocol sections, SAP shells, and DMC charters anchored in precedent. They can perform structured and quality focused review of analysis plans for alignment between specification and data, and scaffold real-world evidence studies with confounder libraries, directed acyclic graphs, and sensitivity panels tailored to payer questions. Retrieval-augmented generation keeps analyses grounded in precedent rather than speculation.

Acceleration, however, requires brakes. If a language model can influence anything that touches a patient, it must be governed like a medical device: documented, monitored, versioned, and equipped to abstain when confidence is low [7]. Hallucinations and overconfidence should be limited by automated fact-checking against verified knowledge sources, calibrated uncertainty, and conformal prediction (a statistical framework that provides a way to make reliable predictions with a guaranteed level of confidence). Guardrail erosion in extended interactions requires conversation state monitoring and adversarial stress testing [8]. Bias and harm-

ful content require structured audits, counterfactual testing, and fairness-constrained training or reranking to preserve subgroup equity [9]. Large language models can automate plumbing, but never judgment.

All of these point to who we must become. Think of a T-skilled statistician. The horizontal bar of T represents breadth, the ability to think throughout the system, from molecule to market, trial to access, seeing the full chessboard of regulators, payers, investigators, supply chains, and, most importantly, patients. The vertical stem represents depth, subject matter expertise in disease biology, endpoints, trial operations, health technology assessment, and the complex mathematical foundations that connect them. We are the ones who recognize when a data collection plan invites missingness, when an endpoint lacks sensitivity, or when a method rests on unverifiable assumptions, and we propose what will work instead. The boldface T is a reminder to act boldly, but with guardrails: use large language models for drafting and scaffolding, yet insist on calibration, provenance, and prespecified rules for trustworthiness. Automate the plumbing; never automate the judgment.

In a systems-biostatistics model, our role is not diminished by AI; in fact, it is strengthened to enable sound decisions in an accelerated world. We design evidence that speaks to both regulators and HTA bodies. We weave randomized and real-world evidence into coherent narratives. We stress test portfolios against disruption and fragmentation. We keep fairness, interpretability, and safety visible in every adaptive step. So, what remains for statisticians in an AI-accelerated world? Everything that matters in this new board game. Think broadly. Integrate deeply. Act boldly - with guardrails. Do that and we will not simply keep up with AI; we will ensure that it delivers what truly counts: better, faster, more trustworthy outcomes for patients.

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THE EVOLVING ROLE OF STATISTICIANS IN THE PHARMACEUTICAL INDUSTRY: LEVERAGING ADVANCED STATISTICAL ANALYTICS AND ARTIFICIAL INTELLIGENCE

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Highlights:

- Over the past century, the role of statisticians in the pharmaceutical industry has evolved—from service analysts to strategic decision drivers who define evidence, quantify uncertainty, design clinical plans, and embed statistical rigor into model-driven decisions across the value chain.
- Today, technology is rapidly advancing, and the definition of data is expanding beyond traditional tabular formats to encompass multimodal sources such as images, text, audio, video, omics, wearables, and real-world data. Guided by sound statistical principles, we are moving from digitization to datafication, to knowledge creation, and ultimately to intelligent decision-making—where statisticians ensure rigor, quality, and trust.
- Looking ahead, statisticians will continue to evolve as architects of the analytical ecosystem—integrating AI, automation, and reproducible workflows to accelerate insights while maintaining transparency, interpretability, and regulatory compliance.

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Abstract

In today's pharmaceutical industry, statisticians play a central role in turning large and complex data into reliable evidence and actionable insights. Their work connects data, science, and technology to support faster and more efficient drug discovery and development. With growing access to real-world data, genomics, and digital health information, along with rapid advances in computing and artificial intelligence (AI), the role of the statistician has expanded far beyond traditional boundaries. This paper reviews the evolution of statisticians in the pharmaceutical field, starting from their early focus on sample size justification and data analysis in late-stage clinical trials to their current position as part of key decision-making throughout the entire drug development process—including discovery, clinical trial design, manufacturing, and commercialization. We highlight major changes that supported this shift, such as improvements in statistical computing, new regulatory guidance, and the adoption of advanced methods like adaptive designs, Bayesian approaches, and simulation studies. We also examine how statisticians are using AI and machine learning for drug discovery, and to improve trial efficiency, generate insights from real-world evidence, and support innovation across the value chain. These changes create new opportunities but also require statisticians to develop broader skills in programming, data science, and cross-functional communication. Looking ahead, we believe that statisticians will continue to be at the forefront of innovation in pharmaceutical research. By combining strong statistical thinking with modern tools and technologies, we can lead efforts to deliver better, safer treatments to patients more quickly. This paper offers a forward-looking view on how the profession can continue to grow and lead in a data-driven future.

Key Words and Phrases: Adaptive designs; Bayesian methods; Data science; De novo design; Drug discovery; Real-world evidence.

Short title: Evolving Role of Statisticians in Pharma

1 Introduction

Pharmaceutical statisticians have come a long way over the past half-century, evolving from backroom number-crunchers to essential contributors across the entire drug development spectrum. Once viewed primarily as support staff ensuring regulatory compliance, statisticians today are equal partners in research and development teams, influencing decisions from early drug discovery, clinical development to manufacturing and commercialization (International Council for Harmonisation, 2009, 2020; Chuang-Stein et al., 2010a) . This expanded role has been driven by multiple converging forces. Advances in computing and the advent of new data sources (e.g. genomics, real-world clinical data) have enabled innovative statistical methodologies, while the rise of artificial intelligence (AI) and machine learning offers powerful tools to extract insights from electronic information which was hard to analyze before (International Human Genome Sequencing Consortium, 2001; 1000 Genomes Project Consortium, 2015; U.S. Food and Drug Administration, 2023b; Concato and Corrigan-Curay, 2022; Vamathevan et al., 2019; Harrer et al., 2019). At the same time, the pharmaceutical industry's external environment has grown more challenging – fewer new therapies are approved each year with increasing costs, and stakeholders demand greater transparency and evidence of value (Wouters et al., 2020). Statisticians have responded by embracing new analytic techniques and stepping into leadership and collaboration roles that were virtually unheard of decades ago (Chuang-Stein et al., 2010a; Senn, 2021). This article explores the trajectory of statisticians' responsibilities in the pharmaceutical industry, with an emphasis on how advanced analytics and AI are shaping the present and future. We review the historical context that set the stage for today's trends, analyze key drivers of change (from big data to Bayesian designs to AI) (U.S. Food and Drug Administration, 2019; Chen et al., 2023), discuss current and emerging applications of AI in drug development (Vamathevan et al., 2019), and examine how the statistician's influence now extends across the pharmaceutical value chain. We also highlight the growing importance of interdisciplinary collaboration – including engagement with regulatory agencies like the FDA – and consider what educational enhancements are needed to prepare the next generation of pharmaceutical statisticians. Ultimately, we aim to demonstrate that statisticians are not only adapting to an evolving landscape but are increasingly leading innovation in pharmaceutical R&D and beyond.

The following sections are structured as follows: Section 2 delves into the historical context of the evolving role of statisticians, setting the foundation for current trends. Section 3 examines the key drivers of change, including advancements in statistical computing, methodological and design innovations, and the emergence of new data types. Section 4 explores the current and emerging applications of AI within pharmaceutical companies and how statisticians' influence now permeates the entire pharmaceutical value chain. Section 5 concludes with a discussion on the increasing importance of interdisciplinary collaboration and the educational advancements necessary to equip the next generation of pharmaceutical statisticians.

2 Historical Context of Statisticians' Roles in Pharmaceutical Industry

The use of data and statistics to improve patient outcomes has been a part of healthcare for thousands of years and remains crucial today. An early example of data-driven healthcare is in the Bible's "Book of Daniel" from 500 BC. King Nebuchadnezzar of Babylon believed a diet of meat and wine would keep his people healthy. However, some young men chose to eat vegetables and drink water for 10 days. They appeared healthier, so the king allowed them to continue their diet. This was an early instance of using an experiment to make a health decision. In the 18th century, James Lind, a ship's surgeon, conducted one of the first controlled clinical trials. He tested treatments for scurvy and found that oranges and lemons were effective (Lind, 1753).

Modern biostatistics in drug development began in 1946 with the introduction of randomization and controlled trials (Crofton, 2006). Randomization was first introduced in 1923, and Sir Austin Bradford Hill conducted the first randomized controlled trial in 1946, showing that streptomycin was effective for tuberculosis (Bothwell and Podolsky, 2016; Chalmers, 2003). This study demonstrated how randomization, control groups, and statistical testing could guide medical decisions. A significant change came with the 1962 amendments to the U.S. Food, Drug, and Cosmetic Act (Goodrich, 1963),

following the thalidomide tragedy. These amendments required the FDA to demand "substantial evidence" from controlled trials to prove a drug's effectiveness, not just safety. This led drug companies to realize the necessity of statistically designed trials for approval, leading to a surge in hiring statisticians to meet FDA requirements (Rodda et al., 2001). By the late 1960s and 1970s, statisticians were key members of clinical research teams, mainly designing trials, calculating sample sizes and analyzing data for regulatory submissions (Meadows, 2006).

In the 1970s and 1980s, the role of statisticians in pharma grew with new regulatory initiatives. A key development was the FDA's New Drug Application (NDA) rewrite in the early 1980s, which required a formal statistical review for every new drug application and a statistician as a co-author of clinical trial reports (U.S. Food and Drug Administration, 1988, 1985). These changes solidified statisticians' roles in the drug approval process. However, they were still seen as technical support, ensuring analyses were correct and compliant. As Rockhold (2000) noted, even after NDA reforms, statisticians mainly executed analyses and calculated sample sizes, rather than shaping study designs or development programs. Most focused on late-phase clinical trials and some manufacturing quality assessments, with little involvement in early research phases or non-clinical areas (Chuang-Stein et al., 2010a).

By the 1990s, several factors increased statisticians' influence. Pharmaceutical R&D became more global and complex, with larger trials and more data. Regulatory agencies worldwide adopted harmonized standards for trial conduct and statistical practice. The International Conference on Harmonisation (ICH) issued guideline E9: Statistical Principles for Clinical Trials (Guideline, 1999), emphasizing the importance of statistics in trial design, analysis, and interpretation. According to Rockhold (2000), ICH E9 gave statisticians more "leverage and authority in drug development," highlighting the need for a strong statistical foundation for credible evidence. Statisticians began contributing strategically, advising on clinical programs and study designs. The industry recognized that information is the key output of R & D, boosting the demand for statistical thinking to maximize data value in discovery, preclinical studies, clinical trials, and post-market surveillance.

Another milestone in the 1990s was the rise of powerful statistical software and personal computing, enabling advanced analyses and simulations. Statistical programming languages like SAS became essential tools for pharma statisticians. In the late 1990s and early 2000s, statisticians expanded into new areas: safety data mining for adverse event detection, support for epidemiological studies, and clinical pharmacology modeling (e.g., PK/PD analyses for dose selection). In the 2000s and 2010s, the statistician's role expanded significantly. The FDA's 2004 Critical Path Initiative aimed to modernize medical product development science, advocating for innovative statistical approaches (U.S. Food and Drug Administration, 2004). The initiative highlighted challenges like biomarker validation, enrichment trial designs, missing data handling, multiplicity issues, and model-based evidence, all requiring sophisticated statistical input. In the following decades, regulators released guidance documents on adaptive trial designs, non-inferiority trials, multiple endpoints, and real-world evidence, expanding statisticians' toolkit and responsibilities in clinical development. By the 2010s, statisticians were seen as essential partners in drug R&D. As noted that statisticians were "absolutely critical for efficient and effective drug development", serving as key contributors or consultants in all R&D areas. The role evolved from a support role to a strategic, interdisciplinary one, preparing statisticians to tackle 21st-century challenges, including the big-data revolution and AI integration in pharmaceutical research.

3 Key Catalysts for the Evolution of the Statistician's Role

Several interrelated factors have accelerated the evolution of statisticians' responsibilities in the pharmaceutical industry. Key among them are: advances in computing and software that exponentially widened analytic possibilities (such as SAS and R) (Ihaka and Gentle- man, 1996; Chambers, 1998; Segreti et al., 2001); the development of innovative statistical methodologies (such as Bayesian methods and adaptive designs) coupled with regulatory encouragement that fostered their adoption (Pallmann et al., 2018; U.S. Food and Drug Administration, 2019; Woodcock and LaVange, 2017; International Council for Harmonisation, 2025); and the emergence of new data types and large datasets (from real-world evidence to genomics and digital health) that demanded novel analytical approaches (Concato and Corrigan-Curay, 2022; U.S. Food and Drug Administration, 2018; Morris and Baladandayuthapani, 2017). These factors together have reshaped what pharmaceutical statisticians do day-to-day. We examine how each of these catalysts has contributed to the deepening and broadening of statisticians' responsibilities in pharma, and we illustrate

how statisticians' skill sets, and influence have grown in response. We review the historical con- text that set the stage for today's trends on the rise of AI in pharmaceutical research(Liu et al., 2023b; U.S. Food and Drug Administration, 2025b).

3.1 Advances in Statistical Computing and Hardware

Early pharmaceutical statisticians worked in an era of limited computing power, often per- forming calculations by hand or with basic mechanical aids. The mid-20th century saw the introduction of mainframe computers, but computational resources remained scarce and specialized. This inherently constrained the complexity of analyses that statisticians could practically undertake. Over time, however, revolutions in computing hardware and the advent of statistical software radically transformed the toolkit of the pharmaceutical statistician. By the late 20th century, improvements in processing speed and data storage (following Moore's Law) (Moore, 1965) enabled routine execution of intensive methods that were previously impractical. In parallel, the development of high-level statistical programming languages and software packages – notably the Statistical Analysis System (SAS) in the 1970s and the open-source S language (and later R) in the 1990s – provided user-friendly platforms to implement complex analyses (Chambers, 1998; Ihaka and Gentleman, 1996). The widespread adoption of these tools in industry meant that statisticians could manage larger datasets and apply more sophisticated models with relative ease. The practice of statistics in pharma changed markedly over 35 years in tandem with advances in computational power (Segreti et al., 2001).

One direct outcome was the rise of simulation-based analysis and design. With greater computing resources, statisticians began to use Monte Carlo simulations to evaluate trial properties and optimize study designs before any patients were enrolled. For example, by the 2000s it became routine to simulate thousands of trial iterations to assess a design's probability of making correct/incorrect decisions or to model various what-if scenarios for adaptive trials (U.S. Food and Drug Administration, 2019). Such computationally intensive work simply was not feasible in earlier decades. The increasing availability of fast computing also facilitated resampling and modern methods – techniques like the bootstrap (for estimating confidence intervals) and Markov chain Monte Carlo (for Bayesian analysis) gained traction in clinical research once computers could handle the necessary iterative calculations (Efron, 1979; Gelfand and Smith, 1990). The net effect was an expansion in statisticians' capabilities: rather than being limited to relatively simple trial designs and analyses, they could now explore a much richer design space and fit more complex models to data. Indeed, contemporary statisticians often write extensive code (in SAS, R, or Python, etc.) to manipulate datasets, implement custom analyses, and even create interactive dashboards for data visualization, reflecting a blending of traditional statistical skills with what we now call data science (Chuang-Stein et al., 2010b).

Importantly, better computing didn't just change how fast statisticians work – it changed what they work on. Previously, statisticians' contributions might begin only after data collection (analyzing final trial results), but modern computing power allowed them to influence studies from the planning and design stage onward, running simulations to inform optimal sample sizes, endpoint definitions, and decision criteria. For instance, clinical trial simulation became an established practice for complex trial planning by the 2010s (U.S. Food and Drug Administration, 2019), allowing statisticians to quantify the trade-offs of various design choices under myriad scenarios. As data sets grew from tens of patients in the 1960s to tens of thousands of patients (or millions of observations) in the 21st century, the statistician's role expanded to include ensuring data integrity, traceability, and reproducibility through efficient programming and validation (Segreti et al., 2001). The long history of success of SAS as a de facto industry standard is one testament to how central computing environments became to pharma statistics. More recently, open-source tools (R and Python in particular) have gained acceptance, further empowering statisticians to use cutting-edge techniques and share reproducible code (Chuang-Stein et al., 2010b). In summary, the dramatic improvements in hardware and the parallel evolution of statistical software over roughly 1950 to the present have been fundamental catalysts for change – transforming the statistician's role from a manual calculator of p-values to a computational strategist capable of exploring vast design and analytic possibilities (Segreti et al., 2001; Rockhold, 2000).

Looking forward, we believe the next wave of computing advances will continue to shape the statistician's role. For example, the current trial simulations primarily focus on addressing scientific questions such as family-wise type I error control, power, or the posterior probability

of trial success. These simulations are often conducted before running a clinical trial. As computing power continues to grow, we expect statisticians to increasingly leverage real-time data during ongoing clinical trials to run simulations that address not only scientific questions but also operational questions, such as the consequences of opening additional sites to speed up enrollment. Addressing these questions can further lead to optimizing clinical trial operations at each step, conditional on what has already happened in the trial. We envision that statisticians, collaborating with cross-functional teams, will be responsible for designing and implementing such real-time simulations, which will be a key component of the next generation of clinical trials.

3.2 Growth of Advanced Statistical Methodologies and Regulatory Encouragement

As computing capabilities grew, so too did the development of novel statistical methodologies for clinical trials. From approximately the 1980s onward, statisticians began proposing innovative trial designs and analysis methods that could make drug development more efficient and informative. Two prominent examples are adaptive trial designs and the increasing use of Bayesian statistical methods.

Innovative designs represented a break from the fixed, one-size-fits-all designs that had dominated clinical research since the standardization of randomized controlled trials in the post-war era. At the same time, the industry has recognized the increasing cost for drug development, and the need to improve the efficiency of drug development. However, the uptake of such innovations in industry was initially slow – until regulatory bodies, and particularly FDA, actively encouraged their adoption. Regulatory guidance has been a crucial catalyst in legitimizing and accelerating the use of advanced methods by pharmaceutical statisticians (U.S. Food and Drug Administration, 2019, 2023c; International Council for Harmonisation, 2025). Adaptive designs allow pre-planned modifications to certain aspects of a clinical trial (such as sample size, randomization ratios, or even treatment arms) based on interim analysis of accumulating data. The conceptual appeal of adaptive trials is clear: they can make clinical research more flexible and efficient, potentially finding effective treatments faster or using fewer patients (Pallmann et al., 2018). For example, an adaptive trial might start with multiple dose groups and use interim results to seamlessly drop ineffective doses or reallocate more patients to promising treatments, rather than sticking to a static design. By utilizing ongoing results, adaptive designs can ethically benefit patients (more patients get the better treatments) and scientifically improve the chance of trial success or reduce resources needed. These advantages were recognized in the statistical literature by the 1990s, but early on there was hesitation in the conservative regulatory environment to accept trials that depart from the traditional fixed protocol (Pallmann et al., 2018). This began to change in the 2000s and 2010s. A milestone was the FDA's 2010 Draft Guidance on adaptive design, followed by a comprehensive FDA Guidance in 2019 explicitly outlining principles for adaptive trials in drug development (U.S. Food and Drug Administration, 2019). This guidance not only provided industry with a clear roadmap on how to plan and analyze adaptive trials rigorously, but also sent a strong signal that regulators welcome well-justified adaptive approaches, such as currently an ICH E20 guidance on adaptive design for clinical trials is underway to delineate the principles of adaptive designs and regulatory considerations (International Council for Harmonisation, 2025). Statisticians were central to this shift: they had to develop new statistical methods to ensure, for instance, that making mid-course modifications would not inflate the family-wise type I error (false positive rate). They also engaged in extensive simulations, as recommended by FDA, to demonstrate operating characteristics of adaptive designs before implementation. As a result of these efforts, adaptive designs are now increasingly common in clinical trials across therapeutic areas (from oncology to cardiology), and pharmaceutical statisticians have expanded responsibilities in designing interim analyses, setting adaptation rules, and liaising with Data Monitoring Committees. Indeed, adaptive methods have moved from an experimental idea to a mainstream tool, catalyzed by regulatory acceptance.

Bayesian methods have similarly grown in prominence. The Bayesian framework for data analysis offers an intuitive and flexible approach in which evidence is accumulated sequentially, and prior knowledge can be formally incorporated into current trial analysis. For decades, classical (frequentist) statistics dominated drug trials, but Bayesian statistics began gaining traction for problems where traditional methods were less efficient – such as trials in rare diseases or early-phase studies requiring use of prior data, as well as other applications in safety signal detection and evaluation (Xia et al., 2011; Xia and

Price, 2014), and meta-experimental design and analysis (Ibrahim et al., 2012). Bayesian analyses can produce direct probability statements about treatment effects (e.g., the probability a drug is better than control), which are appealing to decision-makers, and can allow more continuous learning from data rather than an all-or-nothing hypothesis test. Bayesian methods, such as probability of study success (PrSS) evaluation, have been broadly used for internal decision making (Wang et al., 2013). However, adopting Bayesian approaches in regulated clinical trials required convincing both scientists and regulators of their validity and robustness. A key turning point was in the area of medical devices: in 2010, the FDA's Center for Devices and Radiological Health released a Guidance for the Use of Bayesian Statistics in Medical Device Trials (U.S. Food and Drug Administration, 2010). This document explicitly acknowledged that Bayesian methods, when properly applied, could reduce required sample sizes or study durations by incorporating prior evidence, as well as offer other benefits in flexibility of trial design. Notably, by formally addressing "Why are Bayesian methods more commonly used now?" and similar questions, the FDA guidance clarified misconceptions and provided best practices for sponsors. This endorsement catalyzed a surge of interest in Bayesian designs not only for devices but eventually in drug trials as well. In drug development, Bayesian methods have seen increased use in exploratory Phase II trials, in adaptive dose-finding (e.g., Bayesian dose-escalation methods in oncology), and even in some confirmatory trials with regulatory acceptance (especially in rare disease settings where leveraging external or prior trial data is invaluable). For example, the pivotal Pfizer/BioNTech mRNA COVID-19 vaccine study (BNT162b2) employed a design and analysis framework described as Bayesian (Polack et al., 2020). Notably, in autoimmune disease development, Amgen's programme for Systemic Lupus Erythematosus (SLE) entered the FDA's Complex Innovative Trial Design (CID) pilot programme, proposing that endpoint will be evaluated using a Bayesian Hierarchical Model (BHM) with non-informative priors Food and Drug Administration (FDA) (2021). By 2024, a Lancet review noted that Bayesian statistics offers a flexible and informative approach that facilitates both design and interpretation of trials, and advocated for its broader use in clinical research (Goligher et al., 2024). The authors emphasized that owing to its different conception of probability, the Bayesian paradigm can incorporate evidence in ways that enrich inference and decision-making. It is telling that FDA leadership has also highlighted Bayesian and adaptive designs as promising innovations in the context of modernizing clinical trials (e.g., in discussions around the 21st Century Cures Act, which encouraged the exploration of novel trial designs and analytical methods for speeding therapy approvals) (Concato and Corrigan-Curay, 2022). Recently, the Food and Drug Administration's Center for Drug Evaluation and Research (CDER) launched the Bayesian Statistical Analysis (BSA) Demonstration Project to foster the use of Bayesian methods in "simple" phase-III drug trials (e.g., non-adaptive or sequential designs). The programme allows sponsors to use Bayesian analyses — either as the primary or a supplemental analysis — and offers regulatory interaction and methodological support (U.S. Food and Drug Administration, Center for Drug Evaluation and Research, Center for Clinical Trial Innovation (C3TI), 2025). In practice, statisticians' roles have expanded to include mastering these advanced methodologies, educating project teams and regulators about them, and developing the technical justifications needed for their use. Where a 1970s-era statistician's toolkit might not have extended far beyond t-tests and chi-squares, a statistician today might design a complex adaptive Bayesian trial with multiple interim looks and dynamic randomization, confident in its theoretical soundness and regulatory acceptability (Goligher et al., 2024; U.S. Food and Drug Administration, 2019), as well PUDUFA VII requirement (U.S. Food and Drug Administration, 2022b), and FDA is about to publish a draft guidance on Bayesian methods by the end of 2025.

Another example of methodological innovation is the emergence of master protocols (platform trials, basket trials, umbrella trials) which allow evaluation of multiple therapies and/or multiple diseases within a single trial infrastructure. These designs, which became especially prominent in the 2010s (notably in oncology), require sophisticated statistical coordination – for instance, sharing control groups, dropping or adding treatment arms on the fly, and possibly using Bayesian borrowing of information across sub-studies. Statisticians were instrumental in conceiving these designs, but their broad adoption was again facilitated by regulators. In 2017, Woodcock and LaVange from the FDA authored a New England Journal of Medicine review explaining the value of master protocols and providing a regulatory perspective on how to conduct them rigorously (Woodcock and LaVange, 2017). They illustrated that such designs can accelerate drug development by studying multiple hypotheses under a common protocol, but also cautioned on the statisti-

cal complexities that must be managed. Following this, the FDA issued a formal guidance on master protocol trials (in 2018 draft, finalized 2022), further cementing regulatory encouragement (U.S. Food and Drug Administration, 2022a). The net effect of these trends is that statisticians are now far more deeply involved in trial design strategy than before – they are not just answering "How do we analyze the data?" but also "What is the optimal way to design this study to begin with?". As a 2010 industry review put it, statisticians in pharma have evolved into "full and equal partners with clinical and regulatory scientists" in trial planning and drug development strategy. This cultural shift, partly driven by the need to implement cutting-edge methods properly, means statisticians today often co-lead discussions on a program's evidence generation plans. They ensure that innovative designs like adaptive and Bayesian trials are used appropriately and transparently, satisfying scientific rigor and regulatory standards. In summary, the growth of advanced methodologies – and crucially, the feedback loop of regulatory guidance and endorsement – has been a key catalyst expanding statisticians' responsibilities. It pushed them into new roles: methodological innovators, architects of novel trial designs, and front-line communicators who articulate the benefits and limitations of these designs to regulators and clinical teams.

3.3 New Data Types and Large Datasets

The modern pharmaceutical landscape is awash with data sources that scarcely existed a few decades ago. In early times (1950s-1980s) clinical trial results were captured via paper-based Case Report Forms (CRFs) and were the primary data source for statisticians. With limited computation tools, the analysis was often restricted to basic descriptive statistics and simple statistics methods such as t-tests, ANOVA, and chi-squared tests. Later, longitudinal data from electronic CRFs and databases became more common, allowing for richer analyses of treatment effects over time, methods such as mixed-effects models, and more complex statistical techniques become standard. Nowadays, companies contend with real-world data from healthcare databases, genomic and other "omics" data from advanced laboratory technologies, and digital health data from wearable sensors and electronic patient devices. The advent of these new data types – often high-volume, high-velocity, and high-variety – has changed the statistician's job. Statisticians have had to develop and adopt new methodologies for analyzing such data, expand their expertise into realms traditionally outside classical biostatistics, and often collaborate closely with experts in fields like bioinformatics and machine learning. In short, the rise of large, complex data sets has been another catalyst that broadened the statistician's role from trial-centric analysis to a more holistic "clinical data science" role (Morris and Baladandayuthapani, 2017).

A key area is Real-World Data (RWD) and Real-World Evidence (RWE). RWD are data relating to patient health status and/or the delivery of health care routinely collected from a variety of sources. It could include EHRs, claims and billing data, data from product and disease registries, patient-generated data including in home-use settings, and data gathered from other sources that can inform on health status, such as mobile devices. RWE is the clinical evidence regarding the usage and potential benefits or risks of a medical product derived from analysis of RWD (U.S. Food and Drug Administration, 2018; Concato and Corrigan-Curay, 2022). Historically, RWD was not heavily used in regulatory decisions due to concerns about bias and quality. However, efforts, especially in the U.S., have increased to use RWE for regulatory and clinical insights. The 21st Century Cures Act of 2016 required the FDA to explore RWE for drug approvals (U.S. Food and Drug Administration, 2018). By 2021-2022, the FDA had issued guidance on using RWE and approved some drugs based on real-world studies (U.S. Food and Drug Administration, 2024a, 2021a, 2023d). Statisticians play a crucial role in analyzing these datasets, dealing with issues like bias, confounding and missing data, and ensuring the data's quality. They must also explain to regulators how observational data can approximate randomized trial evidence. This expansion means statisticians now work in outcomes research, safety surveillance, and policy. The FDA's 2021 guidance on using electronic health records for regulatory decisions further expands their responsibilities, and FDA published a series of guidance documents related to RWD/RWE in regards to data, design, conduct and regulations since 2021 (U.S. Food and Drug Administration, 2021b, 2023b,d, 2024a).

Another important area is genomics and other "omics" data. Advances like genome sequencing have introduced large-scale data to drug development. These data are complex and require sophisticated modeling. Statisticians have been key in developing tools to analyze this data, contributing to bioinformatics. They design experiments, preprocess data, and develop algorithms to identify important genes or biomarkers. As precision medicine grows, statisticians help identify patient subgroups with

genomic markers that predict drug response. They also work on companion diagnostics, linking biomarkers to treatment outcomes. Their role has expanded from asking "Does the drug work on average?" to "For whom does the drug work?" This requires skills in multivariate modeling and machine learning, and collaboration with lab scientists. Statisticians also ensure data validity in new analytical domains (Morris and Baladandayuthapani, 2017).

Digital health data is another new area. Devices like smartphones and wearables collect real-time patient data, creating "digital endpoints" in trials. These endpoints offer a more comprehensive view of patient health. Statisticians validate and analyze these endpoints, addressing challenges like data volume and missing data. They work with clinicians to ensure digital measures correlate with clinical benefits. The FDA has shown interest in digital health technologies, issuing guidance on using digital tools in trials. The COVID-19 pandemic increased the acceptance of digital endpoints. Statisticians now work with data scientists to refine algorithms and design trials with remote data capture.

Finally, underpinning all these new data domains is the rise of AI and machine learning (ML) techniques in drug development. Pharmaceutical companies are increasingly using ML models for tasks ranging from drug discovery (e.g., predicting molecule-target interactions) to patient/site selection and outcome prediction in clinical trials. This work is often led by statisticians, which often collaborate closely or lead the validation of such models. Notably, regulatory agencies have begun to acknowledge AI/ML in submissions. By 2025, the FDA reported seeing over 500 product submissions (across drugs and biologics) that incorporated AI/ML approaches, spanning discovery, trial optimization, and post-market safety analysis (U.S. Food and Drug Administration, 2025a). This marks a significant new responsibility for statisticians: evaluating and perhaps even developing predictive algorithms and ensuring they meet appropriate standards of evidence and lack undue bias. The FDA has encouraged sponsors to employ cutting-edge analytical tools – for example, using ML on real-world data to detect safety signals or to interpret complex endpoints – but with the expectation that they are rigorously assessed (U.S. Food and Drug Administration, 2025b). Statisticians thus find themselves contribute in cross-functional teams, bringing their expertise in validation: for instance, applying principled cross-validation, setting up prospective vali- dation studies for algorithms, and quantifying uncertainty in model predictions (Liu et al., 2023b; Morris and Baladandayuthapani, 2017). In essence, the data science revolution has not obviated the need for statisticians – it has expanded their purview. This breadth is a direct consequence of the influx of novel data types that require novel analytic thinking and methods.

4 Emerging AI Technologies in Pharmaceutical Research

Perhaps the most transformative catalyst in recent years has been the rise of artificial intelligence and machine learning in pharmaceutical research. AI technologies are reshaping how data are generated, analyzed, and even how trials are conducted. The following subsections present key trends.

4.1 Expanding Data Definition

In the past, pharmaceutical data was mostly just numbers in tables. Now, AI has expanded what we consider "data" to include things like molecular sequences, medical images, text, and even audio. Machine learning models can now learn from this unstructured information that we couldn't analyze before. For example, large language models have been trained using diverse text sources like Wikipedia. Wikipedia, once just a simple reference, is now a key dataset for training large language models, showing how text can be turned into valuable scientific data (Devlin et al., 2019; Brown et al., 2020). Similarly, AI in biotechnology has used protein databases to create new functional proteins in a computer (Anishchenko et al., 2021; Watson et al., 2023). This means protein databases, once used for manual searches, are now used for AI-driven protein design, allowing us to create enzymes with specific functions from scratch (The UniProt Consortium, 2023; Berman et al., 2000). These examples show how the idea of "data" is growing and how new data types are driving unexpected advances in pharmaceuticals.

Statisticians play an important role in understanding this flood of digital data. AI gives statisticians the chance to work with complex datasets that were too difficult to analyze before. There's a clear path for turning raw data into useful insights: (1) Digitalization – turning paper records into digital form; (2) Datafication – organizing these digital records so they can be analyzed; (3) Knowledgefication – finding patterns and insights from the data and to answer various what-if questions; and (4) Intelligencefication – using AI to recommend optimal decisions based on that knowledge. We see this happening in pharmaceutical research and development. Big compa-

nies have digitized years of clinical trial protocols, patient records, and regulatory documents. Once these documents are digitized, statisticians can start analyzing them, linking trial criteria to outcomes and study designs to success rates. This allows them to ask important questions like, "What makes some trials succeed while others fail?" or "How do certain criteria affect patient enrollment and outcomes?" Recent studies using real-world patient data have shown that many traditional trial restrictions don't significantly affect outcomes, and relaxing these restrictions could increase the number of eligible patients without harming results (Liu et al., 2021). This is an example of knowledgefication – turning large, unstructured data into insights that can improve trial design.

The last step, intelligencefication, is about to happen: using AI to make the best recommendations based on the knowledge gained. In pharmaceutical companies, this could mean AI helping design trials. For example, after learning from many past trials, an AI agent might suggest the best inclusion and exclusion criteria for enrolling patients to best differentiate treatment efficacy and safety, and it can also recommend the best schedule of activities to maximize trial success (Hutson, 2024). We can imagine AI tools that combine information from regulatory documents, scientific publications, conference abstracts, and early experiments to predict what concerns regulators might have about a new drug. Statisticians, with their skills in data analysis and experiment design, will be crucial in checking and using these AI recommendations. By leading the digitalization and analysis of diverse data, and by carefully evaluating AI's suggestions, statisticians help ensure that the pharmaceutical industry's new data is turned into reliable knowledge and smart actions. In short, the growth of "data" in pharmaceutical research – from text and images to real-world patient data – is increasing the influence of statisticians both in organizing data and in making decisions, highlighting their role as key players in AI-driven research.

4.2 Go Beyond Traditional Statistical Methods

Modern AI is not just improving traditional statistics; it often surpasses them, opening new scientific areas. A great example is AlphaFold2 by DeepMind, which revolutionized how we predict protein structures. Before, predicting a protein's 3D shape from its amino acid sequence required expert-crafted features and significant domain knowledge. AlphaFold2 changed this by using deep learning to directly predict structures from sequences, skipping the extensive human interventions. It achieved high accuracy, even without similar known structures, and matched experimental results for many targets. This breakthrough, published in Nature in 2021, showed that AI can learn complex biological patterns from data without needing detailed chemistry or physics rules (Jumper et al., 2021).

Crucially, this shift opens a new "swimming lane" for quantitative scientists with strong mathematical and programming skills. Complex biological and chemical problems that used to be the domain of specialized computational biologists are increasingly being tackled with general-purpose data-driven methods. Statisticians, given their training in rigorous modeling and algorithm development, are well positioned to contribute to this emerging domain often referred to as "digital biology." The nature of work in digital biology (such as de novo protein design or ligand generation) often involves advanced mathematics and computation that go beyond classical computational chemistry training. For instance, modern generative models for molecular structures exploit concepts from differential geometry and Lie group to enforce physical symmetries (e.g. rotational or translational invariances of molecules) in the learning process. Geometric deep learning frameworks have been developed to handle data on non-Euclidean domains like protein surfaces or molecular graphs, encoding invariances under rotations/reflections by design (Bronstein et al., 2017; Fuchs et al., 2020; Garcia Satorras et al., 2021). Implementing and extending these models requires fluency in linear algebra, group representations, and high-performance computing – skill sets much more akin to those of statisticians or applied mathematicians than to traditional wet-lab scientists or computational biologists/chemists. In effect, drug discovery is becoming as much an algorithmic science. This creates ripe opportunities for statisticians to lead methodological innovation in areas like protein engineering and small-molecule drug design, where sophisticated modeling (rather than domain-specific intuition alone) drives breakthroughs.

Beyond AlphaFold, numerous other examples illustrate how algorithmic approaches are reshaping pharmaceutical R&D. For statisticians, each of these advances signals a domain where their expertise can be applied in novel ways: designing the modeling strategy, ensuring rigorous validation, and quantifying uncertainty in predictions. Notably, many such AI-driven discovery techniques emphasize prediction and optimization (e.g. finding a molecule that maximizes a predicted efficacy

score) rather than classical inferential statistics. This highlights an important cultural shift that renowned statistician Leo Breiman presciently discussed in his "Two Cultures" essay two decades ago Breiman (2001). Breiman argued that much of traditional academic statistics focused on data models and inference under an assumed "true" model, whereas a different culture – exemplified by machine learning – focused on algorithmic models aimed at predictive accuracy. He urged statisticians to embrace this algorithmic approach for complex problems where the goal is often prediction or discovery, not estimating a pre-specified parameter. The current wave of AI in pharma is a testament to Breiman's point: many breakthroughs (like protein folding or de novo molecule generation) are essentially large-scale prediction problems where flexible algorithms trump analytical formulas. Statisticians who adapt to this mindset – valuing predictive performance and computational experimentation alongside traditional inference – can substantially broaden their impact.

In summary, the rise of AI methods is pushing the boundaries of what quantitative scientists can do in pharmaceutical research. Statisticians equipped with strong coding abilities and mathematical depth are in an excellent position to drive these innovations. They can develop new algorithms, rigorously evaluate AI models, and ensure that these methods are applied soundly. By venturing beyond the confines of traditional statistical methodology – while still upholding standards of rigor and clarity – statisticians can become key players in cutting-edge domains like AI-driven drug discovery, precision medicine, and digital health. Their contributions will complement those of domain specialists, blending data-centric problem-solving with scientific insight to accelerate pharmaceutical progress.

4.3 Broadening Responsibilities and Impact of Statisticians Across the Value Chain

The role of statisticians in the pharmaceutical industry have expanded dramatically in recent years, evolving from a narrow focus on clinical trials to a broad involvement across the entire drug discovery and development lifecycle. Historically, a pharmaceutical statistician's influence was largely confined to Phase II/III clinical development: designing trials, analyzing efficacy and safety data, and supporting regulatory submissions. Today, statisticians are increasingly embedded in cross-functional teams from early discovery and preclinical research, through manufacturing and quality control, all the way to post-marketing surveillance and health economics. This expansion is driven by the growing recognition that the statistician's core skill set – quantitative reasoning, experimental design, data interpretation, and uncertainty quantification – is invaluable at every stage where data are generated and decisions are made. Enas and Andersen (2001) presciently noted that statisticians are uniquely trained to improve decision-making "from the very early stages of drug discovery until patients, payers and regulators are satisfied," essentially advocating for statisticians to become key contributors in all phases of the enterprise. Two decades later, this vision is being realized. Statisticians now collaborate with chemists and biologists in discovery research, optimize processes with engineers in CMC (Chemistry, Manufacturing, and Controls) groups, and partner with physicians and epidemiologists to assess real-world outcomes post-approval. The modern pharmaceutical statistician often serves as a quantitative strategist, not only ensuring analyses are sound but also guiding what data to collect, how to collect it efficiently, and how to interpret it to drive business and scientific decisions.

Besides drug discoveries, the role of statisticians is rapidly evolving as AI technologies become integral to various fields beyond traditional statistics. In clinical development, statisticians are leveraging AI to enhance trial design and execution. Natural language processing algorithms are being used to analyze study protocols and electronic health records (Jin et al., 2024). Image technology and digital biomarkers are developed to help enrollment, particularly in complex oncology trials, by quickly finding eligible patients across extensive health networks. Moreover, AI is being used to simulate or augment control arms in trials through the creation of "digital twins" – virtual patient avatars generated from historical data. This innovative approach augmented the data analysis, making trials more efficient and ethically palatable. Statisticians play a crucial role in validating these AI models to ensure they accurately represent patient outcomes and maintain scientific and regulatory rigor (Davi et al., 2020; Thorlund et al., 2022).

In the manufacturing and supply chain sectors, AI is driving the transition to Pharma

4.0, a new paradigm of smart, data-driven production. Statisticians are collaborating with engineers to implement AI-based process monitoring and control systems. Machine learning models analyze process development data to identify optimal parameters and scaling condi-

tions, accelerating the development process. AI-driven advanced process control systems can make real-time adjustments during production, ensuring critical quality attributes remain within target ranges. The FDA has acknowledged the potential of AI in drug manufacturing, highlighting its ability to reduce development time and waste through improved process design (U.S. Food and Drug Administration, 2023a). Statisticians are essential in deploying these advancements, from designing experiments to train AI models to validating their performance and integrating statistical process control with AI technologies.

In the realm of commercialization, AI and advanced analytics are empowering statisticians to drive better business decisions (Huanbutta et al., 2024). AI algorithms are used for demand forecasting and inventory optimization, analyzing historical sales and external data to predict drug demand accurately (Dong et al., 2009; Liu et al., 2023a). This helps reduce stockouts and oversupply, optimizing the pharma supply chain. In marketing, AI tools assist in segmenting healthcare providers and patients, tailoring outreach to those most likely to benefit. Predictive analytics guide field sales strategies by integrating data on prescribing habits and patient demographics, enhancing targeting precision (Dong et al., 2009; Manchanda and Chintagunta, 2004). Statisticians collaborate with AI to develop pricing strategies, using machine learning models to analyze market data and recommend optimal pricing (Fazekas et al., 2024). These advancements demonstrate that data-driven decision-making is becoming the norm in pharma, with statisticians translating AI-driven analytics into actionable business insights.

Finally, as the question of data collection for AI arises, statisticians will influence future data strategies too (ICH E9(R1) Expert Working Group, 2019). Traditionally, pharma's data collection in trials was solely focused on regulatory approval of the molecule at hand. In the future, we envision that companies will deliberately collect data not just to advance the current product, but also to improve the next generation of AI models that assist in drug design and development. This might entail, for instance, designing clinical studies that also create high-quality datasets for machine learning (such as rich biomarker panels or digital sensor data), recognizing that these datasets could inform many programs beyond the original trial. Statisticians will be key in planning such dual-purpose studies, balancing immediate needs with the long-term value of data. Techniques like adaptive sampling and active learning – where the data collected is dynamically guided by algorithmic learning needs – could become part of trial design considerations. By advising on how to gather the most informative data for both human decision-making and machine learning, statisticians ensure that pharmaceutical data resources continuously feed the cycle of innovation.

In summary, AI are expanding what scientists can do in pharmaceutical research (Vamathevan et al., 2019; Topol, 2019). Solving today's tough problems often requires complex models and heavy computation. Statisticians with strong coding and math skills are well- positioned to lead these innovations (Cruz Rivera et al., 2020; Liu et al., 2020; Collins et al., 2024). They can create new algorithms, evaluate AI models, and ensure these methods are used correctly. By moving beyond traditional statistics, statisticians can play key roles in AI-driven drug discovery, precision medicine, digital health, manufacturing and commercialization space (Vamathevan et al., 2019; Topol, 2019; Helleckes et al., 2023). Their work will complement that of domain experts, combining data-driven problem-solving with scientific insight to advance pharmaceutical research (Topol, 2019).

5 Conclusion

The role of statisticians in the pharmaceutical industry has undergone a remarkable evolution, expanding in scope, influence, and importance over the past 50 years. From the early days following the 1962 FDA reforms – when a handful of statisticians were brought in to ensure new drugs had statistically sound evidence of efficacy – to the present day where statisticians are at the forefront of AI-driven drug development, the transformation is pro- found. We have seen how historical milestones, such as regulatory changes (e.g. the 1980s NDA guidelines, ICH E9) and technological advances (the computing revolution, big data), set the stage for statisticians to move from the periphery to the core of decision-making in pharma.

Driving this evolution are key factors like statistical computing, the proliferation of new data types, which demanded novel analytical methods, and the willingness of industry and regulators to embrace innovative statistical designs that can make drug development more efficient. The recent surge of artificial intelligence has further catalyzed a paradigm shift, positioning statisticians as vital contributors to data science initiatives that span discovery through post-market use. This breadth of impact across the value chain - from molecule to market – exemplifies how the statistician's remit has grown far beyond tradi-

tional boundaries.

Crucially, statisticians have not just grown in number or technical capability, but also in their leadership and collaborative roles. They are increasingly recognized as strategic partners who bring a data-driven lens to interdisciplinary teams. Whether it's guiding a cross-functional team through the design of an adaptive platform trial, negotiating the use of a novel surrogate endpoint with regulators, or explaining to commercial colleagues how an observational study supports a product's value proposition, statisticians are influencing critical decisions at every step (Woodcock and LaVange, 2017; Prentice, 1989; U.S. Food and Drug Administration, 1992, 2018; Franklin et al., 2023). The statistician often serves as the bridge between the company and regulators on complex methodological issues, an intermediary role that has smoothed the adoption of things like complex innovative trial designs and real-world evidence considerations.

Looking to the future, the trajectory points toward statisticians continuing to be agents of innovation in pharmaceutical R&D. With the ongoing integration of AI, the growth of personalized medicine, and the increasing reliance on real-world data, there will be even greater demand for statisticians who can blend quantitative rigor with creativity and strategic thinking (Collins and Varmus, 2015; U.S. Food and Drug Administration, 2024b; Sadybekov and Katritch, 2023). We can anticipate statisticians playing leading roles in the effort of quantitative decision making for every single step in pharmaceutical research. Realizing these opportunities will require concerted effort in training and professional development. As discussed, academia and industry have to work together to equip statisticians with a modern skill set that includes evolving technical skills on advanced modeling, machine learning, statistical computing (in particular for high performance parallel computing), algorithms, mathematical optimization, and software engineering basics (Pitman et al., 2019). The curriculum adjustments and competency development recommended in this paper are intended to future-proof the profession.

In conclusion, the evolving role of statisticians in pharma is a success story of how a profession can adapt and expand to meet new challenges. Statisticians have leveraged advanced analytics and AI not to replace their traditional work, but to augment and elevate it, driving better decisions and outcomes. They have transitioned from behind-the-scenes advisers to frontline leaders ensuring that evidence and data quality remain the bedrock of pharmaceutical innovation. The fruits of this evolution are evident: more efficient trials, more robust evidence of drug benefits and risks, and ultimately, a more informed approach to bringing therapies to the patients who are waiting for us. Our evolving role will continue to be characterized by leadership, innovation, and an unwavering commitment to using data for the betterment of public health.

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PRACTICAL CONSIDERATIONS FOR INTEGRATING AI/ML IN CLINICAL TRIALS

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Highlights:

- PROCOVA represents an example of AI integration in clinical trials.
- Successful AI/ML implementation involves careful evaluation of external data comparability, balancing model complexity with interpretability.

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Introduction

The rapid advancement of artificial intelligence (AI) and machine learning (ML) offers unique opportunities to enhance the design and conduct of clinical trials. While these technologies are not intended to replace traditional methodologies, they can be thoughtfully integrated to improve efficiency, precision, and interpretability. Recent developments, such as the PROCOVA approach, illustrate this potential. PROCOVA uses AI-derived prognostic scores to adjust for covariates, enhancing treatment effect estimation even when external data differ from the current trial setting. The method has been qualified by the European Medicines Agency (EMA) and acknowledged by the U.S. Food and Drug Administration (FDA), demonstrating growing regulatory openness to AI-informed methodologies. [1,2].

Despite this progress, practical implementation remains challenging. Issues such as data quality, comparability of external sources, model transparency, and interpretability remain central concerns. Moreover, ensuring that AI-driven approaches meet regulatory standards for validity and reproducibility is critical. This paper presents pragmatic insights for researchers, statisticians, and regulators on the integration of AI/ML methods in clinical trials, encompassing considerations for PROCOVA implementation, external data utilization, and the evaluation and interpretability of models. The following sections elaborate on these key considerations, beginning with the application of PROCOVA as a practical example of AI/ML integration in clinical trials.

Considerations for PROCOVA

PROCOVA can be conceptualized as an advanced application of covariate adjustment, same as analysis of covariance (ANCOVA). It uses AI-derived prognostic scores as covariates to enhance treatment effect estimation and maintain validity even when external data differ from the current trial setting [1]. An enhanced variant, PROCOVA-MMRM, further incorporates time-matched prognostic scores for longitudinal continuous outcomes, improving precision and potentially enabling sample size reduction [3]. In practice, however, translating these analytical gains into study design requires caution. When incorporating covariate adjustment into sample size calculations, a conservative estimation approach is recommended due to several sources of uncertainty. The correlation between the prognostic score and the outcome may be weaker than anticipated, reducing the expected efficiency gains. Historical data used to inform the model may have limited relevance to the current study population or setting, thereby affecting generalizability. In addition, the statistical assumptions underlying the prognostic model may not hold in practice, potentially undermining its performance. Finally,

variability in the prognostic score may be lower than expected based on historical data, further diminishing the anticipated benefit of covariate adjustment.

Considerations for External Data

When incorporating external data (e.g., for prognostic modeling), careful evaluation of comparability is essential. FDA guidance on externally controlled trials highlights key areas to assess: demographic similarities, endpoint consistency, timing of follow-up, missingness, and mitigation of immortal time bias [4]. ICH E10 further clarifies differences between internal and external controls [5]. Robust modeling practices include splitting external data into distinct training and testing subsets and ensuring adequate sample size to avoid overfitting or inappropriate modeling assumptions [6]. Beyond data comparability, appropriate handling of missing data is another critical component of model reliability. Imputation approaches must be both statistically sound and clinically meaningful. For example, imputing age via group average may be acceptable statistically, but its clinical plausibility must be justified and documented [8].

Model Selection, Evaluation, and Interpretability

Complex AI models (e.g., neural networks) may offer high accuracy but are often opaque. In contrast, simpler models such as random forests provide greater interpretability and can be more easily visualized for clinical stakeholders. Choosing between them involves evaluating stakeholder needs, regulatory expectations, and clinical relevance [7]. Once an appropriate modeling approach is selected, careful evaluation becomes essential to ensure that model performance aligns with its intended clinical purpose. Selecting evaluation metrics should reflect both the model's architecture and the underlying clinical question. There is no universal metric, so alignment with intended use is critical. When merging external datasets (e.g., from different Alzheimer's disease cohorts), differences in diagnostic or rating standards must be critically examined before pooling [3,6].

Conclusion

AI and ML can serve as powerful complements to traditional clinical trial methodologies when applied thoughtfully. Regulatory precedents such as EMA's qualification of PROCOVA and FDA's acknowledgment reinforce the feasibility of this integration [1,2]. Building on this foundation, the continued advancement of AI/ML in clinical research will increasingly depend on multidisciplinary collaboration among statisticians, clinicians, data scientists, and regulators. Ultimately, the path forward lies not in replacing traditional methodologies but in harmonizing innovation with regulatory and clinical principle, ensuring that AI/ML enhances the credibility, efficiency, and impact of clinical trials in the years to come.

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UNLEASHING AI-GENERATED DIGITAL TWINS TO DELIVER MORE EFFICIENT RANDOMIZED CLINICAL TRIALS

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Highlights

- The integration of artificial intelligence (AI) into clinical development is rapidly reshaping the landscape of randomized controlled trials (RCTs).
- Recent advances in AI-generated "digital twins", defined as predictive models that simulate the entire trajectory of control potential outcomes for trial participants, unlock new statistical methods that can improve the power, precision, and efficiency of clinical trials.
- Specifically, summaries of the digital twins constitute "super covariates" for the design and analysis of RCTs, with the corresponding covariate adjustments reliably yielding precise and powerful causal inferences in a regulatory-acceptable manner.
- Ultimately, the integration of AI-generated digital twins with statistical methods can effectively address critical challenges in modern clinical trials.

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The Challenge: Eroom's Law and the Need for Innovation

Modern clinical development faces a daunting challenge. Despite technological progress, the cost and time required to bring new drugs, biologics, devices, and other interventions to market continue to rise. This unfortunate phenomenon is the antithesis of the well-known Moore's Law, and consequently is known as Eroom's Law (Lower, 2012; Scannel et al., 2012). Clinical trials, especially RCTs, are a major driver of these costs, often requiring many years and millions of dollars to complete (Sertkaya et al., 2014). There is an urgent need for innovative solutions to counteract Eroom's Law.

Covariate Adjustment and the Rise of Super Covariates

Covariate adjustment provides a regulatory-acceptable approach to address Eroom's Law. Regulatory agencies, including the FDA (2023) and the EMA (2015), have provided guidance on the appropriate use of covariate adjustment for RCTs, emphasizing the careful selection of a small number of covariates for adjustment. By identifying a covariate that is highly correlated with the outcome, one can obtain treatment effect inferences that are more precise and powerful based on the adjustment for the covariate compared to unadjusted analyses, or compared to other analyses that adjust for covariates that are less correlated with the outcome. This helps to reduce the necessary sample size, and consequently shorten the enrollment period, for RCTs.

Enter the "super covariate": a prognostic score (Hansen, 2008) obtained via AI-generated digital twins that effectively summarizes a multidimensional covariate vector (consisting of baseline data, demographics, and other covariates) into a scalar that is highly correlated with control outcomes. The AI algorithms involved in constructing super covariates should be pretrained on historical control data that are external to a target RCT,

and should predict the control potential outcomes for participants in the target RCT as a function of their baseline covariates. The predictive distribution for a trial participant's control potential outcome obtained from the pretrained AI algorithm is their digital twin distribution (Alam et al., 2024). As a result of the pretraining process, the digital twin generator is prespecified prior to the target RCT. Furthermore, as the digital twin generator has the baseline covariates as its inputs, summaries of the generated digital twins are themselves covariates. In particular, the mean of a participant's digital twin distribution corresponds to their prognostic score, and serves as a super covariate that enables more powerful and precise treatment effect inferences without inflating bias or Type I error rates (Schuler et al., 2022).

Regulatory Acceptance and Methodological Advances

Prognostic covariate adjustment (PROCOVATM) is Unlearn.AI's (EMA, 2022) statistical approach for the design and analysis of RCTs based on the prognostic score obtained from AI-generated digital twins. The essential steps for PROCOVA are:

1. Pretrain an AI model on historical control data.

2. Apply the pretrained AI model to the baseline covariates for treated and control participants in the target RCT to calculate their prognostic scores.

3. Fit a linear regression model for the RCT data in which the response variable is the outcome and the predictor variables are the treatment indicator and the prognostic score.

4. Estimate the treatment effect via the linear regression model.

5. Obtain the standard error of the treatment effect estimate using the sandwich estimator approach.

The EMA qualified PROCOVA as "an acceptable statistical approach for primary analysis" of Phase 2 and 3 trials with continuous endpoints (EMA, 2022). Furthermore, the FDA stated that they concur with the EMA and that PROCOVA does not deviate from their current guidance (Fisher, 2024) .

Two extensions of PROCOVA, referred to as Weighted PROCOVA (Vanderbeek et al., 2023) and Bayesian PROCOVA (Vanderbeek et al., 2024), further enhance the power, precision, and efficiency of PROCOVA by incorporating the variances of the digital twin distributions, and dynamically borrowing information from historical controls, respectively. These methods further reduce necessary sample sizes, increase statistical power, and maintain rigorous control of bias and Type I error rates compared to PROCOVA. In particular, Bayesian PROCOVA increases the precision of treatment effect inferences without adding significant bias when historical controls and trial participants are exchangeable, and can discount historical controls when they are discrepant with trial participants so as to control bias and Type I error rates.

AI-generated digital twins are not limited to continuous outcomes. Consequently, statistical methods that incorporate digital twins for RCTs have also been specified for time-to-event (Li et al., 2023), binary (Li et al., 2024), and repeated measures endpoints (Ross et al., 2024).

Broader Implications for the Future of Clinical Development

The integration of AI with statistics can help to address Eroom's Law, and usher in a new generation of regulatory-acceptable clinical trials that can be more adaptive, efficient, and informative, thereby accelerating clinical development and improving patient outcomes. Key stakeholders across pharmaceutical companies, biotech, regulatory agencies, and technology companies must work together to realize the full potential of AI in transforming the future of medicine.

For further discussion or collaboration, connect with Arman Sabbaghi (@SabbaghiArman) on LinkedIn or at Santen Inc.

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HOW REGULATORY STATISTICIANS CAN ADAPT TO NEW CHALLENGES IN THE AI ERA

Feiming Chen (FDA)

Highlights

- Statisticians must deeply understand health problems and device design, while continuously learning and staying open to new methodologies for evaluating AI-enabled medical products.
- Effective collaboration and clear communication—including plain language and visualizations—are important for solving complex challenges and ensuring scientific integrity.
- Developing AI literacy and maintaining human oversight are part of responsible evaluation and use of advanced technologies in regulatory settings.

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Disclaimer: This article reflects the views of the author and should not be construed to represent FDA's views or policies.

The primary role of regulatory statisticians in the Center for Devices and Radiological Health (CDRH) at the FDA is to evaluate study protocols and data submitted for new medical devices to demonstrate reasonable assurance of safety and effectiveness. As a statistician at CDRH, I focus on reviewing in-vivo medical diagnostic devices that increasingly incorporate artificial intelligence/machine learning (AI/ML)-enabled technologies in diverse applications such as ophthalmic, cardiovascular, reproductive, urological, surgical, or neurological devices. Such AI/ML-enabled devices, which can have a variety of outputs for users, provide ample evaluation challenges. Such challenges make our review work more interesting; for example, if an application of AI technology claims to solve a previously unsolved health problem (or solve it in a better way than existing solutions), then we consider how we can have enough confidence to evaluate such a claim statistically using adequate data evidence, especially when ready-made traditional methods are not available to use. I would like to make the following five observations where statisticians can learn and contribute.

Firstly, during medical product reviews, it is important for statisticians to understand the specific health problem and design features of the device, to assist in asking the right questions to best evaluate the adequacy of the study design or propose analyses to better assess the underlying health problem. For example, it is helpful to understand the target condition, the process by which an AI model is developed and trained, the data that are proposed to validate it internally and externally, factors affecting the benefit-risk profile in its intended use setting, including prevalence in the target population, predictive values, characterization of repeatability and reproducibility, and potential AI biases.

Secondly, staying informed about relevant statistical methodologies and participating in various seminars or workshops enables statisticians to learn new methods that can extract meaningful evidence from fit-for-purpose data. For example, in recent years, FDA Statistical Association hosted many seminars, often with invited speakers from academia and industry, that introduced many interesting non-traditional methods, such as the win ratio method for hierarchical endpoints [1], the desirability of outcome ranking method for holistic effectiveness and safety analysis [2], the propensity

score method for real-world evidence analysis [3], the promising zone method for adaptive design [4], the estimand framework methods for handling intercurrent events [5], the Bayesian methods for complex design [6], etc. An innovative proposal offers interesting challenges: to determine whether it can be verified to answer the right question, to not introduce unacceptable bias, and to be statistically sound. Statisticians can play a pivotal role in adopting and disseminating sound non-traditional methods that can increase the efficiency of clinical studies and support better interpretations of clinical data. Recall a famous observation attributed to Abraham Maslow, "When all you have is a hammer, every problem looks like a nail." [7] A good understanding of the health problem and a big toolbox (with traditional and non-traditional methods) may help a statistician to overcome inherent cognitive bias and select/adapt the relevant statistical tool to a unique study or review challenge.

Thirdly, statisticians can embrace appropriate collaborations internally and externally, actively involving people from academia, industry, and regulatory agencies. What's more, every meeting or interaction can be viewed as a form of collaboration that allows people to solve the same health problem together as a team, where different perspectives are incorporated (e.g., the need for protecting public health, the process of bringing health innovations to markets, etc.). In this collaborative process, statisticians can especially serve as a sounding board to the team and contribute critical statistical thinking to uphold scientific integrity.

Fourthly, statisticians can be more effective when complex statistical methods and findings are communicated in plain language as much as possible to all stakeholders, whether in writing or speaking. For example, instead of stating "propensity score methodology approximates randomization", it could be explained that this is a statistical technique to construct a fair comparison between treatment and control groups when subjects are not randomized to treatment or control groups. Another valuable communication skill that statisticians can continue developing is the use of statistical visualization to convey complex data relationships (e.g., Bland-Altman plot [8], Sankey diagram [9], calibration plot [10], likelihood ratios graph [11], ROC curve [12], decision curve [13], predictiveness curve [14]).

Lastly, it is beneficial to develop a deeper understanding of rapidly advancing AI technologies, from machine learning to generative AI, tools that can produce increasingly complex mathematical mapping functions meant to substitute for traditional human labor through computing. At the same time, it is important to recognize that such technologies still possess limited capacity for independent and critical thinking and therefore human oversight for high-stakes applications is critical. Statisticians can play a vital role in the evaluation of AI systems by applying our expertise in statistical reasoning and critical analysis.

In conclusion, regulatory statisticians play a pivotal role in FDA's mission of protecting and promoting public health. In the face of new challenges in the AI era, we can still apply basic, broadly applicable principles for achieving professional excellence: understanding a problem deeply, learning continuously (including statistical and AI technology), embracing collaborations, enhancing communication skills, and consistently upholding scientific integrity.

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NATURAL LANGUAGE PROCESSING MEETS FDA: MY AI ADVENTURE IN THE POST-MARKETING SPACE

Yong Ma (FDA)

Highlights

- Below is a summary of some FDA's examples using natural language processing (NLP) in the post-marketing space over the past few years.
- FDA Adverse Event Reporting System (FAERS) Enhancement: Evolving from simple rules to advanced language models, NLP applications have delivered measurable improvements in pharmacovigilance using the FAERS system, going from reducing missing demographics (e.g. age, gender) information, to the conceptual piloting in de-duplicating adverse event reporting.
- Electronic Health Record (EHR) Processing: NLP technologies effectively address a fundamental challenge in pharmacoepidemiology by extracting meaningful data from unstructured physician notes. This capability was demonstrated through successful implementations in anaphylaxis identification and extracting outcomes and potential confounders information in the Multi-source Observational Safety study for Advanced Information Classification using NLP (MOSAIC-NLP) project.
- Social Media Surveillance for Public Health: During public health emergencies, NLP models may analyze social media narratives to identify disease trends and symptoms in real-time. FDA's intermural research demonstrated that NLP models such as Bidirectional Encoder Representations from Transformers (BERT) can successfully extract COVID infections and symptoms from Reddit posts.

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Disclaimer: This article reflects the views of the author and should not be construed to represent FDA's views or policies.

When ChatGPT suddenly became the talk of every conference, coffee break, and dinner party in recent years, I found my FDA colleagues were also chatting: what is the FDA doing with this new technology at work? Is it going to be a useful tool? Or is it going to replace us?

Reassuringly, my experience with AI in the post-marketing surveillance landscape confirmed that we've been experimenting with NLP for the past few years—before it became the must-have technology that everyone claims they're "leveraging." While the world was just discovering ChatGPT's charm, we had already been extracting key information from texts, by using something simple as a rule-based algorithm, to much more sophisticated language models.

At the FDA's Center for Drug Evaluation and Research (CDER), statisticians support post-marketing

drug safety surveillance and work closely with our colleagues in the divisions of Pharmacovigilance and divisions of Pharmacoepidemiology at the Office of Surveillance and Epidemiology. Over the years, our roles went beyond those of traditional statisticians as we stepped into the wonderful world of natural language processing.

In this article, I'll take you behind the regulatory curtain to share our encounters with AI, revealing the surprising fact that NLP has been our workplace companion all along. These projects span from 2018 to present and are organized by research area: pharmacovigilance (project 1-2), pharmacoepidemiology (project 3-4) and public health emergency (project 5).

1. Capturing key missing demographic information from the fixed field in FAERS report using case narratives

My first encounter with language processing was back in 2018 when our team was asked to help evaluate an algorithm developed to capture missing age data in the FDA's adverse event reporting system (FAERS). FAERS, a spontaneous reporting system capturing adverse events associated with drug use and medication error, is the corner stone in pharmacovigilance. Demographic information, such as age, sex and race/ethnicity, are usually captured in the fixed fields. However, many adverse event reports were missing patient age information in their structured data fields, and it is worsening over time - the percentage of reports with missing age data doubled from about 22% in 2002 to nearly 44% in 2018. This created real issues, especially when trying to monitor pediatric safety where age is critical.

My epidemiologist colleagues tackled this with a simple NLP approach. A rule-based algorithm (Wunnava S, 2017) was built to search for numbers followed by key words like "years" or "years old", "months" etc. and converted those to years. The tool would extract the first age it found in each report's narratives. This straightforward approach didn't need any training data and could work across different FAERS runs.

Although we were not involved with the development of the algorithm, we were asked to help develop a validation study to evaluate the performance of the algorithm. We worked with our pharmacovigilance colleagues and designed a study to test this tool on 1,500 randomly selected reports (Pham P, 2021). The algorithm correctly identified 98.5% of ages that were present in the narratives. It also avoided false alarms 92.9% of the time, meaning it rarely claimed to find an age when there wasn't one. When it identified an age, it was right 94.9% of the time.

When we applied this tool to the entire FAERS database covering 2002 to 2018, we extracted age information for an additional one million reports. This brought the overall percentage of reports missing age data down from 37% to 27% (Figure 1). The impact was especially notable for pediatric cases, where they more than doubled the number of reports with known ages for children under 6 years old.

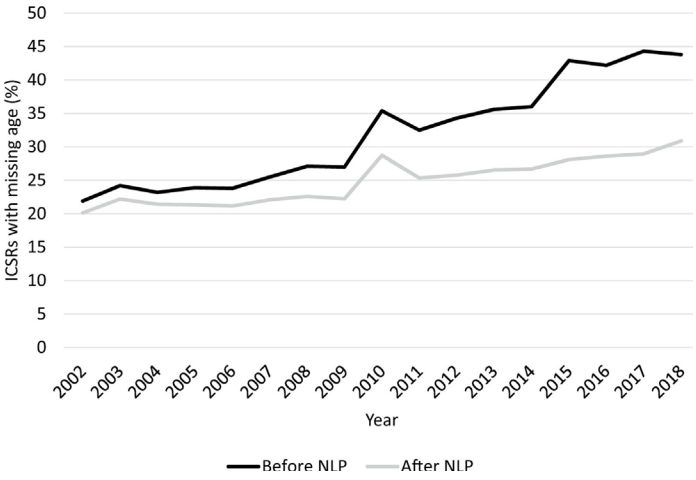

Figure 1. Percentage of FAERS ICSRs with missing age before and after NLP implementation. FAERS FDA Adverse Event Reporting System, ICSR individual case safety report, NLP natural language processing (Reprinted from (Pham P, 2021) under CC BY-NC 4.0)

We noted that although we could bring down the missingness in the structured age data from 37% to 27% by supplementing data from the non-structured field, 27% is still substantially high. This high number is largely because age is simply not entered into the FAERS report. In such a case, NLP has reached its limit, and efforts should be directed to ensure better data entry. This demonstrates the ultimate limit of NLP – when there is no information, NLP won't be helpful. We also noticed this phenomenon when we tried to capture other demographic data, specifically gender, weight, race, and ethnicity from the unstructured field (Dang V, 2022). A rule-based NLP mini-algorithm for each demographic variable was developed to be tailored to each specific

feature. The gender algorithm, for instance, looked for terms like "male," "female," "his," and "her," while the weight algorithm hunted for numbers followed by units like "lb" or "kg." The gender extraction tool performed well with 98.6% sensitivity and helped reduce missing gender data in FAERS by a 33%— over 470,000 reports found to contain usable gender data hidden in the text. Unfortunately, the weight, race, and ethnicity algorithms showed high specificity but low sensitivity—not because the tool underperformed, but because the information just wasn't there. It turns out, you can't extract what doesn't exist.

2. An Evaluation of Duplicate Adverse Event Reports Characteristics in the Food and Drug Administration Adverse Event Reporting System

Our journey with pharmacovigilance continued. In 2023, we were asked to help with one of the long-standing challenges in post-market drug surveillance - determining when multiple adverse event reports in FAERS describe the same event. It's not uncommon for different reporters—patients, physicians, manufacturers—to submit slightly different narratives for what may be the same case. These duplicates can inflate counts, distort safety signal, and make safety signal detection more challenging. While our pharmacovigilance colleague provided reports already identified manually as duplicates, our task was to see if narrative-level similarity in the duplicate reports were indeed distinguishable from the non-duplicate reports (Janiczak S, 2025) .

To tackle this, we deployed Sentence-BERT (SBERT)—a model designed to convert sentences into embeddings that capture semantic meaning. Using the all-MPNet-base-v2 variant, we transformed each report narrative into a vector and then measured cosine similarity between pairs of narratives. If the narratives were telling the same story (e.g., "the patient developed a rash and shortness of breath" vs. "rash and trouble breathing began after dose"), they'd show up as close in this vector space and have a cosine similarity close to 1. We found that confirmed duplicate reports had a median cosine similarity of 0.87, while random non-duplicate pairs had a median of just 0.48. As shown in Figure 2, with a threshold of 0.73 as a classifier, we could achieve a sensitivity of 96% and specificity of 96%.

The cosine similarity measure appears to be a promising tool facilitating duplicate identification; however, certain practical considerations remain. Computing all possible pairwise similarities across the massive FAERS database would require large computing power and time and may not be feasible; model and threshold need to be carefully chosen. Plus, while narrative similarity is a powerful flag, it doesn't replace expert review or structured field analysis. Instead, this method may serve as a decision support tool: a fast, consistent way to surface likely duplicates that can then be reviewed more carefully.

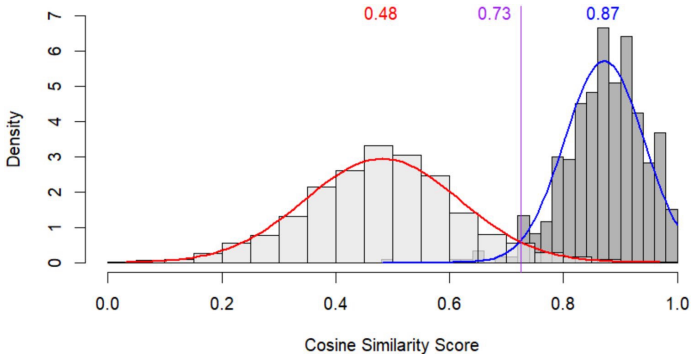

Figure 2: Distribution of cosine similarity analysis of narrative text. reprinted from: (Janiczak S, 2025) Licensed under CC BY 4.0.

3. Improving Methods of Identifying Anaphylaxis for Medical Product Safety Surveillance Using Natural Language Processing and Machine Learning

If capturing missing data and de-duplicate reports from FAERS narrative are relatively simple with NLP application, this third project has certainly taken a big step forward. This study (Carrell DS, 2023) addressed the critical challenge of accurately identifying anaphylaxis events in electronic health records for FDA medical product safety surveillance. Anaphylaxis is a rare but severe, potentially life-threatening allergic reaction with rapid onset. It is often caused by medications, food, or other exposures. Lifetime anaphylaxis prevalence estimates in the US range from 0.05% to 2% and incidence is increasing. Anaphylaxis mortality rates are increasing for medication-induced

cases. The FDA's Sentinel Initiative monitors medical product safety using real-world data through the Active Risk Identification and Analysis (ARIA) System. However, it has been insufficient for identifying anaphylaxis due to the condition's complex clinical presentation and its reliance on structured medical claims data. Existing automated algorithms, including the 2013 Walsh algorithm, achieved only 63% positive predictive value when identifying anaphylaxis events. This falls short of the commonly used ≥80% threshold for FDA ARIA analyses. This identification challenge stems from several factors. Anaphylaxis has diverse clinical presentations. There are frequent "rule-out" coding practices. Diagnosis codes show high sensitivity but low specificity. These issues create a major barrier to effective disease surveillance and prevent clinicians from identifying actionable health risks.

To overcome these limitations, the study team developed machine learning algorithms incorporating NLP. The goal was to better discriminate between actual and potential anaphylaxis events using rich electronic health record text data. The NLP methodology included creating a custom dictionary of anaphylaxis-related concepts through clinical expert review. The study team also augmented this with Unified Medical Language System (UMLS) concepts from published literature. The dictionary was enriched with synonyms and misspellings discovered through manual chart review. A locally developed NLP system, like Apache cTAKES, identified dictionary terms in clinical notes. It used a tailored ConText algorithm to distinguish affirmative mentions from negated, historical, or hypothetical references. The team manually engineered 468 candidate NLP-derived covariates. These included rules for multi-organ system involvement, symptom categories, normalized mention counts, and treatment indicators. Ultimately 100 covariates were selected through expert judgment and frequency analysis and added to a prediction model already containing structured data.

The NLP-enhanced models significantly outperformed structured data-only approaches. The best performing model achieved a cross-validated area under the curve (AUC) of 0.71 compared to 0.62 for structured data alone (Figure 3). At a classification threshold yielding 66% cross-validated sensitivity, the model achieved 79% cross-validated positive predictive value. This represents a substantial improvement over existing methods.

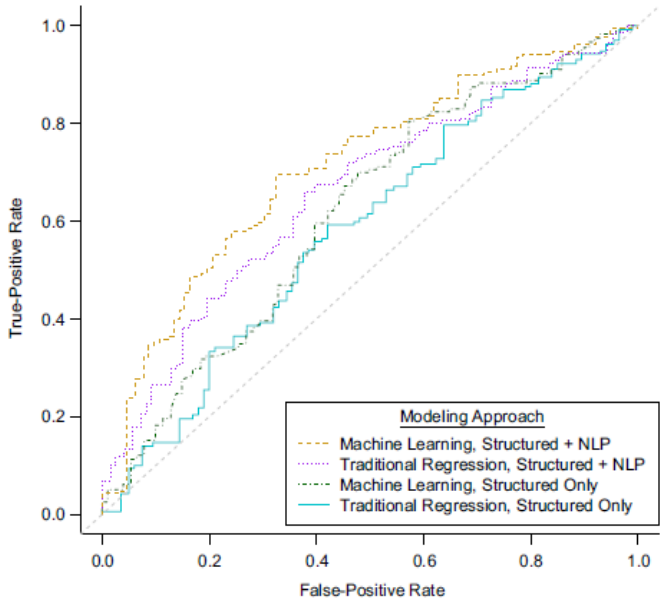

Figure 3. Weighted cross-validated area under the receiver operating characteristic curve for Kaiser Permanente Washington algorithms identifying actual anaphylaxis events in Kaiser Permanente Washington data (2015–2019) using the best machine-learning approach applied to structured and all natural language processing (NLP) data, traditional logistic regression approach applied to structured and all NLP data, machine-learning approach applied to structured data only, and traditional logistic regression approach applied to structured data only. (Figure reproduced from: (Carrell DS, 2023) Reused under the terms of the Creative Commons Attribution License.)

4. Natural Language Processing in Pharmacoepidemiology: Lessons from the Multi-Source Observational Safety study for Advanced Information Classification Using NLP (MOSAIC-NLP)

FDA's Sentinel initiative integrates innovation to drug safety monitoring and the Multi-Source Observational Safety study for Advanced Information Classification Using NLP (MOSAIC-NLP) project applied NLP in pharmacoepidemiology (Jaffe, 2024). When using real-world data (RWD) from electronic health records (EHRs), important information on confounders and outcomes is contained in clinical notes. The MOSAIC-NLP study demonstrated the feasibility of applying NLP to a data set including 17+ million notes from over 100 healthcare systems to extract key information on outcomes and potential confounders. In this retrospective cohort study, the study team examined EHR-claims linked structured and unstructured data

(2015-2022) from multiple national sources. Patients with asthma newly initiated montelukast (monotherapy) were compared to those who initiated inhaled corticosteroids for their neuropsychiatric events.

The study found that including structured and unstructured EHR data significantly increased the number of detected suicidality and self-harm events related to both mediations, both at baseline and during the follow up. Other baselines covariate information such as GERD, Cough, COPD and substance abuse was also captured more. The broadened scope and scale of clinical information extracted from the structured and unstructured EHR data enriched the measurement of patient and disease characteristics and enhanced the strength and accuracy of risk estimates, compared to that from the claims data alone. Although the finds on the association between montelukast use and neuropsychiatric events did not differ from prior studies, integrating relevant entities extracted from clinical text using NLP added extra evidence and strength to the study conclusion.

5. Identifying COVID-19 cases and extracting patient reported symptoms from Reddit

In 2021, as the COVID-19 pandemic continued to unfold, traditional surveillance systems struggled to keep pace with real-time symptom reporting, especially from underrepresented or non-clinical populations. Meanwhile, millions of people were openly sharing their symptoms, frustrations, and theories on social media platforms like Reddit. Epidemiologists at the FDA saw an opportunity: could social media be used to provide meaningful health data—specifically, COVID-19 case identification and patient-reported symptoms? And we statisticians quickly pitched in by approaching this with automation so that we were not limited to the cumbersome manual process. The goal was to develop a fully automated, scalable method to detect self-reported COVID-19 cases and extract symptoms with clinical relevance (Guo M, 2023).

To accomplish this, we built a two-stage NLP pipeline. First, we tackled case identification using a BERT-Large model, applied to comments from a "COVID" sub-Reddit users which was aggregated into "author documents." These were split into 512-token segments (due to BERT's limit) and then encoded and passed through a neural network classifier that aggregated the chunk-level outputs. The model achieved 91.2% accuracy in distinguishing COVID-positive, demonstrating robust performance despite the presence of colloquial language, sarcastic expressions, and the prevalence of unsubstantiated claims regarding the pandemic.

Once positive cases were flagged, the next challenge was to extract symptoms from unstructured, often creatively phrased narratives. For this, we introduced QuadArm, a four-step NLP framework. It began with a BERT/BioBERT-based question-answering model to identify rough symptom mentions. These were expanded using word embeddings (GoogleNews word-2vec) to capture related keywords and modifiers—so the model could learn that "burning lungs" and "tight chest" might live in the same semantic neighborhood. The refined symptom phrases were then clustered using Adaptive Rotation Clustering (ARC), which dynamically groups similar terms without needing to predefine the number of clusters. Finally, the clusters were mapped to standardized UMLS concepts, translating Reddit slang into medically meaningful terms. In the end, this NLP approach revealed evolving symptom trends across the pandemic's early, Delta, and Omicron waves—showing, for example, a drop in loss of smell and a rise in sore throat, consistent with CDC reports. The study demonstrates that with the right combination of transformer models, semantic feature expansion, and optimized clustering methodologies, social media discourse can be systematically analyzed to extract clini-

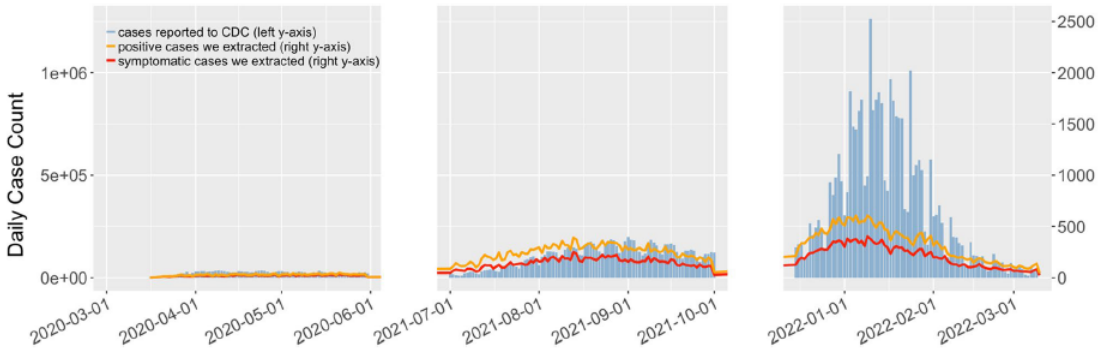

Figure 4. Daily trends in number of COVID-19 cases reported to the CDC and we extracted, for the corresponding three periods. (Reused from (Guo M, 2023), under CC BY 4.0)

Reflecting on the projects I've worked on, NLP appeared to be a powerful tool and can be applied in pharmacovigilance and pharmacoepidemiology, or public health emergency. While the text narrative could come from different sources: spontaneous reporting for pharmacovigilance, doctors' notes for pharmacoepidemiology, social media posting for public information, all require efficient automated text processing to extract key information accurately. Language modeling tools demonstrate significant potential for these applications, and I anticipate expanded utilization of evolving natural language processing technologies, with continued algorithmic improvements contributing to enhanced public health outcomes.

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CELEBRATING EXCELLENCE: 2025 ASA FELLOWS AND THEIR IMPACT ON STATISTICAL SCIENCE

Maria Kudela (Pfizer)

We are thrilled to celebrate members of our community who were named ASA Fellows in 2025 and recognized at the Joint Statistical Meetings (JSM) in Nashville, Tennessee. This distinction—bestowed annually by the ASA Committee on Fellows—is one of the highest honors in our profession, reserved for statisticians whose contributions, leadership, and service have had a sustained impact on statistical science and the ASA. Under ASA bylaws, the Committee on Fellows may elect up to one third of one percent of the association's membership each year.

How Fellows Are Selected: ASA Criteria

The Committee on Fellows evaluates nominees' overall contributions to the advancement of statistical science, placing due weight on (source: *https://www.amstat.org/your-career/awards/asa-fellows*):

- Professional activities (scientific impact and leadership in practice or research)
- Service to the ASA (section, chapter, and association-level contributions)
- Positions held and organizational impact (e.g., building teams, mentoring, advancing mission through statistical excellence)
- Published works (quality, influence, and breadth of scholarship)
- Membership and accomplishments in other societies (professional recognition across the broader community)

In this article, we are excited to shine a spotlight on several of this year's Biopharmaceutical Section nominees for ASA Fellow, recognizing their outstanding contributions to our profession.

Robert A. Beckman,
Georgetown University

Dr. Robert Allen Beckman is an oncology clinical researcher and mathematical biologist, whose goals are to develop cancer therapies and to improve the way cancer therapies are developed and deployed in patients. He is Professor of Oncology and of Biostatistics, Bioinformatics and Biomathematics at Georgetown University Medical Center, Scientific Advisor to the Senior Vice President for Research, Georgetown University, and chair of the Innovative Design Scientific Working Group (IDSWG), an international volunteer organization dedicated to improving clinical trials for more efficient development of experimental medical therapies.

Dr. Beckman's father, an electrical engineer and computer scientist who had worked on the first electronic computer, influenced him early in life. He developed a passion for science and medicine at 13, teaching himself from his father's books, getting a research grant at 15, and earning recognition as one of the top 40 STEM students in the US in the 1974 Westinghouse (now Regeneron) Science Talent Search. Dr. Beckman's father inspired him to extensively apply mathematics to biological problems.

Dr. Beckman also had a brother who predeceased him. He spoke with his mother about this painful experience, spurring him to prioritize patients and caregivers. He established one of the first pharmaceutical research programs in childhood cancer. As chair of IDSWG, he has recruited patient advocates and promoted bidirectional communication between patient and caregiver communities and clinical trial professionals.

After entering Harvard College as a sophomore and graduating with high honors, he also earned his MD from Harvard. He trained in pediatrics at Stanford University and pediatric cancer medicine at the University

of Michigan. He served on the faculty in Biophysics at the University of Michigan and was a Member in Systems Biology at the Institute for Advanced Study in Princeton.

Dr. Beckman's career spanned both academia and industry. His early research investigated physical mechanisms of preserving genetic information when cells divide, how cells store and release energy, and the atomic structure and interactions of biomolecules. After this he moved to industry, where he held leadership positions in experimental clinical cancer research in 5 pharmaceutical companies, led teams responsible for nearly two dozen first in human studies of cancer drugs, and contributed to approval of therapies for use in lung and prostate cancers. During these years, he combined his mathematical and clinical interests to co-invent clinical study designs that could test drugs at lower costs and with fewer clinical trial participants. The breadth and interdisciplinary nature of his interests is reflected in his numerous scientific publications and service as a reviewer for over 50 disparate scientific journals

In 2015, he joined the Georgetown faculty. He is most recently known for his theories of cancer evolution, which in turn led to dynamic precision medicine, a new approach to cancer medicine that holds promise for significantly improved patient outcomes. He also has continued developing improved clinical trial designs for testing experimental drugs.

Election as an ASA fellow is especially meaningful for Dr. Beckman, who is an interdisciplinary scholar without formal training in statistics. The election reflects extensive collaborations within the statistics community.

Freda Cooner,
Center for Biologics Evaluation and Research, FDA

Dr. Freda Cooner is a biostatistician with extensive experience in clinical research and development, spanning early-phase studies through post-marketing trials across diverse therapeutic areas, including pediatric drug development. Her work centers on the application and advancement of statistical methodologies to improve the design, conduct, and interpretation of clinical studies.

Dr. Cooner began her career at the U.S. Food and Drug Administration (FDA), where she continued her doctoral research in Bayesian statistics and applied it to regulatory science. In this role, she advanced the development and implementation of Bayesian methods in clinical trial research. She provided statistical consultation across multiple review divisions and promoted the use of model-informed, evidence-based approaches to support regulatory decision-making. She also helped establish internal forums for knowledge exchange on Bayesian methodologies, fostering professional development within the agency and encouraging broader adoption of modern statistical frameworks. Having since returned to the FDA, Dr. Cooner continues her mission to advance modern clinical trial science.

During her time in industry, Dr. Cooner further expanded the application of innovative statistical strategies to enhance clinical development programs. She collaborated with multidisciplinary teams on model-based and adaptive trial designs and contributed to methodological advancements for integrating data across studies and populations.

Dr. Cooner has been deeply engaged in advancing pediatric extrapolation and small population trial design. Her work supports the use of quantitative approaches to address challenges inherent in pediatric and rare disease studies, with an emphasis on efficient data utilization and statistical rigor. These efforts have informed trial strategies and contributed to broader discussions on applying Bayesian methods in complex clinical settings.

Beyond her scientific contributions, Dr. Cooner has maintained an active and sustained presence in the statistical community. She has led and participated in multiple scientific working groups focused on advancing statistical innovation and fostering collaboration between regulatory and industry statisticians. Within professional societies, she has served in leadership and committee roles that support knowledge sharing, mentorship, and professional development among statisticians at all career stages. Dr. Cooner has also been involved in organizing conferences, workshops, and educational events aimed at promoting emerging methodologies and practical applications in clinical development. In addition, she contributes to the field through editorial service on statistical journals, where she helps facilitate scholarly exchange and maintain scientific standards.

Dr. Cooner's career reflects a sustained commitment to both the methodological and applied aspects of biostatistics, particularly in Bayesian statistics. Her work emphasizes practical, data-driven solutions to challenges in clinical development and ongoing support for the advancement of the statistical profession.

Ying Ding,
University of Pittsburgh School of Public Health

Ying Ding, Ph.D., is Professor of Biostatistics and Health Data Science and Associate Dean for Graduate Academic Affairs at the University of Pittsburgh School of Public Health. She is internationally recognized for her contributions to survival analysis, semiparametric inference, and integration of modern machine learning methods into biomedical research, particularly in precision medicine and public health, with major applications in ophthalmology and psychiatry.

Dr. Ding earned her Ph.D. in Biostatistics from the University of Michigan. Following her doctoral training, she worked as a Senior Research Scientist at Eli Lilly and Company, where she gained valuable experience in early-phase drug development, biomarker discovery, and tailored therapeutics. She joined the University of Pittsburgh in 2013, rising through the ranks to full professor in 2024 and assuming key leadership roles including Vice Chair for Education, Director of the Ph.D. Program, and now Associate Dean.

Her recent research focuses on developing statistical and deep learning methods for complex time-to-event data, with applications to disease progression modeling and prediction, heterogeneous treatment effects estimation, and individualized treatment rule evaluation. She has been PI and co-I on numerous NIH grants from NIGMS, NEI, NIMH, and NIA, leading projects such as New Statistical Methods for Modeling Complex Multivariate Survival Data with Large-Scale Covariates and Deep Learning for Prediction of Age-Related Macular Degeneration Progression. Her research publication has appeared in many leading journals such as Annals of Statistics, Biometrics, Biostatistics, Journal of the Royal Statistical Society (Series C), Statistics in Medicine, Nature Communications, and PNAS, advancing both statistical methodology and its application to impactful biomedical research. Her exemplary scholarship has earned institutional and national recognition, including the Ascending Star Award at the University of Pittsburgh and the ASA Lifetime Data Science (LiDS) Section Outstanding Service Award.

Beyond her scholarly impact, Dr. Ding is a dedicated mentor and educator. She has advised numerous doctoral and master's students, many of whom have received national awards from ENAR, ASA, and ICSA. She is also deeply committed to faculty mentorship, helping junior colleagues secure independent NIH funding and establish successful research programs. Her excellence in teaching and mentorship was recognized through the James L. Craig Excellence in Education Award at the University of Pittsburgh.

Dr. Ding has also provided exceptional professional service to the American Statistical Association, including leadership roles as Program Chair of the ASA LiDS Section, Chair of the Statistical Partnerships Among Academe, Industry, and Government (SPAIG) Committee, and President of the ASA Pittsburgh Chapter. She has contributed extensively to advancing collaboration between academia and industry, promoting mentorship and visibility for early-career statisticians, and strengthening the statistical community. Her contribution to public health was further recognized through her induction into the Delta Omega Honorary Society in Public Health in 2022.

Elected as a Fellow of the American Statistical Association in 2025, Dr. Ding is honored for her innovative contributions to survival analysis and precision medicine, leadership in statistical education, and outstanding service to the profession, including her leadership roles with the ASA Lifetime Data Science Section and the Pittsburgh Chapter. She views the ASA Fellowship not only as a recognition of past accomplishments but as an inspiration to continue advancing statistical science through impactful collaboration, mentorship, and community building.

Yixin Fang
AbbVie

Dr. Yixin Fang received his PhD in Statistics from Columbia University in 2006 and then worked for one year as Postdoctoral Research Fellow at Columbia University Medical Center. From 2007 to 2018, he had been working in academia, first as Assistant Professor at Georgia State University and New York University School of Medicine and then as Associate Professor at New Jersy Institute of Technology.

In January 2019, Yixin joined the Medical Affairs and Health Technology Assessment (MA&HTA) Statistics group at AbbVie, bringing with him his 12 years of academic experience and expertise in machine learning and causal inference. In April 2019, he delivered an introduc-

tory presentation at AbbVie during a MA&HTA Stats "lunch-and-learn" session, where he advocated for the use of targeted learning as a crucial causal inference tool in the pharmaceutical industry.

As the Therapeutic Area Head of Eyecare and Specialty within the MA&HTA Statistics group, Yixin's agile and accountable leadership has enabled him to successfully manage his team and lead medical affairs researches and HTA submissions. His pioneering spirit led to the founding of the Causal Inference Center (CIC) at AbbVie in 2022, where he offers consultations and training on causal inference, the estimand framework, and the targeted learning approaches to his colleagues at the MA&HTA Statistics group. Yixin was the first statistician at AbbVie to promote and apply targeted learning to analyze data from clinical trials and real-world studies. He trained numerous statisticians in this framework, which offers greater efficiency in confounding bias adjustment and missing data handling than parametric modeling approaches.

Yixin has authored or co-authored over 120 peer-reviewed publications, with more than 60 being methodological contributions to statistical journals. In 2024, he published a book titled "Causal Inference in Pharmaceutical Statistics," which introduces clinicians and statisticians to causal inference concepts and methods with practical applications. Additionally, he co-edited the book with his colleagues Weili He and Hongwei Wang, "Real-World Evidence in Medical Product Development," published in 2023.

Jianchang Lin,
Takeda

Dr. Jianchang Lin is Executive Director and Head of Statistical & Quantitative Sciences (SQS) Neuroscience and Chief Statistical Office (CSO) at Takeda Pharmaceuticals. With over a decade of experience in the pharmaceutical industry, Dr. Lin is widely recognized as a visionary leader in statistics and data science. His pioneering contributions span innovative trial designs, real-world data and evidence (RWD/RWE), and the application of artificial intelligence and machine learning (AI/ML) across global drug development.

In his current dual role, Dr. Lin leads a high-performing SQS team that provides strategic and operational support across Takeda's Neuroscience Therapeutic Area—including sleep-wake disorders, neurodegenerative diseases such as Alzheimer's, and rare neurological conditions. Also, as Head of the Chief Statistical Office (CSO) within Takeda's SQS organization, he leads a matrix team and methodologies hubs supporting a global community of hundreds of statisticians, data scientists, and programmers. Under his leadership, the CSO has developed and implemented cutting-edge statistical methodologies, tools, and guidance, while fostering best practice sharing and a vibrant learning community. These efforts have helped accelerate drug development and improve patient outcomes across Takeda's portfolio on Oncology, Gastrointestinal & Inflammation and Neuroscience.

Previously, Dr. Lin served as Senior Director and Director of SQS Oncology at Takeda, where he led teams supporting the development and global approval of several novel cancer therapies, including treatments for multiple myeloma (MM), non-small cell lung cancer (NSCLC), and metastatic colorectal cancer (mCRC), among others. His innovative quantitative approaches contributed to expedited drug approvals, earning him the highest Takeda Executive Team (TET) Award and numerous R&D Project Awards.

Dr. Lin is deeply committed to advancing the integration of modern quantitative science in drug development. He has published over 90 peer-reviewed articles, with more than 4,000 citations in leading journals such as Biometrics, Statistics in Medicine, NEJM, JAMA Oncology, JCO, Blood, and Cancer Discovery.

His dedication to service is reflected in his leadership within the broader statistical and data science community. Dr. Lin currently serves as President of the ASA Boston Chapter, Industry Co-Chair for the ASA Biopharmaceutical Section and Regulatory-Industry Statistics Workshop (RISW) 2024, and Board Director for the International Chinese Statistical Association (ICSA). He is a strong advocate for industry-academia partnerships, including the Takeda-MIT Artificial Intelligence Program (2020–2024) and Takeda-Yale Biostatistics collaborations. He also serves on editorial boards for the *Journal of Biopharmaceutical Statistics and Statistics in Biosciences.*

Passionate about mentorship, Dr. Lin has guided over 15 PhD interns, many of whom have gone on to thrive in academia, industry, and regulatory agencies. He is deeply grateful for the support of colleagues and the statistical community throughout his career and remains committed to "paying it forward" by mentoring the next generation of statisticians and fostering a culture of learning and innovation.

Dr. Lin strives to promote excellence, integrity, and innovation in statistics and data science—with the ultimate goal of improving patient health worldwide.

Yan Ma,
University of Pittsburgh

Dr. Yan Ma is Professor and Chair of the Department of Biostatistics and Health Data Science at the University of Pittsburgh School of Public Health. He earned his PhD in Statistics from the University of Rochester.

Dr. Ma's theoretical and computational statistical research interests include missing data imputation, machine learning, meta-analysis, methods for assessing interrater reliability, causal inference, complex sample surveys, and longitudinal methods. Through his collaborative research, Dr. Ma has become a statistician specializing in team science, translational science, and comparative effectiveness research. His areas of application include orthopedics, anesthesiology, health disparities, cancer, HIV/AIDS, psychiatry, and emergency medicine.

Dr. Ma has authored over 100 peer-reviewed publications, including methodological, biomedical, and health services research articles in journals such as Biometrics, Statistics in Medicine, Psychometrika, Health Services Research, JAMA, Anesthesiology, Anesthesia & Analgesia, Circulation Research, Clinical Orthopaedics and Related Research, Journal of Bone & Joint Surgery, and Regional Anesthesia and Pain Medicine. His research has been supported by R01 grants from AHRQ and NIH to advance statistical methods for addressing missing data in health disparities research.

Dr. Ma has served the profession in multiple editorial and leadership roles. He is an Associate Editor for The American Statistician and was an Editorial Board Member of The American Journal of Public Health. He has also served on numerous NIH, PCORI, and VA review panels, and the ENAR Regional Advisory Board. Dr. Ma has been an active member of the American Statistical Association (ASA). He has helped develop the next generation of statisticians through his instrumental role in the ASA Section on Statistics in Epidemiology's mentoring program. He was a member of the ASA's Mentoring Award Committee.

Dr. Ma's contributions have been recognized with numerous honors, including the ASA Statistics in Epidemiology Young Investigator Award, an Oak Ridge Institute for Science and Education (ORISE) fellowship at the FDA, and the Achievement in Academia Award from the APHA Applied Public Health Statistics Section. Together with his collaborators, he received the distinguished Team Science Award, which honors exceptional success in translating research discoveries into clinical applications and advancing them into routine medical practice. This award was jointly presented by the Association for Clinical Research Training, American Federation for Medical Research, Association for Patient-Oriented Research, and the Society for Clinical and Translational Science. Dr. Ma is an ASA Fellow and, notably, a Fellow of the American College of Chest Physicians—an honor rarely awarded to statisticians.

Kannan Natarajan,
Pfizer

In 2025, Dr. Kannan Natarajan was recognized as an ASA Fellow, a distinction representing the highest achievement in applied statistics within the industry. Dr. Natarajan's career in the pharmaceutical sector began unexpectedly, but over three decades, he learned that success requires not only theoretical expertise but also a deep understanding of the problems at hand and the ability to communicate statistical solutions clearly to diverse audiences.

As Senior Vice President and Global Head of Biometrics and Data Sciences at Pfizer, Dr. Natarajan has dedicated his career to advancing the role of statistics, data science, and artificial intelligence in drug development. Dr. Natarajan manages a global organization of statisticians, data scientists, engineers, and statistical programmers, building a culture of rigorous, data-driven decision making. One of Dr. Natarajan's proudest achievements has been establishing and leading the AI/ML Quantitative and Digital Sciences Center of Excellence at Pfizer, which drives the development and deployment of AI/ML solutions across R&D, supporting digital medicine initiatives and transforming approaches to clinical trials and data analysis.

Dr. Natarajan spearheaded the creation of AI-driven tools such as Smart Data Query, piloted during the pivotal COVID-19 vaccine trial. This innovation reduced the median time from data capture to query generation from 25 days (in typical vaccine studies) to just 1.7 days for the COVID vaccine, dramatically accelerat-

ing the ability to deliver critical data and make timely decisions. Dr. Natarajan also led the development and regulatory qualification of Bayesian dose-response modeling and R-shiny applications, which have been broadly adopted across the industry.

Throughout his career, Dr. Natarajan has championed the integration of statisticians and data scientists as core members of asset and study teams, ensuring that data-driven insights are central to clinical strategy and decision-making. He has also focused on building platforms for innovation, such as the Pfizer Analytics Summit and the refocused Global Statistics Conference, to foster knowledge sharing and best practices across the organization.

Diversity and mentorship are deeply important to Dr. Natarajan. He transformed his leadership team to achieve nearly 50% representation of women and racial/ethnic minorities, and established university fellowships supporting minority statisticians.

Methodological leadership includes championing Bayesian methods in clinical trials, such as interim monitoring for the COVID-19 vaccine trial, which enabled early stopping and expedited global emergency use authorization, as well as advancing synthetic control and real-world evidence approaches for regulatory approvals.

Prior to Pfizer, Dr. Natarajan led oncology biometrics at Novartis, contributing to the approval of multiple breakthrough therapies and the adoption of Bayesian and AI/ML methods in clinical trial design. His journey began at Bristol-Myers Squibb and Abbott, supporting landmark therapy approvals in pulmonary, immunology, cardiovascular, and metabolic diseases and shaping regulatory guidance.

Dr. Natarajan earned a Ph.D. in Statistics from the University of Florida, anchoring a lifelong commitment to methodological rigor and translational impact. Above all, Dr. Natarajan is proud that his work has helped place statistics, data science, and AI/ML at the heart of drug development, accelerating innovation and improving patient outcomes worldwide.

Zhenming Shun,
Daiichi Sankyo

Dr. Zhenming Shun received his Ph.D. in Statistics from the University of Chicago and an M.S. in Mathematics from Peking University. He has built a distinguished career of more than 30 years in the pharmaceutical industry and academia, specializing in biostatistics, data management, and clinical drug development.

Dr. Shun has held senior global leadership positions, including Global Head of Biostatistics in Oncology at Sanofi and Vice President, Global Head of Biostatistics and Data Management at Daiichi Sankyo. In these roles, he supported strategic business decisions and led international teams responsible for clinical trial design, statistical analysis, and regulatory submissions. His leadership was instrumental in establishing robust biostatistics and data management functions and in achieving multiple successful drug approvals in oncology and cardiology—advancing therapies that have improved patient outcomes worldwide.

Beyond his industry leadership, Dr. Shun has authored influential papers in peer-reviewed journals and presented extensively at international scientific conferences.

In recognition of his impact, he was elected a Fellow of the American Statistical Association (ASA) for his leadership in drug development and statistical research.

Chenguang (CG) Wang,
Regeneron Pharmaceuticals

Dr. Chenguang Wang is Executive Director and Head of Quantitative Innovation and Statistical Strategy at Regeneron Pharmaceuticals. Combining expertise in statistics and computer science, Dr. Wang has contributed to advancing missing data analysis, causal inference, Bayesian methods, and the integration of real-world evidence into clinical trials. His work aims to bridge the gap between statistical theory and practical application, striving to make complex methodologies more accessible to the broader scientific community.

Dr. Wang earned his Ph.D. in Statistics from the University of Florida and began his career as a Mathematical Statistician at the FDA Center for Devices and Radiological Health. In 2011, he transitioned to academia, joining Johns Hopkins University, where he became an Associate Professor in the Departments of Oncology and Biostatistics. In 2021, he joined

Regeneron Pharmaceuticals to establish and lead the Statistical Innovation Group, contributing to the Senior Leadership Team within the Biostatistics and Data Management Department.

Dr. Wang's work has helped improve how clinical researchers address challenges such as missing data and causal inference. His efforts in leveraging real-world data for regulatory decision-making were recognized with two FDA Scientific Achievement Group Awards in 2020, including the Excellence in Analytical Science Award for developing innovative statistical methods to incorporate real-world evidence into clinical trials. With close to 100 peer-reviewed publications in journals such as Journal of the American Statistical Association, Biometrics, Statistics in Medicine, and Journal of Statistical Software, Dr. Wang's research has made a meaningful impact on the field of biostatistics.

Dr. Wang is a strong advocate for making statistical methods more accessible. He has developed numerous R packages, which include user-friendly tools with web-based graphical interfaces. These tools have made advanced statistical methods more approachable for both statisticians and non-statisticians. His philosophy emphasizes that statistical innovation has the greatest impact when paired with practical and easy-to-use implementation tools.

Beyond his technical contributions, Dr. Wang has been deeply involved in advancing the statistical profession through service and leadership roles. He currently serves as Secretary of the ASA NYC Chapter and as an Associate Editor for Biometrics and Pharmaceutical Statistics. His prior leadership roles include serving as Associate Program Chair for ENAR in 2019. In 2023, he played a key role in launching the inaugural Statistical Innovation Community Summit and helped establish the ASA Biopharmaceutical Section's Statistical Innovators in Medical Product Development subcommittee.

Dr. Wang's election as an ASA Fellow in 2025 reflects his major contributions to missing data methodology, causal inference, and leveraging real-world evidence in the evaluation of medical products. Dr. Wang's collaborative approach, focus on practical innovation, and commitment to the advancement of biostatistics continue to contribute to the development of life-saving medicines and the growth of the statistical profession.

The 2025 ASA Fellows represent excellence, innovation, and service in statistical science. Their achievements—from advancing methodology to mentoring future leaders—show the impact of collaboration and commitment to our profession.

As we honor these distinguished Fellows, we celebrate their contributions and look forward to continued progress in research, medicine, and society.

Congratulations to all the 2025 ASA Fellows—your work inspires us to aim higher and support the next generation of statisticians.

Figure 1. All 2025 ASA Fellows

SURVEY REPORT ON THE FUTURE OF NONCLINICAL STATISTICS

Aili Cheng (Pfizer), Eve Pickering (Pfizer), Charles Tan (Pfizer)

Executive summary

A survey of nonclinical statistics leaders in March 2025 gathered 21 anonymous responses on the impact of advanced technology and organizational changes. While artificial intelligent (AI) and machine learning (ML) are expected to influence the field over the next 10–20 years, human expertise remains crucial. Respondents emphasized skills in ML, digital twins, deep learning, and neural networks, and showed a preference for centralized structures with strong scientific and business collaboration. Leaders are encouraged to focus on advanced analytics training, cross-functional teamwork, and balanced organizational models.

Survey Overview

Objective: This survey aims to gather insights from nonclinical statistical leaders in various pharmaceutical companies to inform discussions on the future of nonclinical statistics with respect to mandatory skills, impact of AI/ML and organizational structures.

Methodology: Online questionnaire via Microsoft office forms

Number of Respondents: 21

Period: April 14, 2025 to May 21, 2025

Key Findings

This brief survey comprised five questions in total. Below is a summary of the responses to each question.

1. Question #1: Which emerging skills will be essential for nonclinical statisticians in the future?

Responses were distributed relatively evenly among deep learning, neural networks, digital twins, and other categories. "Machine learning" received the highest proportion of votes at 35% (see Figure 1). It is noteworthy to highlight three comments submitted under the "others" category:

- "Marketing skills, business savviness."
- "The ability to combine statistics and scientific/risk-based thinking; this is the only way to distinguish ourselves from AI."
- "Statistical computing and software engineering."

It is important to note that soft skills such as marketing abilities are likely to become increasingly vital as we move into the era of AI.

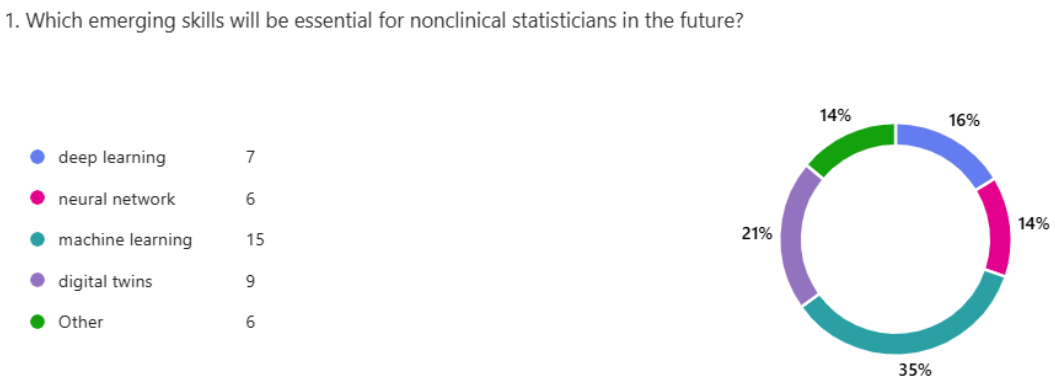

Figure 1. Question 1 response summary

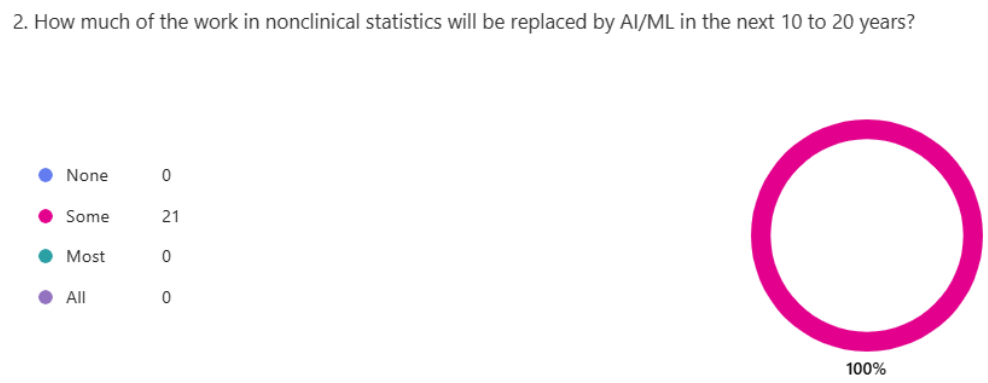

Figure 2. Question 2 response summary

Figure 3. Question 3 response summary

2. Question 2: How much of the work in nonclinical statistics will be replaced by AI/ML in the next 10 to 20 years?

All respondents answered "some" to question #2 (Figure 2), indicating confidence that our nonclinical statistics skills are so unique that we are confident that we will not be fully replaced by AI/ML.

3. Question #3: Which line do nonclinical statisticians report to in your organization?

Nonclinical statisticians' reporting lines vary by company; about 33% report to central statistics (Figure 3)

4. Question #4: What do you think is the best organizational structure for nonclinical statistics?

As a follow-up to Question #3, Question #4 asked what the best organizational structure is for nonclinical statistics. Except for one respondent who answered "NA", 20 respondents honestly expressed their experience and opinions.

- A majority of respondents (over 50%, with 13 out of 20) expressed a preference for centralized organizational structures, such as a central statistics group or data science department. However, two of these thirteen raised concerns regarding centralization with clinical statistics: one noted that nonclinical statistics might be deprioritized when the statistics function reports under clinical

development, while another acknowledged both advantages and disadvantages of integrating clinical statisticians into a centralized organization.

- Four respondents indicated a clear preference for reporting within a scientific line or related business unit.

- Two respondents were neutral, recognizing both strengths and limitations in any reporting structure. They emphasized the importance of maintaining strong connections across all relevant functions, adapting to circumstances, and upholding high standards of statistical practice irrespective of organizational design.

Many respondents stressed maintaining strong ties with both supported lines and the statistical line. Some suggested that if reporting to one line, a dotted line connection with others should remain.

5. Question #5: As leaders in nonclinical statistics, what can we do to make positive changes?

Similar to Question #4, this item is open-ended. Out of 21 respondents, 20 provided responses. The actions suggested by the respondents can be organized into four categories:

1. Collaboration: Expand and enhance collaborations with all surrounding functional lines, including CMC, regulatory, AI/ML/modeling/data sciences.

2. Business influence: Address challenges that deliver value to the business.

3. Staff training: Offer opportunities and support for statisticians to develop non-statistical knowledge and skills such as biology, chemistry, regulatory, software, and soft skills like communication and stakeholder engagement.

4. New technologies: Adopt new technologies such as AI and ML and demonstrate leadership in digital transformation.

See more details in Table 1.

Table 1. The suggested actions for question #5

Category	Key Actions
Collaborations	Develop CMC and regulatory strategies together; engage in question-asking and problem-solving; work with IT, scientific, regulatory affairs, and QA teams to clean, standardize, and structure data for AI-readiness; ensure compliance and model validation; engage with partners and stakeholders; participate in cross-discipline activities; encourage visibility and inclusion; promote integration with science, data science, and modeling groups; foster collaboration and curiosity
Business Influence	Drive use of statistics to solve high-value business challenges; demonstrate measurable business impact; advocate for data practices (FAIR principles); quantify risks; visualize data; design experiments; communicate impact of statistical work; contribute to improved experimental design
Staff Training	Ensure statisticians understand processes and methods; provide opportunities for non-statistical skills; support development in biology, chemistry, software, communication, stakeholder engagement; encourage ongoing learning and cross-disciplinary growth; support participation in diverse projects
New Technologies	Embrace AI/ML as tools to enhance statistical work; champion responsible, explainable AI; integrate AI into workflows; make data AI-ready; pilot AI tools for study design, dose selection, outcome prediction; set guardrails for responsible AI use; ensure transparency, validation, compliance; promote adoption of new technologies; demonstrate best practices for AI/ML integration; show leadership in digital transformation; encourage proactive attitude toward change

Conclusion

The aggregated survey responses reveal several key insights:

- Most participants believe that only some aspects of nonclinical statistics will be replaced by AI/ML in the next 10 to 20 years, suggesting a continued need for human expertise and collaboration.

- The most frequently mentioned emerging skills for nonclinical statisticians are ML, digital twins, deep learning, and neural networks, highlighting the importance of adapting to new technologies and interdisciplinary approaches.

- There is a strong preference for centralized organizational structures (such as a central statistics line or data science department), but many also emphasize the value of close collaboration with scientific and business functions to maximize impact and visibility.

These findings indicate that leaders in nonclinical statistics may benefit from enhancing statistician skills in advanced analytics, AI, and related soft skills, promoting cross-functional collaboration, and supporting organizational approaches that balance centralization with integration into scientific teams. This approach can enable nonclinical statisticians to contribute effectively to the business rather than focusing solely on model development.

BOLD MOVES: HOW AN EARLY PIVOT TO BIOTECH ACCELERATED ONE EXECUTIVE'S RISE

Emily Butler (ProKidney)

In today's life sciences ecosystem, career paths rarely follow a linear trajectory. While many professionals spend decades in large pharmaceutical organizations before moving to biotech, others choose to pivot early—often with transformative results. This article profiles one senior executive who made that bold leap early in her career, sharing how the decision shaped her leadership journey and what lessons it offers for the next generation of industry leaders.

An Early Leap of Faith

For Emily Butler, the choice to leave big pharma early was driven by both fit and opportunity. She found that her role in a large company misaligned with her skill set and cultural expectations. After exploring roles at other pharma companies, it became clear the same challenges would persist. Instead, she accepted a position at a small, cash-strong biotech—a move that would redefine her career.

"I believed, you're not a tree—you can move," she explained. "I was young enough that if it turned out to be a mistake, I could go back. The bigger risk was staying in a role that wasn't a good fit and always wondering, what if?"

The Biotech Acceleration Effect

The shift into biotech resulted in what the executive described as "exponential" progression. Where big pharma offered defined career paths but limited agility, biotech provided speed, visibility, and direct access to decision-makers. With fewer layers of hierarchy, her ideas reached the CEO quickly, often influencing company direction.

Resource constraints, while challenging, also opened opportunities. "I stepped in wherever there were gaps, even outside statistics," she recalled. This breadth of responsibility honed her learning agility and strengthened her confidence. She also discovered the importance of trusting intuition—initially deferring to more senior colleagues but later realizing that her own instincts could drive critical company pivots.

Leadership Lessons in Real Time

Biotech demanded leadership skills that would have developed much later in big pharma: managing teams, working with boards, and influencing senior peers. With constant change and resource constraints, adaptability became essential. "Change will never stop. The best we can do is adapt and not take it personally," she told her team.

Her hands-on approach also built credibility. By staying close to the work and stepping in during critical moments, she earned the trust and respect of colleagues at every level—an asset that amplified her visibility and influence.

Innovation as a Non-Negotiable

Innovation emerged as a consistent theme throughout our conversation. For this executive, innovation is not optional—it is the only path forward in drug development. She recalled multiple instances where seemingly impossible challenges were overcome through persistence, creativity, and strategic risk-taking.

"Sometimes there's no precedent, no regulatory example, no literature to point to," she reflected. "That's when I remind myself, someone has to be first."

What Biotech Teaches Executives

The biotech environment also shapes a distinctive style of leadership. It requires grit, agility, and creative problem-solving. Unlike big pharma, it does not provide a safety net—leaders must speak up, even in uncomfortable situations, because silence can jeopardize the mission.

While many leaders with strong resumes struggle in biotech, success is less about credentials and more about fit. Effective leaders are either able to pivot between large and small organizations or recognize which environment suits them best.

Advice for Emerging Leaders

For early-career professionals considering a pivot, the executive offered clear guidance: start by building a foundation in big pharma. Understanding the regulatory and operational rules of the industry is essential before attempting to break them. Once that foundation is set, the agility and exposure of biotech can accelerate growth.

Her advice to rising leaders includes:

- Be prepared to work harder and wear more hats than you expect.
- Advocate for your discipline.
- Embrace self-driven learning.
- Treat mistakes as catalysts for growth.
- Lead with authenticity and transparency.

Final Reflection

Looking back, the executive expressed no regrets about leaving pharma early. The decision provided breadth, resilience, and the confidence to lead authentically. Ultimately, the move was less about leaving one environment and more about becoming the kind of leader who could succeed in both worlds—a leader defined by agility, intuition, and an unwavering commitment to patients.

ADVICE FOR STATISTICIANS IN CLINICAL TRIALS

Scott Evans (George Washington University)

Thank you to the Biopharmaceutical Section for the kind invitation to contribute an article for Biopharmaceutical Report on professional development and the evolution of role of statisticians in clinical trials.

I recently completed my term as the President of the Society for Clinical Trials (SCT). In one issue of the SCT newsletter, I was asked if I had advice for statisticians in clinical trials. The question reminded me of a lecture from a PERI training course for new statisticians in clinical trials. I took the course when I was beginning my career. I recall a lecture given by Dan Anbar on the role of the statistician in clinical trials. It contained valuable advice from a non-technical and big picture point of view. Years later I was a faculty member for the same PERI course and gave the same lecture to a new cohort of clinical trial statisticians. I have updated it over the years. Below is a bullet list of pieces of advice drawing upon that lecture and lessons accumulated over the years.

• Understand the research question; ensure it is the right one.

- o Work hard at finding and understanding the question before searching for answers.
- o Place increased interest on questions of a pragmatic origin. These are the most important questions for patients and clinicians.

• Be inquisitive.

- o Be a detective.
- o Ask a lot of questions before answering one.
- o It is better to know how to learn than to know. Go beyond what, into why.

• Be thoughtful.

- o Do not rush your answers.
- o Think about a problem, develop your own ideas for solutions, before researching how others have approached it. This is how novel thinking begins.

• Protect scientific integrity. Clinical trials are our strongest tool.

- o Be motivated to do things better rather than faster than cheaper.
- o Strive for objectivity, robustness, and transparency.
- o When sacrifice is necessary, and sometimes it is, sacrifice quantity based on feasibility while protecting quality. Otherwise, we will be unable to fully understand the evidence.
- o Identify options and their pros and cons.
- o Learn to distinguish innovations advancing science vs. compromises advertised as such. It is better to walk alone than in a crowd in the wrong direction.
- o Voice scientific opinions. Ensure they are well-rationalized.

• Educating yourself and others is never-ending.

- o Keep learning. Science does not stand still.
- o Own and learn from your mistakes.
- o Know the statistical literature.
- o Know the medical literature. Interpret it critically.
- o Tactfully teach others regarding clinical trial concepts and sound approaches.
- o Educate colleagues about what you do and learn from them about what they do.
- o Find mentors. Use your references and resources.
- o Develop a library of key papers different topics in the design, monitoring, analyses, and reporting of clinical trials
- o Participate in professional societies, attend professional meetings, and take short courses.

- **Keep developing content of character.**
    - o Pretend to be the best person you can imagine; you will become that person.
    - o Find opportunities for others.
    - o Be proactive.
- **Develop effective communication skills.**
    - o This involves listening, writing, speaking, and presenting.
    - o Tailor to your audience.
    - o Avoid being isolated.
    - o Learn to explain complicated things in simple ways.
- **Finish the job.**
    - o The goal is to understand the results, not simply obtain them. Thoroughly understand and help others to understand the result, beyond producing it.

Learning statistics is one thing. Learning to be a statistician is another. Becoming a statistician is not like learning the state capitals or a collection of methods that can be checked off as completed. Certainly we learn about inference tools for estimation and testing, modeling approaches and their assumptions for handling different types of data and complex data challenges, new technological advancements, and how statistical science is a grounded scientific thought process for understanding data in the presence of uncertainty. Being a statistician is as much a road as a destination, being an ever inquisitive student and scientific educator. We are a critical part of team science, collaborating in an effort to improve the lives of our fellow humankind through sound, principled, high-integrity research. Developing the non-technical skills as well as the technical skills are critical for maximizing our important contributions.

JSM 2025 BIOPHARMACEUTICAL SECTION: INNOVATION, COLLABORATION, AND COMMUNITY

Jianchang Lin (Takeda), Biopharmaceutical Section Program Chair, 2025

Figure 1 2025 Biopharmaceutical Section Mixer and Exhibit Booth at JSM 2025.

The Biopharmaceutical Section (BIOP)'s presence at JSM 2025 in Nashville, Tennessee was nothing short of inspiring. The BIOP sponsored program brought together statisticians, researchers, and industry leaders for a week that celebrated both scientific progress and the spirit of collaboration.

This year's agenda was packed, featuring 6 invited sessions, 16 topic-contributed sessions, and 17 contributed paper sessions. The program also shone a spotlight on emerging talent, with a special session dedicated to the winners of the ASA BIOP Student Paper Competition.

A recurring theme throughout the conference was the transformative role of artificial intelligence and machine learning in drug development. Attendees explored how advanced statistical and AI methods are being used to analyze data from digital wearables, detect anomalies in clinical trials, and drive innovation across the biopharmaceutical landscape. These discussions made it clear that AI/ML is not just a buzzword—it's reshaping the way that research is conducted and how therapies are developed.

Bayesian and adaptive trial designs also took center stage. Presenters shared practical insights on implement-

ing these approaches in real-world drug development, from dynamic borrowing to innovative Bayesian analyses. The emphasis on adaptive and complex trial designs reflected a broader industry shift toward more flexible, efficient, and informative studies.

Precision medicine and biomarkers were another highlight. Sessions delved into integrating PK/PD and biomarkers for greater accuracy in clinical trials, as well as strategies for enrichment designs and dose optimization. These conversations underscored the growing importance of tailoring treatments to individual patients and leveraging data to make smarter decisions.

Patient-centered outcomes remained a core focus. Experts discussed the standardization of patient-reported outcomes in oncology, and the increasing use of real-world evidence and patient experience data. The message was clear: keeping patients at the heart of research leads to better science and, ultimately, better care.

Regulatory science and collaboration were also in the spotlight. Sessions addressed sponsor-regulatory interactions on estimands, innovations in covariate adjustment, and the use of master protocols. These topics highlighted the ongoing need for clear communication and partnership between industry and regulators as the field evolves.

Beyond the technical sessions, the conference highlighted community engagement. Special recognition was given to winners of the student paper competition, while roundtable discussions fostered deeper dialogue and networking among attendees. The ASA Biopharmaceutical Section also hosted its booth at JSM, where members connected, shared resources, and showcased initiatives.

For those interested in exploring the full program or learning more about specific sessions, the official 2025 JSM website offers a comprehensive overview (*https://ww2.amstat.org/meetings/jsm/2025/*).

Beyond the scientific sessions, JSM 2025 was also a wonderful opportunity to reconnect with old friends and make new ones. The well-attended Biopharmaceutical Mixer was a highlight for many, offering a relaxed and lively setting for networking and conversation. During the mixer, the section recognized outstanding student contributions with awards for the best papers, and provided important updates on section activities and initiatives. The sense of community was palpable, reminding everyone that BIOP is not just about advancing science, but also about building lasting professional relationships and supporting the next generation of leaders. We can't wait to keep the momentum going—join us at JSM 2026 for more innovation, collaboration, and connection!

RECAP OF THE 2025 BOSTON PHARMACEUTICAL STATISTICS SYMPOSIUM

Gautier Paux (Sanofi), Maria Kudela (Pfizer), Tu Xu (Novo Nordisk), Kush Kapur (argenx), Kristin Baltrusaitis (Harvard), Wenting Cheng (Biogen), Zhaoyang Teng (Astellas), Jianchang Lin (Takeda)

Organized by the Boston Chapter of the American Statistical Association (ASA) and hosted by Novo Nordisk, the 2025 Boston Pharmaceutical Statistics Symposium brought together over 200 professionals and students from industry, academia, and CROs for two days of learning, connecting, and discussions. The theme for this year's symposium - "Transforming Clinical Development Through Data Science, Innovative Design, and Statistical Excellence" - was particularly timely as our field is entering an era when AI/ML methods are reshaping drug development. Statisticians play a critical role, not only as data analysts but as strategic partners who bring scientific rigor, transparency, and translation of complex models into actionable drug development decisions. The symposium spotlighted how statistical teams can lead and shape smarter trials, guide key decisions, and influence outcomes for patients.

Short course

Following the success of last year's short courses, the scientific committee created two short courses on November 6th. Over 60 attendees (in-person and virtual) had the opportunity to learn from Susan Gruber (TL Revolution) who delivered an insightful short course on Targeted Maximum Likelihood Estimation in drug development and Haolin (Leo) Lin, who shared An Overview of Machine Learning Methods for Survival

Data. These two short courses offered hands-on training and highly interactive discussions, fostering an excellent platform for deeper engagement and peer learning.

Keynote and Invited Sessions

On November 7th, the main event welcomed 150 participants. Two keynote speakers were invited to provide their insights into two different topics:

- Brian Millen (Biogen; ASA 122nd President-Elect), who spoke on "The Future of Our Profession" and painted a forward-looking picture of how statisticians will shape the evolving pharmaceutical landscape.
- Josh Chen (Vertex Pharmaceuticals), whose talk "Adaptive Designs: Applications and Practices" focused on how adaptive trial methodologies can support innovative drug development.

Complementing the keynotes, seven invited speakers (Kentaro Takeda (Astellas), Yunqi Zhao (Takeda), Krishna Padmanabhan (Madrigal Pharmaceuticals), Yoni Sidi (Sanofi), Jake Gagnon (Biogen), Junwei Lu (Harvard T.H. Chan School of Public Health) and Foroogh Shamsi (Novo Nordisk)) delved into a variety of topics including dose optimization, AI/ML-powered innovation in drug development, knowledge graphs, and targeted learning for healthcare applications. The sessions offered a rich blend of methodological innovation and practical case examples, highlighting how statistical science is translating into strategic development decisions.

Poster and Lighting Talk Sessions

This year the symposium poster session hosted 20 poster contributions, including 15 students who participated in the Best Student Poster award. This session continues to grow as one of the most energizing parts of the program, offering a visible platform for emerging talent and innovative ideas. The lightning talk session offered a lively and engaging preview of poster content, inviting attendees to visit the posters directly, ask questions, and meet the authors. After a voting panel from the poster sub-committee, Eric Zhou (University of Florida) *https://www.wayup.com/profile/Eric-Zhou-78b04d9637/* and Aaron Apostadero (Harvard Univer-

Symposium Co-Chair and Program Chair of BCASA Gautier Paux provides welcome address

Some Symposium Scientific Committee Members

Symposium Co-Chair and Chair of Speakers and Short Course Subcommittee Maria Kudela gives closing remarks

sity) were recognized for the 1st place, and Yuyang Jin (Boston University) and Yixin Zhang (Boston University) won the 2nd place.

The full event agenda and presentation slides can be found on the BCASA website: 2025 - BostonChapter (*https://community.amstat.org/bostonchapter/new-page/new-page9*)

Acknowledgements

The Scientific Committee, comprising 23 members, played a crucial role in organizing the symposium. The leaders of the Scientific Committee included Co-Chair and Program Chair of BCASA, Gautier Paux (Sanofi); Co-Chair and Chair of Speakers and Short Course Subcommittee, Maria Kudela (Pfizer); Vice-Chair and Venue Host, Tu Xu (Novo Nordisk); Vice-Chair and Chair of Communication Subcommittee and Webmaster of BCASA, Kush Kapur (argenx); Chair of Poster and Lightning Talks Subcommittee, Hailu Chen (Alkermes); Past Co-Chair and Student Volunteer Liaison, Kristin Baltrusaitis (Harvard); Past Co-Chair and Past President of the Boston Chapter of ASA, Wenting Cheng (Biogen); Past Co-Chair, Zhaoyang Teng (Astellas); President of the Boston Chapter of ASA, Jianchang Lin (Takeda).

We extend our heartfelt gratitude to the entire Scientific Committee for their exceptional work: Brooks Clark (Cytel), Jinghui Dong (Kite, Gilead Science), Jimmy Efird (VA CSPCC – Boston), Kosalaram Goteti (Seaport Therapeutics, Inc.), Ina Jazic (Vertex), Fotios Kokkotos (Boston University), Haolin Li (Boston University), Xihao Li (UNC-Chapel Hill), Rachel Liu (Takeda), Jameson Luks (MaxisIT), Abigail Sloan (Pfizer), Ting Wang (Biogen), Disa Yu (Sanofi), Jing Yu (Novo Nordisk).

Last, we deeply appreciate our generous sponsors.

- Our venue host, Novo Nordisk, especially Tu Xu, Jing Yu, and the team, for venue support and event logistics.
- The Boston Chapter of the ASA for their ongoing leadership in fostering the regional statistical community.

Student Poster Award Winners and the Student Poster Award Judges

- Our sponsors Sanofi, Pfizer, Insilicom (Platinum Sponsors); Vertex, Cytel, MMS, Takeda (Gold Sponsors); Astellas, Metrum (Silver Sponsors); Servier (Short Course Sponsor); and the ASA Biopharmaceutical Section (Poster Sponsor), for their financial support.

As the statistical and drug development landscape continues to evolve at pace, the role of biostatisticians has never been more critical. Bringing together methodological innovation, strategic translation, and collaborative networking, the 2025 symposium strengthened our community's ability to lead in this transformation. We look forward to building on this momentum, through new events, continued engagement, and even deeper focus on how statistics can shape the future of drug development.

NCB 2025 SUMMARY

Paul Faya (Eli Lilly and Company), John Kolassa (Rutgers University)

The 2025 ASA-BIOP Nonclinical Biostatistics Conference took place from June 16-18 at Rutgers University. A total of 128 participants attended the conference, which kicked off with two short courses: A Primer on Spatial Transcriptomics Analysis taught by Dr. Joon Sang Lee from Sanofi and Making Projects Work Better with R taught by Max Kuhn from Posit. Day one concluded with the ASA Presidential Address delivered by Dr. Ji-Hyun Lee. Dr. Lee shared how statistical thinking and leadership drive scientific advancements and patient care. On the second day of the conference, Daniel Lee from Teamworks gave an engaging keynote talk titled "Beyond the Box Score: Bayesian Models for Evaluating Player Performance". Daniel explored how Bayesian models provide a deeper, more nuanced evaluation of athletic performance by incorporating rich, granular data.

The NCB 2025 technical program included four tracks: Chemistry, Manufacturing, and Controls (CMC); Discovery and Biomarkers; Safety and Pharmacology; and Data Sciences and Emerging Tools.

The CMC track hosted 1 invited speaker, 1 panel discussion, 6 contributed speakers, and 8 posters. Peter Goos from KU Leuven gave an invited talk on optimal experimental designs for process robustness studies while Yiming Peng from Genentech led a discussion panel on bridging pharma and medical device technologies through collaborative statistical practices. The contributed talks led to some engaging discussions and focused on topics such as dilution strategies for genetic medicines, shelf-life estimation and internal release limits using Bayesian methods, setting acceptance criteria for gage R&R studies, statistical assessment for analytical comparability studies, leveraging experimental databases to inform OMARS experimental designs, and using Bayesian methods to address common data challenges in CMC.

The Discovery/Biomarker track sponsored 2 invited speakers, 6 contributed speakers, and 6 contributed posters. Dr. Michael Lingzhi Li from Harvard Business School gave an invited talk on statistical inference for heterogenous treatments defects discovered by machine learning in randomized experiments, while Veavi Chang from Eli Lilly gave a second invited talk on comparative transcriptional profiles of preclinical lupus models and their relevance to human diseases. The contributed talks focused on applicable methodology for daily practitioners, examples of using data to answer questions, and details of specific issues that arise in this track within industry.

The safety & pharmacology track hosted 2 invited speakers, 3 contributed talks and 1 poster. The track showcased the breadth of nonclinical areas in which statisticians are innovating and adding value. These talks covered using Bayesian statistics for sample size reduction, simulations for choosing an optimal experimental design for cardiovascular safety studies, a comparison of methods for early-stage prediction of drug-induced liver injury, an overview of current methodology and workstreams for using virtual control groups in preclinical safety assessment, and how innovative statistics education within companies can maximize the scientific impact of statisticians. Even though these talks all covered different application areas, a common theme that emerged was the value in collaborating with other statisticians and subject-matter experts to ensure that rigorous and scientifically beneficial statistical approaches and methods will be adopted.

The Data Sciences and Emerging Tools track hosted 2 invited talks, 3 contributed talks, and 1 poster. The track brought together a set of talks that highlighted how emerging statistical and ML/AI methods are reshaping the pharmaceutical pipeline, all the way from discovery and preclinical research through development and manufacturing. Common threads across topics included flow cytometry analysis, modern tools for preclinical translation, quality-document retrieval, GenAI, formulation analytics, and causal inference for manufacturing: the need for trustworthy, data-driven tools that can handle complexity and scale (or lack of), the centrality of rigorous statistical thinking in principled application of modern AI methods, and an emphasis on integration into real life workflows as opposed to chasing benchmarks. Together, the discussions showed that this is a field moving toward methods that both enable leading-edge analyses and

strengthen confidence in the insights that guide critical scientific and operational decisions.

The student outreach section was led by a team of five committee members. It featured discussions on career opportunities in nonclinical statistics and included student presentations to the NCB community. The highlight was a one-hour panel on career paths in nonclinical statistics for students. The student outreach section also hosted career opportunities talk in nonclinical statistics and student presentations. Three oral presentations and one poster presentation were given by students. The best oral presentation was awarded to Mahan Dastgiri from Rutgers University for her talk titled "Differential Projection Pursuit: A machine learning method to find regions with maximal difference between distributions" and was accompanied by a cash prize. Each of the student presenters (oral/poster) received a statistical book. Additionally, travel stipends to students were awarded to facilitate their participation.

Finally, the 2025 Stan Altan Best Nonclinical Biostatistics Paper Awards were also announced during the conference. The awards are listed in order below.

1st Place: Chau, J., Altan, S., Burggraeve, A., Coppenolle, H., Kifle, Y. W., Prokopcova, H., Van Daele, T., Sterckx, H. (2023). A bayesian approach to kinetic modeling of accelerated stability studies and shelf life determination. Aaps Pharmscitech, 24(8), 250.

2nd Place: Li, D., Garren, J., Mangipudy, R., Martin, M., Tomlinson, L., & Vansell, N. R. (2024). Statistical applications of virtual control groups to nonrodent animal toxicity studies: An initial evaluation. Regulatory Toxicology and Pharmacology, 154, 105733.

3rd Place: Mallick, H., Chatterjee, S., Chowdhury, S., Chatterjee, S., Rahnavard, A., & Hicks, S. C. (2022). Differential expression of single-cell RNA-seq data using Tweedie models. Statistics in medicine, 41(18), 3492-3510.

Finally, the ASA-BIOP NCB Best Student Presentation was awarded to Mahan Dastgiri from Rutgers University for her talk on Differential Projection Pursuit: A machine learning method to find regions with maximal difference between distributions.

The organizing committee of the NCB Conference along with the Nonclinical Biostatistics Leadership Forum and Steering Committee are looking forward to the 10th anniversary of this biennial conference, which will take place in the summer of 2027.

HIGHLIGHTS FROM THE 13TH INTERNATIONAL CONFERENCE ON MULTIPLE COMPARISON PROCEDURES — A SUCCESSFUL GATHERING IN PHILADELPHIA

Jie Chen (Taimei), Dror Rom (Prosoft Inc), Wenjin Wang (Pfizer Inc)

Upper-left: Introductory remarks by Professor Sanat Sarkar; upper-right: Keynote speech by Professor Emeritus Yoav Benjamini; bottom-left: Keynote speech by Professor Mark van der Laan; and bottom-right: keynote speech by Dr. Florian Klinglmueller

The 13th International Conference on Multiple Comparison Procedures (MCP2025) took place from August 12 to 15 at Temple University in Philadelphia. Commemorating three decades since the seminal work of Benjamini and Hochberg introduced the False Discovery Rate (FDR), the conference brought together more than 120 statisticians and research scientists from around the world.

The program opened with welcome remarks by Professor Sunil Wattal, Associate Dean of Research and Doctoral Programs at the Fox School of Business. Professor Sanat Sarkar then offered brief remarks before introducing Professor Emeritus Yoav Benjamini of Tel Aviv University, who delivered the opening keynote address. In his lecture, Professor Benjamini reflected on the emergence of FDR and its impact on medical research, highlighted how major scientific advances have shaped both past and present developments in FDR methodology, and shared his perspective on future challenges, particularly those posed by Big Data and generative AI—that call for continued refinement of FDR concepts and methods.

On Day 2, Professor Mark J. van der Laan of the University of California, Berkeley delivered the second keynote speech. He traced the development of targeted learning and demonstrated its application to multiple testing in causal inference with real-world evidence. On Day 3, Dr. Florian Klinglmueller, Head of the Expert Group Statistics at the Austrian Agency for Health and Food Safety in Vienna started the third keynote speech, who discussed current regulatory challenges and methodological perspectives on multiplicity in confirmatory clinical trials.

Preceding the main conference, three short courses were offered that attracted many graduate students and statisticians from pharmaceutical industries:

- An introduction to graphical testing procedures for group-sequential designs, instructed by Dr. Michael Grayling and Dr. Yevgen Tymofyeyev (Johnson & Johnson)
- Adaptive sequential design for phase 2/3 seamless combination and for multiple comparisons, instructed by Dr. Ping Gao (Innovatio Statistics)
- Good Software Engineering Practice for R Packages, instructed by Daniel Sabanes Bove (RCONIS)

The scientific program featured 24 parallel sessions with more than 90 speakers presenting on a wide range of topics in multiple comparisons and multiple testing, including FDR control, familywise error rate control, causal inference with real-world data, regulatory perspectives on multiplicity, graphical approaches, group sequential designs, platform trials, conformal inference, e-values, online inference, and ranking and selection methods.

MCP2025 was organized by the International Society for Biopharmaceutical Statistics (ISBS) and sponsored by the Department of Statistics, Operations, and Data Science, and the Data Science Institute of Temple University; the Biopharmaceutical Section of the American Statistical Association (ASA); the Philadelphia Chapter of the ASA; Prosoft Clinical; Advanced Medical Services; Springer Publishing; and DuBu Research. The conference was a resounding success with strong support of the other committee members such as Scientific Program Committee, local volunteers, Temple alumni and graduate students --- including Qin Liu, Yanping Liu, Katie Pheysey, Fang Liu, Aiying Chen, Li He, and Frank Fan --- as well as Alan F. Karr and Ana Omana, whose outstanding assistance ensured seamless conference logistics.

SUMMARY OF ASA BIOP SECTION'S VIRTUAL DISCUSSION WITH REGULATORS ON DESIGN AND ANALYSES CONSIDERATIONS IN THE EVALUATION OF CONTRIBUTION OF EFFECT IN RANDOMIZED CANCER CLINICAL TRIALS

Rajeshwari Sridhara (FDA), Olga Marchenko (Bayer), Qi Jiang (Pfizer), Brittany Mckelvey (LUNGevity Foundation), Yiyi Chen (Pfizer), Gautam Mehta (FDA)

On April 8, 2025, the American Statistical Association (ASA) Biopharmaceutical Section (BIOP) and LUNGevity Foundation hosted a virtual forum to discuss Design and Analyses Considerations in the Evaluation of Contribution of Effect in Randomized Cancer Clinical Trials. This forum was part of a series conducted under the guidance of the U.S. Food and Drug Administration (FDA) Oncology Center of Excellence (OCE)'s Project SignifiCanT (Statistics in Cancer Trials). The goal of Project SignifiCanT is to advance cancer drug development through collaboration and engagement among various stakeholders in the design and analysis of cancer clinical trials. The discussion was organized jointly by the ASA BIOP Statistical Methods in Oncology Scientific Working Group, the FDA OCE, and LUNGevity Foundation.

This discussion is a continuation of two prior discussions held in August 2023 and April 2024. The 2023 discussion focused on design considerations for evaluating the contribution of effect for each component in combination therapy, while the 2024 discussion centered on the contribution of effect for each phase in a sequence of treatments. Recently, Korn EL et.al. (2024) demonstrated that in a three-arm study of combination therapy (AB), monotherapy (A), and control (C), it is crucial to conduct formal testing of AB vs. A, in addition to comparing AB vs. C and A vs. C, to support use of combination therapy. This type of comparison may also be applicable in evaluating the contribution of phases (CoP) in a sequence of treatments, wherein it is important to assess the perioperative regimen vs. neoadjuvant only or the perioperative regimen vs. adjuvant therapy, in addition to comparing perioperative vs. control, neoadjuvant only vs. control, adjuvant only vs. control to determine if the entire perioperative regimen is necessary. The current forum (2025) discussed the advantages and disadvantages of this approach with multi-disciplinary experts, along with alternative design and analysis options to facilitate the evaluation of the contribution of effect for each component or phase.

The speakers/panelists* for the discussion included members of the BIOP Statistical Methods in Oncology Scientific Working Group representing pharmaceutical companies, representatives from international regulatory agencies (FDA, Health Canada (HC), Medicines and

*** Speakers/ Panelists:**

Dr. Keaven Anderson (Merck), Dr. Michael Coory (TGA, AU), Dr. Boris Freidlin (NCI, NIH), Dr. Tim Friede (Medical University of Göttingen), Dr. John Heymach (University of Texas, MD Anderson Cancer Center), Dr. Qi Jiang (Pfizer), Mr. Stephen Lane (Bristol Myers Squibb), Mr. Barry Nelson (LUNGevity, Patient Advocate), Dr. Gautam Mehta (FDA), Dr. Pallavi Mishra-Kalyani (FDA), Dr. Brittany McKelvey (LUNGevity), Dr. Olga Marchenko (Bayer), Mr. Andrew Raven (Health Canada), Dr. Khadija Rerhou Rantell (MHRA, UK), Dr. Gary Rosner (Johns Hopkins & FDA), Dr. Satrajit Roychoudhury (Pfizer), Dr. Rajeshwari Sridhara (FDA), Dr. Yevgen Tymofyeyev (Johnson & Johnson), Dr. Jonathon Vallejo (FDA).

Healthcare products Regulatory Agency (MHRA), and Therapeutic Goods Administration (TGA)), clinicians, academicians, patient advocates, and expert statisticians. In addition, over 100 participants attended the virtual meeting, including representatives from other international regulatory agencies (European Medicines Agency (EMA), Brazilian Health Regulatory Agency (ANVIS), Health Sciences Authority (HAS), Singapore; Ministry of Health, Israel; Pharmaceuticals and Medical Devices Agency (PMDA), Japan). The discussions were moderated by the BIOP Statistical Methods in Oncology Scientific Working Group co-chairs, Dr. Olga Marchenko from Bayer and Dr. Qi Jiang from Pfizer; and Dr. Rajeshwari Sridhara, consultant from OCE, FDA.

In the introductory presentation, the presenter from OCE leadership emphasized the importance of demonstrating the contribution of effect for combination therapies in randomized cancer clinical trials. Factorial designs (A vs. B vs. AB vs. Control [Standard of Care]) are ideal for evaluating combination therapies but are often limited in feasibility due to the required large sample size. The presenter summarized the two relevant previous discussions held in August 2023 and April 2024. The 2023 discussion focused on establishing efficacy and safety of combination therapies while exposing the least number of patients to potentially less effective monotherapy. It was agreed that overtreatment is a concern for combination therapies and data from early trial phases could inform later phase 3 trial designs on patient exposure to the different regimens. The 2024 forum discussed design considerations, including innovative designs such as SMART design, in assessing contribution of a phase for perioperative trials with neoadjuvant and adjuvant treatment phases. The presenter outlined specific points for panelists from academia, industry, and regulatory agencies to consider and discuss.

The first speaker from academia presented a practical 3-arm "AB-A-C" design (AB vs. A vs. control) in evaluating combination therapies involving experimental drugs A and B. A recent analysis revealed that most trials using the AB-A-C design lacked a formal statistical comparison of AB vs. A, leading to ambiguous treatment recommendations regarding if the combination treatment was more efficacious than the single agent (Korn EL et.al., 2025). To facilitate best practices, three analytical strategies (strawman, sequential and parallel testing) were assessed through simulations, which demonstrated that sequential and parallel strategies both effectively control type I error. When drug B is likely to add more toxicity, parallel strategy is preferred to minimize overtreatment. When drug B has modest toxicity, sequential strategies should be used to maximize the probability of correct treatment recommendations. The speaker recommended employing a sufficiently powered "AB-A-C" design, testing AB vs. A. This test should be performed after demonstrating superiority of both drugs to the control, controlling for multiple comparisons, and choosing sequential or parallel testing strategies based on the anticipated toxicity level of the B component.

The second speaker from an academia presented innovative trial designs for effectively evaluating the CoP in perioperative combination therapies. The proposed designs included an initial randomization before neoadjuvant treatment and surgery, with safety and efficacy results from the neoadjuvant phase supporting a potential accelerated approval based on pathological complete response (pCR) for the neoadjuvant phase alone. This is followed by a second randomization post-surgery to evaluate the adjuvant component and full perioperative regimen using event-free survival (EFS) to support traditional approval of either the neoadjuvant therapy alone or the full perioperative regimen, depending on the EFS results. The speaker highlighted that the sample size required for such designs could be substantial to achieve adequate power, specifically in the adjuvant phase after the second randomization, given that the anticipated patient dropout rate after surgery is approximately 33% or higher, resulting in a reduced sample size for the adjuvant phase.

The discussion covered the advantages and disadvantages of these designs, with the speaker arguing that they could provide significant net benefits to patients with resectable non-small cell lung cancer.

The key points raised in the panel discussion following the presentation were:

- For AB-A-C design, some panelists supported flexible estimation-based approaches, while others argued that formal comparison between AB and A is critical, especially to prevent overtreatment when added benefit is uncertain.
- There was strong overall support for re-randomization after surgery in the perioperative setting to assess CoP, although concerns were raised about operational challenges.
- Adaptive designs may be employed to add flexibility and potentially reduce required sample size for multi-arm trials.
- Results of early-phase trials could be useful in understanding the biological effects of different components in combination therapy and in gathering meaningful evidence to better inform phase 3 designs.
- A transparent method for comprehensively assessing different clinical outcomes, including efficacy, toxicity and tolerability, is needed to make overall recommendations.
- It is desirable not to overcomplicate the trial design by attempting to answer too many questions in a single trial.
- Better communication with patients regarding treatment expectations, risks, and eligibility is essential.
- There is continued interest in balancing practicality of trial designs with statistical rigor, ensuring that data are of high quality and adequate for regulatory decision-making while avoiding over treatment as well as overly burdensome trials.

This forum provided an opportunity to have open scientific discussion among a diverse multidisciplinary stakeholder group – clinicians, and statisticians from academia and pharmaceutical companies, patient advocates, and international regulators- focused on emerging statistical issues in cancer drug development.

Acknowledgement: Authors thank Joan Todd (FDA) and Syed Shah (FDA) for technical support.

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SUMMARY OF ASA BIOP SECTION'S VIRTUAL DISCUSSION WITH REGULATORS ON STATISTICAL CONSIDERATIONS IN THE DESIGN OF RANDOMIZED PRAGMATIC CANCER TRIALS

Rajeshwari Sridhara (OCE, FDA), Olga Marchenko (Bayer), Qi Jiang (Pfizer), Elizabeth Barksdale (LUNGevity Foundation), Yiyi Chen (Pfizer), Donna Rivera (FDA), Marc Theoret (FDA)

On July 16, 2024, the American Statistical Association (ASA) Biopharmaceutical Section (BIOP) and LUNGevity Foundation hosted a virtual forum to discuss Statistical Considerations in the Design of Randomized Pragmatic Cancer Trials. This forum was part of a series conducted under the guidance of the U.S. FDA Oncology Center of Excellence's Project **SignifiCanT** (Statistics in Cancer Trials). The goal of Project SignifiCanT is to advance cancer drug development through collaboration and engagement among various interested parties in the design and analysis of cancer clinical trials. The discussion was organized jointly by the ASA BIOP Statistical Methods in Oncology Scientific Working Group, the FDA Oncology Center of Excellence (OCE), and LUNGevity Foundation.

Traditional prospective randomized clinical trials in oncology are designed to maximize the likelihood of demonstrating efficacy of an experimental treatment by testing it in a controlled setting. Such trials in oncology are often associated with significant monitoring, assessments, tests, and clinical follow-up visits that can be burdensome to trial participants, investigators, and sponsors. In contrast, pragmatic randomized clinical trials are designed to evaluate the effectiveness of an experimental treatment in routine clinical practice conditions. The Oncology Center of Excellence at the FDA has initiated Project Pragmatica with the objective of advancing evidence generation for approved oncology medical products, including medications evaluated as supplemental New Drug Applications (sNDA). This project explores innovative trial design approaches that introduce functional efficiencies and patient centricity through integration with routine clinical practice, by introducing appropriate pragmatic design elements. This open forum discussion among multidisciplinary experts focused on the statistical considerations and challenges in implementing pragmatic elements, including the choice of primary and secondary endpoints that are most important to patients, examining the impact on data collection and minimizing variability in measuring outcomes.

*** Speakers/ Panelists:**

Dr. Keaven Anderson (Merck), Dr. Elizabeth Barksdale (LUNGevity Foundation), Dr. Scott Berry (Berry Consultants), Dr. Alex Bliu (Health Canada), Dr. Somak Chatterjee (FDA), Dr. Michael Coory (TGA, AU), Dr. Leonardo Costa (ANVISA, BR), Dr. Boris Freidlin (National Cancer Institute), Prof. Liz Garrett (ASCO), Prof. Susan Halabi (Duke), Dr. Qi Jiang (Pfizer), Dr. Olga Marchenko (Bayer), Dr. Timil Patel (FDA), Dr. Khadija Rantell (MHRA, UK), Prof. Mary Redman (Fred Hutch Cancer Center), Dr. Donna Rivera (FDA), Dr. Yuan-Li Shen (FDA), Dr. Rajeshwari Sridhara (FDA), Dr. Marc Theoret (FDA), Dr. Zachary Thomas (Lily), Dr. Andrew Thomson (EMA), Dr. Biao Xing (Pfizer)

The speakers/panelists* for the discussion included members of the BIOP Statistical Methods in Oncology Scientific Working Group representing pharmaceutical companies, representatives from international regulatory agencies (Food and Drug Administration (FDA), European Medicines Agency (EMA), Health Canada (HC), Medicines and Healthcare products Regulatory

Agency (MHRA), Therapeutic Goods Administration (TGA), and Brazilian Health Regulatory Agency (ANVIS)), clinicians, academicians, and expert statisticians. In addition, over 100 participants attended the virtual meeting, including representatives from other international regulatory agencies (Health Sciences Authority (HAS), Singapore; Ministry of Health, Israel; Pharmaceuticals and Medical Devices Agency (PMDA), Japan). The discussions were moderated by the BIOP Statistical Methods in Oncology Scientific Working Group co-chairs, Dr. Olga Marchenko from Bayer and Dr. Qi Jiang from Pfizer; Dr. Elizabeth Barksdale from LUNGevity Foundation; and Dr. Rajeshwari Sridhara, consultant from OCE, FDA.

In the introductory presentation, the OCE leadership discussed the rationale for considering pragmatic elements in trial design to increase use of pragmatic clinical trials in oncology research. The presenter contrasted traditional randomized clinical trials, conducted in controlled settings and in populations where rigid eligibility criteria often apply, with randomized pragmatic trials that evaluate treatments in routine clinical care where broader eligibility and routine assessments may be more appropriate. Pragmatic clinical trials can reduce trial burden, enhance representativeness of the US intended use populations, and bring trials to patients in their communities. The presentation highlighted that FDA OCE has initiated Project Pragmatica to explore pragmatic design elements in trials for approved oncology medical products, and the "Project 5 in 5" crowdsourcing initiative seeking ideas for clinically meaningful questions in oncology that may be best addressed using pragmatic elements over the next five years. The key considerations for academia, industry, and regulatory panelists included the benefits and limitations of pragmatic cancer trials, statistical challenges in design, conduct, and analysis, potential barriers, and regulatory perspectives on trials with pragmatic elements. This comprehensive introduction set the stage for a deeper discussion on the implementation and implications of pragmatic trials in oncology.

A speaker from academia, presented the Pragmatica Lung Trial (SWOGS2302), a pragmatic clinical trial for patients with advanced non-small cell lung cancer (NSCLC) who previously received chemotherapy and immunotherapy. Launched in March 2023, the study compares standard of care to pembrolizumab and ramucirumab, with overall survival as the primary endpoint. This trial includes pragmatic elements such as, broader eligibility criteria, reduced data collection including selective safety data reporting, and a focus on care in routine clinical practice. Such pragmatic elements aim to reduce participation burdens and empower investigators to treat patients in routine care without additional burden. At the time of the presentation on July 16, 2024, 544 patients had been enrolled towards a target of 800 participants (616 events). Notably, the study has demonstrated success in rapidly enrolling a representative patient population.

The key points raised in the panel discussion following the presentation were:

- Pragmatic oncology trials reduce design complexity and patient burden by incorporating routine clinical practice elements that could potentially incentivize patients to stay on trials.

- Design decisions to include pragmatic elements depend on the clinical context, route of administration and available prior knowledge, especially about the safety of the drug being investigated.

- Both ASCO and NCI have initiated ongoing trials that include de-centralized and pragmatic elements.

- Potential challenges of pragmatic oncology trials include maintaining randomization, ensuring data quality, appropriate endpoint selection, evaluation of variability due to routine clinical care and variability that may induce measurement error. Interpretation of results could be challenging if there is too much variability. Molecular testing may not be always feasible.

- Most often for pragmatic trials, overall survival is the preferred endpoint. The use of PFS or ORR are often not appropriate due to assessment feasibility (e.g. RECIST) and variability in routine clinical care settings. Alternative endpoints such as time to treatment discontinuation are being explored.

- Accounting for higher variability and potential loss to follow-up leads to larger sample size requirements to detect treatment effects in heterogeneous populations. Statistical considerations should include advanced analytical methods to handle heterogeneity, sensitivity analyses, and transparent reporting of variability sources. The estimand framework can be crucial for interpretation and generalizability of results.

- Design considerations should include all interested parties (regulatory agencies, physicians, and patients). Regulators are open to consideration of innovative design including randomized trials with pragmatic elements, especially for already approved medical products and post-approval studies. Some regulators expressed concerns on suitable candidate drugs appropriate for this design, limited safety data collection, and the trade-off between the pragmatic nature of broader inclusion criteria and explanatory need for answering specific clinical questions.

This forum provided an opportunity to have open scientific discussion among a multidisciplinary scientific group – clinicians, epidemiologists, and statisticians from academia and pharmaceutical companies, patient advocates, and international regulators- focused on emerging statistical issues in cancer drug development.

Acknowledgement: Authors thank Joan Todd (FDA) and Syed Shah (FDA) for technical support.

STATISTICS IN PHARMACEUTICALS 2025: CONFERENCE SUMMARY

UNIVERSITY OF CONNECTICUT, STORRS, CT 06269 | AUGUST 13-15, 2025

Ming-Hui Chen (University of Connecticut)

The Statistics in Pharmaceuticals (SIP) conference, also known as the Conference for Students, was conceived by Dr. Ming-Hui Chen from the UConn, along with Qiqi Deng (Moderna) and Dooti Roy (Boehringer Ingelheim Inc). The conference aims to introduce students and professionals in quantitative fields, particularly statistics and data sciences, to drug development and careers in the pharmaceutical industry and regulatory agencies. The SIP conference serves as an excellent platform for industry, academic, and regulatory organizations to collaboratively enhance the role of statistics in drug development.

In the summer of 2025, the 8th SIP conference was successfully held at UConn again. This year, Dr. Ofer Harel, Dean of the College of Liberal Arts and Sciences (UConn) delivered the opening remarks. The conference featured four keynote speakers: Dr. Xun Chen (AbbVie), Dr. Lei Nie (FDA), Dr. Dean Follman (NIAID) and Dr. Yili Pritchett (MindMed). They offered their insights on artificial intelligence, rare diseases, vaccine trials, and adaptive designs. Additionally, five comprehensive plenary sessions focused on career development in biostatistics, statistical programming, and data science within the pharmaceutical and regulatory sectors. For the second year in a row, SIP offered short courses on its pre-conference day. The three short courses focused on artificial intelligence (Dr. Mark Chang), meta-analysis (Dr. Zhaohui Liu), and Bayesian adaptive designs (Dr. Jack Lee).

In addition to the main conference, the SIP conference features a scholarship program and a student poster competition. This year, we received 33 scholarship applications and granted 8 awards. The recipients were Gogoate Lemea (University at Buffalo, The State University of New York), Yunyi Wang (The University of Texas Health Science Center at Houston), Dennis Baidoo (University of New Mexico), Anika Islam (Drexel University), Shrijana Gautam (University of Connecticut), Oluwafunto

Aladekomo (The University of Texas Health Science Center at Houston), and Yuzhou Peng (Brown University).

The poster competition drew 23 students across various educational levels. Both scholarship applications and poster submissions reached all-time highs for the conference. The poster award recipients were Chuxin Chen (University of North Carolina at Chapel Hill), Yihan Tang (University of North Carolina at Chapel Hill), Xin-Wei Huang (University at Buffalo, The State University of New York), Himani Yadav (Boston University), Zhe Guan (University of Connecticut), and Romario Joseph (Boston University).

The organizing committee for SIP 2025 includes members from Gilead, Takeda, BMS, FDA, UConn, Pfizer, BU, Amgen, Cytel, UMich, Alexion, Vertex, Moderna, Servier, Astellas, OSU, Lilly, Merck, Regeneron, and UMass Dartmouth. This year was the first SIP to introduce a mentoring program, where 14 experienced professionals volunteered to meet with 35 participating students over an extended lunch period. Participants enjoyed expanding their networks, fostering stronger relationships, and discussing specific career-development questions in a friendly social atmosphere. The mentoring program was a fantastic success, organized by our three student committee members: Ruoyuan Qian (Ohio State University), Vindyani Herath (Boston University) and Leo Li (Boston University).

We extend sincere gratitude to our sponsors this year: Amgen, ASA Biopharmaceutical Section, BeOne, Gilead, Lotus Group, Pfizer, Regeneron, and Servier. For SIP 2025, 42 of 98 registrants are members of ASA BIOP.

We are also deeply appreciative of the UConn volunteers - Max Sun, Sana Gupta, Zhengqi (Elsa) Gu, Shike Xu, Zhe Guan, Min Hee Seo, and Mingye Chen (webmaster), as well the supporting UConn staff, Juliet Kapsis and Tracy Burke. Their contributions have been invaluable, and without their dedication, the conference would not have been possible.

We are proud of the achievements of SIP 2025 and are committed to further enhancing the activities for next year. For more information, please visit *https://stat4pharma.org/index.html*

RECAP: IABS 11TH ANNUAL STATISTICS WORKSHOP

Jia Liu (Pfizer), José G. Ramírez (Kite Pharma, a Gilead Company), Ruojia Li (Bristol Myers Squibb)

The 2025 IABS Statistics Workshop, held virtually from October 20-23, brought together leaders from industry and regulatory agencies to discuss the evolving role of statisticians in a data-driven and AI world. The central theme, "Big Tent Statistics", emphasized expanding the reach and visibility of statistical science, advocating for CMC statisticians as strategic partners in decision-making, and highlighting their unique contributions to drug development and manufacturing.

The workshop opened with a keynote address delivered by former ASA president Dr. Robert Rodriguez. He emphasized the most valuable statistical contributions come from clear, helpful explanations that make complex issues understandable and actionable. Statisticians must act as thinking and strategic partners, making their contributions visible and impactful to broader audiences.

Following the keynote, Day 1 featured three presentations under the theme 'Contribution & Differentiation'. James Garrett, Replicate! Statistical planning and analysis, highlighted how statistical principles improve outcomes and urged statisticians to broaden their roles through advocacy and adaptation. Garrett encouraged statisticians to differentiate themselves by articulating their value, building relevant toolboxes, and actively engaging with collaborators to address complex questions and organizational needs. Stan Altan, JJIM, explored how CMC statisticians can move beyond traditional service roles to become strategic partners in drug development. By integrating statistical rigor with process understanding, regulatory insight, and lifecycle thinking, Altan showed that statisticians deliver measurable business value through designed experimentation, Bayesian decision-making, and multivariate approaches, ultimately shaping the future of pharmaceutical quality. Mark DiMartino, Amgen, discussed the evolving landscape of data science in the pharmaceutical industry, positioning CMC statisticians as the original data scientists whose deep domain knowledge and advanced analytical skills remain essential. DiMartino highlighted the importance of advocating for the unique contributions of statisticians, demonstrating

Highlights:

- The IABS 11th Annual Statistics Workshop brought together statisticians and scientists from over 20 organizations across the pharmaceutical and biotech industries, as well as regulatory agencies, to spotlight the evolving role of CMC statistics in a data-driven world. The "Big Tent" theme encouraged statisticians to expand their influence, advocate for their value, and foster cross-disciplinary partnerships.
- Keynotes & presentations: The workshop featured a keynote address by former ASA president Dr. Robert Rodriguez and included 12 presentations; all centered on the theme: "Big Tent Statistics—Conveying the Importance of Statistical Contributions." Presentations were organized into four focused sessions: Contribution & Differentiation, Experimentation & Investigation, Collaboration & Recognition, and Innovation & Acceleration. Each session was further enriched by a dedicated panel discussion and two parallel breakout sessions. Collectively, these sessions showcased the unique value and impact of CMC statisticians in advancing drug development and manufacturing.
- Community Engagement and Impact: The workshop fostered a vibrant sense of community by bringing together statisticians and scientists from diverse backgrounds to share knowledge, best practices, and new ideas. It encouraged cross-disciplinary collaboration, highlighted the importance of advocacy and visibility for statistical contributions, and inspired attendees to broaden their impact both within their organizations and across the broader scientific community. This spirit of engagement not only strengthens professional networks but also reinforces the collective commitment to advancing the field and serving society through statistical excellence.

their impact on drug quality, regulatory compliance, and manufacturing excellence, and positioning them as indispensable partners in a data-driven world.

On Day 2 the session focused on "Experimentation and Investigation". Adam Rauk, Eli Lilly & Co., demonstrated how Bayesian hierarchical models can quantify platform knowledge and enhance experimental design, as shown in a Protein A purification process example. Integrating Bayesian statistics into design not only improves scientist engagement but also ensures that outcomes provide meaningful insights for collaborative teams. Rick Kramer, Ferring Microbiome Inc., explored the use of design of experiments (DoE) as a discovery tool in the development of live biotherapeutic products, emphasizing the importance of early and frequent collaboration to clarify goals, select optimal designs, and deliver clinical assets ahead of schedule in the complex landscape of microbiome research. David Ciciora, Regeneron, focused on empowering method subject matter experts (SMEs) through strategic collaboration with statisticians, illustrating how new regulatory guidance ICH Q2(R2) on assay validations creates opportunities to develop meaningful interval-based criteria for accuracy and precision. By leveraging historical data and fostering mutual understanding, statisticians can elevate their role as strategic partners and ensure scientifically sound, regulatory-compliant practices.

On Day 3, the "Collaboration & Recognition" session highlighted the essential role of statisticians as strategic partners throughout the product lifecycle. Bianca Teodorescu, UCB, described CMC statisticians as the backbone of development and lifecycle management, connecting departments and guiding statistical strategies from early development through commercial manufacturing. Their expertise supports process characterization, specification justification, and continuous improvement, ensuring robust quality by design. John Farris, Kyverna Therapeutics, emphasized that statisticians are most transformative when engaged early in project design, elevating decision quality, compressing timelines, and strengthening regulatory credibility. Lori McCaig, Stability Strategist & Expert (former Seagen/Pfizer), focused on the evolving partnership between stability scientists and statisticians, showing how collaboration and communication are vital for mutual understanding of challenges in stability data generation and evaluation. Statisticians should act as partners, collaborators, and leaders, driving risk-based stability approaches and technical programs. Alongside all the session speakers, Catherine Njue from Health Canada and Andreas Brandt from BfArM also joined the panel discussion, bringing valuable regulatory perspectives to the conversation.

On Day 4, the "Innovation and Acceleration" session spotlighted cutting-edge statistical approaches driving progress in pharmaceutical development. Christopher

Organizing Committee

- Ruojia Li – BMS (Co-Chair)
- Jia Liu – Pfizer (Co-Chair)
- José Ramírez - Kite Pharma, a Gilead Company (Co-Chair)
- Madinina Cox – IABS, France
- Camille Roux – IABS, France

Scientific Committee Members:

- Ruojia Li, Co-Chair – BMS
- Jia Liu, Co-Chair – Pfizer
- José Ramírez, Co-Chair – Kite Pharma, a Gilead Company
- Timo Bailer – Boehringer Ingelheim
- Stan Broskey – Merck
- Catherine Cheng – Novartis
- Jennifer Kirk – FDA
- Irina Gershgorin – Legend Biotech
- Ashley Giambrone – Regeneron
- Kristi Griffiths – Eli Lilly & Co.
- Cristian M. Oliva-Aviles – Genentech
- Oluyemi Oyeniran – Johnson & Johnson
- Laura Pack – Moderna
- Jayda Siggers – Health Canada
- Christopher Thompson – AstraZeneca
- Travis Wolter – Amgen

Their collective expertise and commitment made the 11th IABS Statistics Workshop possible, shaping a program that fostered collaboration, innovation, and scientific excellence.

Kot, AstraZeneca, presented Bayesian methods for qualifying flow cytometry in cell therapies, demonstrating how these techniques address complex analytical profiles and improve accuracy, precision, and regulatory alignment in method validation. Ji Young Kim, Takeda, introduced a Bayesian hierarchical kinetic Arrhenius model for shelf-life estimation and internal release limits, showing how optimal accelerated stability study design and market-specific modeling can reduce risk and improve product reliability, especially when accounting for real-world storage excursions. Shu Yang, Pfizer, showcased the use of interpretable machine learning to uncover nonlinear relationships between process variables and yield, enabling actionable insights and continuous improvement in commercial manufacturing through collaborative workflows with CMC statistician and process scientists. In addition to all the session speakers, Paula Russell from Health Canada and Bernard Francq from GSK joined the panel discussion, bringing further expertise and perspectives to the conversation.

For the full workshop agenda, visit the IABS website: 11th IABS CMC Statistics Workshop

The Organizing Committee of the 11th IABS Statistics Workshop was instrumental in bringing the event to life, ensuring its success through dedicated planning and coordination. The Scientific Committee, composed of experts from leading organizations, provided essential guidance and oversight for the workshop's scientific program:

Last, we deeply appreciate our generous sponsors:
- Gold sponsor: Moderna
- Silver sponsor: Pfizer
- Bronze sponsor: Bristol Myers Squibb.

The workshop fostered vibrant dialogue, highlighted the importance of early and strategic statistical engagement, and demonstrated how collaborative problem-solving drives scientific and operational excellence. As the field continues to advance, the IABS Statistics Workshop remains a vital forum for sharing best practices, building partnerships, and shaping the future of CMC statistics. We look forward to building on this momentum with new topics and broader participation at next year's event, and invite all participants to stay engaged, share their experiences, and help make the next IABS Statistics Workshop even more impactful.

ASA BIOPHARMACEUTICAL SECTION SCHOLARSHIP AWARD WINNERS – 2025

Francis Rogan (Merck)

We are excited to once again recognize the student scholarship award winners from the 2025 Joint Statistical Meetings (JSM), held August 2–7 in Nashville, Tennessee. The scholarship committee—Bruce Binkowitz (2025 Chair, Arcutis Biotherapeutics), Rebbecca Wilson (Johnson & Johnson), Tony Jiang (Amgen), Cindy Chen (Vanderbilt University Medical Center), Rebecca Silva (AstraZeneca), and Yue Song (Merck)—evaluated each application across three key areas:

1. Service and Leadership
2. Impact and Innovation
3. Performance and Achievements

Of 50 submissions representing 34 universities, seven outstanding winners were selected during the Biopharmaceutical Section mixer. We extend our sincere thanks to everyone who participated and offer our heartfelt congratulations to the award recipients!

Ever wondered what's next for our award winners? We asked them about their plans after graduation!

Bella Qian, Harvard University

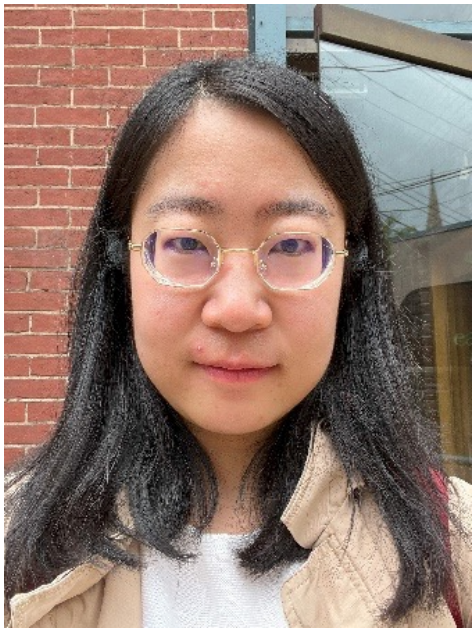
"I hope to leverage my biostatistics knowledge to drive healthcare forward and advance healthcare accessibility and innovation. After I graduate, I plan to pursue opportunities in biopharmaceutical organizations or regulatory agencies where I can support critical research initiatives, strengthen public health systems, and give back to communities."

Emily Alger, Institute of Cancer Research, United Kingdom

"Following my graduation later this year, I am so excited to continue my contribution to the biostatistics community as I actively pursue postdoctoral research opportunities in Bayesian methods."

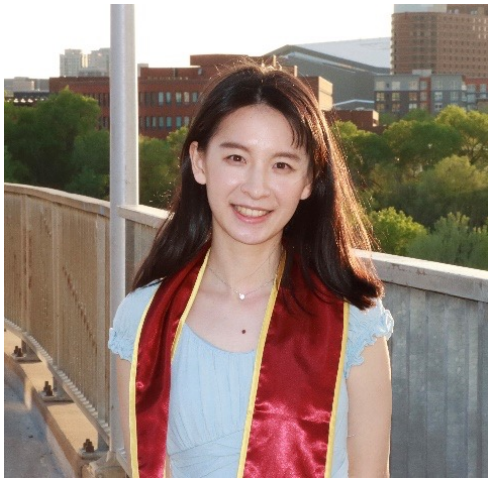
Jack Wolf, University of Minnesota School of Public Health

"After graduation, I will join the University of Pennsylvania Center for Causal Inference as a postdoctoral researcher."



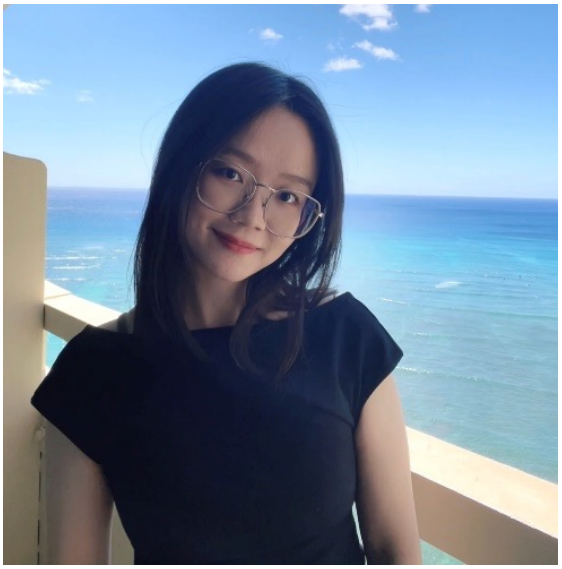
Na Bo, University of Pittsburgh

"I will be starting my new position as a tenure track assistant professor in biostatistics at Virginia Commonwealth University this July and continue to work on biopharmaceutical research including subgroup identification, biomarker selection and causal inference."



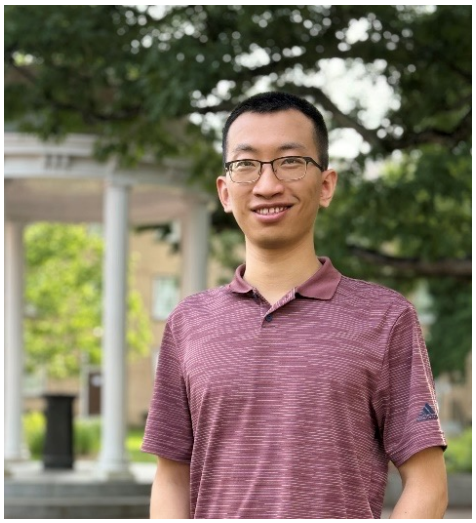
Peijun Liu, University of California, San Francisco

"My plan after graduation is landing a position in the biotechnology industry, specifically focusing on neuroscience or aging research."



Jiachen Chen, Boston University School of Public Health

"I aim to develop and apply statistical methodology to support healthy aging and translational biopharmaceutical research."



Tianhao Song, University of North Carolina at Chapel Hill

"I am seeking a post-doc opportunity in preparation for an academia career in the area of clinical trials and biomedical analysis "

Once more, congratulations to all the winners! The future is shining bright, and we're thrilled to see what's next for them.