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Announcements
- Please check our website for details. (https://community.amstat.org/sectiononstatisticsin/genomicsandgenetics/meetings/upcomingevents)
- Webinar: Multivariate Integration of Multi-Omics Data. 10/24/2022 | 5-6 PM (EASTERN). HTTPS://US02WEB.ZOOM.US/WEBINAR/REGISTER/WW_MATDLDN7RNUGRD4OJ0V5TG

Contents
Get connected ........................................................ 1
Announcements ...................................................... 1
SSGG Business Meeting at JSM 2022 ................... 2
Forum for Justice, Equity, Diversity, and Inclusion (JEDI)................................................................. 4
Reflection and Tips on the Job Search Experience 5
Future Webinar ....................................................... 9
Student Paper Award Competition......................... 10
Call for Topic-contributed Session Proposals ...... 11
Join US ................................................................... 12
Executive Committee ............................................ 12
Member Engagement Committee ......................... 12
Contact Us ............................................................ 12
Keep Connected ................................................... 12
SSGG Business Meeting at JSM 2022

We held our annual business meeting on August 9th via Zoom. For those of you who missed the meeting, below are the highlights.

The Section Chair, Dr. Michael Wu, welcomed the members to the meeting. Participants of the meeting gave brief self-introduction around the table.

1. SSGG Student Paper Awards (Ni Zhao)

The call for application was sent out in October 2021; the submission deadline was December 15, 2021; and the results were available by January 15, 2022. We received 37 submissions for the 2022 ASA Section on Statistics in Genomics and Genetics’ Distinguished Student Paper Competition. Each paper was reviewed by 4-5 referees separately, and 25 referees helped with the reviews, each reviewing 3-6 submissions. Based on reviews, the following five winners were selected in no particular order:

- Nam Nguyen, Department of Statistics, Rice University. Paper: “Bayesian Estimation of a Joint Semiparametric Recurrent Event Model of Multiple Cancer Types with Applications to the Li-Fraumeni Syndrome”

- Luxiao Chen, Department of Biostatistics, Emory University. Paper: “Incorporating cell type hierarchy improves cell type-specific differential analyses in bulk omics data.”

- Jiangcheng Miao, Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison. Paper: “A quantile integral linear model to quantify genetic effects on phenotypic variability.”

- Kyle Coleman, Department of Biostatistics, Epidemiology, and Informatics, University of Pennsylvania. Paper: “SpaDecon: cell-type deconvolution in spatial transcriptomics with transfer learning.”

- Xihao Li, Department of Biostatistics, Harvard University. Paper: “Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole-genome sequencing studies.”

We acknowledge the volunteer judges for the competition: Yijuan Hu (Emory), Wei Sun (FHCRC), Han Chen (UTHSCH), Jennifer Sinnott (OSU), Jun Chen (Mayo Clinic), Lynn Lin (PSU), Mengjie Chen (Chicago), Xuefeng Wang (Moffitt), Zhigang Li (UFL), Xiang Zhan (PKU), Debashree Ray (JHU), Anna Plantinga (Williams College), Ran Tao (Vanderbilt), Zhicheng Ji (Duke), Charles Kooperberg (FHCRC), Weiqiang Zhou (JHU), Wei Chen (UPMC), Hao Wu (Emory), Thomas Hoffmann (UCSF), Jung-Ying Tzeng (NCSU), Mingyao Li (UPenn), Dave Zhao (UIUC), Yuying Xie (MSU), Gen Li (Michigan), Davide Risso (Padova).

2. Report on 2022 Election Results (Michael Wu)

Dr. Michael Wu will become the Past-Chair in 2022. Dr. Nancy Zhang and Dr. Kimberley Siegmund will begin their terms as Section Chair and Program Chair, respectively, from January 2023. Dr. George Tseng and Dr. Xiang Zhou have been elected as the Chair-Elect and Program Chair-Elect, respectively, for 2024.

3. 2022 JSM SSGG Program Report (Lin Chen)

The SSGG section sponsored 12 sessions, including three invited/panel sessions, of which two were allocated, one was won from the competition, two topic-contributed sessions, 6 contributed paper sessions and one roundtable discussion at JSM 2022.

4. 2023 JSM SSGG Program Report (Kim Siegmund)

The SSGG section has been allocated three slots for invited sessions and three for topic-contributed sessions for JSM 2023. The submission deadlines for the invited and topic-contributed sessions were September 8, 2022, and December 8, 2022, respectively. The SSGG section encourages section members and colleagues to submit session proposals via the online system by the deadlines.
5. Treasurer Report (Li-Xuan Qin)

We had a balance of $4,493.44 from the Year 2021. This year, as of June 30th, we have a revenue of $14,329.16 and an expense of $2,000, resulting in a YTD fund balance of $16,822.60. This year’s increased revenue is mainly due to the successful “Deep Learning for Omics Data” workshop held in January 2022. The membership income for the first half of 2022 is 50% more than last year, implying a likely increase in membership. With the increased revenue, the section was able to expand the variety of paid activities, including (1) hosting a professional speaker to give a webinar on mentoring, (2) co-hosting a conference for honoring Prof. Shili Lin, and (3) ordering refreshment for serving at the section’s business meeting at JSM.

6. Membership Engagement Committee Report (Anna Plantinga representing Shili Lin)

The committee currently has a well-balanced membership representation, including members from various sectors (academia and industry) and career stages (senior, mid-career, junior, and students). It welcomes new members, with expectations to rotate off 2+ years old members.

The committee has established multiple communication channels beyond emails, including Facebook, Twitter, and LinkedIn. It has also successfully run virtual activities such as technical webinars and career development panels. More specifically, technical webinars are held monthly featuring speakers from both academia and industry; career development panels are organized on an ad-hoc basis, with one held in June 2022 (on the topic of grant writing and review), another in November 2022 (on the topic of manuscript writing), and more under planning (on topics of such as research collaboration and student internship application); a mentoring webinar was given by Dr. Ruth Gotian, a leadership coach and book author, in Feb 2022. The committee has also conducted a member survey with its results to be used for planning future events.

MEC evaluates the idea of a mentoring program by pairing mentors with mentees. Questions were raised on whether people are interested in volunteering as a mentor, what is expected from a mentor, and how to manage potential conflicts with a mentee’s home advisor. Suggestions were made on potential topics (such as industry readiness for potential career transition) and viable formats (such as limited-time mentoring at a webinar using breakout rooms with possibly multiple mentors per room).

7. Short-Course Topics: for JSM and external to JSM (Katerina Kechris and Nancy Zhang)

Dr. Kechris and Dr. Tseng have been actively planning for a short multi-omics course, with monthly meetings to work on the course materials. The meeting participants brainstormed on additional ideas; past survey ideas included causal inference and mendelian randomization.

Additional potential course topics were suggested on (1) handling biobank scale data, (2) meta-analysis for multiethnic populations, (3) how to teach URM, and (4) how to set up a docket container. Moreover, Dr. Alex Alekseyenko from the Medical University of South Carolina suggested a short course on how to wrangle data from All of US. However, concerns were raised about data access and data privacy issues. We may need to focus on summary statistics.

In terms of teaching style and organization, Yunhui Qi from Iowa State University provided feedback that Zoom is more tiring than in person and that it would be good to have a slower pace with more breaks. Related to this feedback, someone shared that UW Summer Institutes in Biostatistics had 1.5-hour modules in person and switched to 50min when online. Another feedback was to use Slack, rather than the Zoom chat box, for better organizing and archiving questions and answers. Dr. Ni Zhao from Johns Hopkins noted that the Zoom link and YouTube recording for the deep learning short course were not password protected, which may not be fair for the paid participants; others commented that that concern should be weighed with SSGG’s impact. We can ask instructors about their comfort level in posting recordings.

8. Other Business: Diversity Initiatives, New Member Recruitment, etc.

Diversity Initiatives:
Some ideas were brainstormed, including a JSM topic-contributed session on diversity, biomarker research on kidney function, and causal inference research on health equity (e.g., the Kaiser Permanente model).

**New Member Recruitment:**
Prof. Xihong Lin led a roundtable discussion on the TopMed experience at JSM 2022. Future topics can include introducing genomics to non-genomics folks, how to use genetics/genomics and precision medicine, how statisticians work in industry, and how to assemble a data science team. Suggestions were made to invite people in the industry and regulatory agencies to be speakers or round-table leaders. Dr. Aida Yazdanparast from Illumina also suggested ideas on how to engage better industry members, one of which was to invite industry people to serve as mentors for students interested in going into the industry.

**Forum for Justice, Equity, Diversity, and Inclusion (JEDI)**

*Perspective: Informed Consent, Genetic Data, and Minority Populations*

Contributed by Katerina Kechriss (SSGG past Chair) ([KATERINA.KECHRIS@CUANSCHUTZ.EDU](mailto:KATERINA.KECHRIS@CUANSCHUTZ.EDU))

For many statisticians and data scientists, the majority of our time may be focused on data analysis. However, it is also imperative to understand and, when possible, get involved with aspects of study design and data collection, including the informed consent process. Informed consent is multi-tiered and dynamic, and not only does consent for current research need to be considered, but also consent for future research, consent for release of data into public databases, re-consent, and withdrawal from a study. When informed consent is improperly conducted, there can be serious consequences. The Tuskegee Syphilis Study is an example of a direct violation of ethical conduct and informed consent principles, resulting in the death of hundreds of men of a treatable disease.

Here I focus on informed consent for genetic studies and the consequences of improper or unethical practices on minority populations. Collecting genetic information has serious implications regarding privacy, as genetic data are personally identifiable information and used in other contexts besides research, including law-enforcement databases. Informed consent particularly in genetic research has been put in the spotlight recently in the popular media ("The DNA of Roma People Has Long Been Misused, Scientists Reveal" and "Ancient-DNA Researchers Set Ethics Guidelines for Their Work"), in addition to an important example from more than a decade ago ("Indian Tribe Wins Fight to Limit Research of Its DNA"). A common theme in these cases was improper or lack of consent in marginalized or under-represented populations and lack of awareness of cultural practices for human samples and remains.

In the case of the Roma people, a minority group in Europe subjected to discrimination for centuries, genetic data had been obtained and deposited in databases using unethical or questionable practices. Among other negative consequences, some databases became over-represented with Roma people; however, this could introduce bias in law enforcement searches of these databases for crime suspects. Here in the US, the case of the Havasupai tribe in Arizona, where samples were used for additional studies that were improperly consented, also had a negative consequence. Instead of increasing representation by more diverse groups, it resulted in mistrust of genetic research and decreased participation, as was the result of the Tuskegee Syphilis Study. Recent perspectives have addressed what needs to be done to rebuild trust and engage Indigenous and other under-represented groups ("A framework for enhancing ethical genomic research with Indigenous communities"). Finally, the study of DNA from human remains introduces other ethical considerations, as there have been a lack of community engagement with descendants and a lack of awareness of cultural practices on human remains. Furthermore, implications of biological and historical interpretations from research findings can negatively affect current day individuals and communities.
In summary, I found these articles thought-provoking and brought awareness to a process I often take for granted. I became more aware of these issues in my work when we recently learned from our study coordinators that we needed to remove several subjects from the analysis because consent was revoked. As statisticians and data scientists, we should take an active role and be aware of the informed consent process of our studies, especially in populations with a history of misuse, as illustrated in the above articles.

5th Annual Florence Nightingale Day for 8-12th grade students

The upcoming 5th Annual Florence Nightingale Day which will be held on October 29 at Ohio State and virtually, and at other sites on various dates in the US and Canada. Florence Nightingale Day is sponsored by the American Statistical Association, the Caucus for Women in Statistics, the Canadian Statistical Sciences Institute, among others. It aims to celebrate women in statistics and data science while guiding 8-12th grade students, especially women and those from under-represented groups, to discover opportunities in statistics and data science through activities and discussions with professional women and current students in data-related areas. For more information about this one-day free event, please visit https://fndaystats.org/current-year/.

Reflection and Tips on the Job Search Experience

Ananda Datta
Senior Data Scientist at Bayer
Graduation year: 2016

Q: Who besides your advisor did you ask for advice about career paths and applications?

Apart from my advisor, I took advice from a few department professors who taught me multiple courses and knew my strengths and career aspirations. Also, I consulted with my seniors who were already placed in academia or industry. I always had good connections with them, and their suggestions were instrumental in my career choice.

Q: What is the general timeline of job applications and interviews?

For industry applications, the timeline varies from 4 weeks to 8 weeks from the day of application till you have an offer in hand. For academic applications, especially for post-doc positions, the timeline varies from 2 weeks to a month from the day of application to have an offer.

Q: How did you decide on your current position?
Honestly, I did not decide on my current position. Being trained in Statistics and having a computational background, I knew I would do good in analytical or applied statistics or computational-based positions. I followed that, applied, and joined Bayer as an Applied Statistician. The rest of the pathway to being a Data Scientist, followed by a Senior Data Scientist, was pretty much driven by my love for making out stories, driven by metrics and observations from messy data and guided by ownership on several impactful projects.

Q: How did you prepare for the interviews?

Interviews for post-doc positions involved focusing on my research area and its extensions, reading and understanding the recent contributions of the concerned professor (to who’s lab I am applying) and striking a synergy between my expertise and the research professor’s domain of ongoing research. For industry positions, the preparation involved more on brushing up the fundamentals, practicing optimized algorithm coding, knowing about the current applications and trends in data science and software engineering along with hands on practice. Videos on youtube, data science blogs, github projects and bootcamp websites were pretty helpful in the preparation.

Q: How did your graduate research training help your job search or current work?

My graduate research training has been extremely helpful throughout my job search and towards my contribution to any of my previous projects and my current deliverables. Building up on the fundamentals, rigorous and challenging assignments and modelling based coding projects during graduate coursework and research gave me the proper foundation to help enhance my skillset and be able to contribute significantly in my job responsibilities.

Q: What else do you think people currently on the job market should know?

As regards data Science jobs, in this era of big data analytics, apart from the trainings/learnings from the graduate courses and research work, the candidates must also be proficient with cloud computing, distributed computing, advanced machine learning techniques for high throughput computing and have strong communication and soft skills.

Dhanushka Rajapaksha
Senior Data Science Analyst, Discover Financial services
Graduation year: 2022

Q: How did you learn about the different available career paths? How did you decide what area to apply in (e.g., academia vs. industry)?

I attended several workshops organized by the UT Dallas career center that discussed different career opportunities. I always wanted to pursue a career related to data science. However, attending those seminars made me realize that data science is a very diverse field and that I should focus on the job opportunities that are related to my skills and educational qualifications. As an example, the focus of my PhD dissertation is to build risk prediction models for substance use disorders (SUD). In addition, I had completed a professional qualification related to financial and management studies. Therefore, I decided to apply for data science positions related to risk modeling in the financial sector like banks.

Q: What resources did you find helpful when preparing your applications and applying to positions?

I found workshops organized by the UT Dallas career center very useful. In addition, I also took advantage of LinkedIn. These different resources provided a lot of useful information on how to prepare resume, and how to face an interview, etc. The UT Dallas Career Center also offers a resume...
review service, which was really helpful when I was preparing my resume.

Q: What is the general timeline of job applications and interviews?

I think it is best to start the job application process at least 5-6 months prior to your graduation. This way you will have enough time to prepare and find a job. Finding a job within 90 days of graduation is important for international students on an F1 visa. In that timeline I spent the first couple of weeks preparing the resume. Then I researched about suitable job positions according to my skills and started to apply. I mainly used LinkedIn to find suitable job postings.

Q: How did you prepare for the interviews?

I think preparation is the key to a successful job interview. Interviewers can assess you in a number of ways during a job interview. I made an elevator pitch before each interview that is more specific to the job position. At the same time, I carefully reviewed the job description before the interview, as it contains several keywords, and familiarized myself with those. This is very important because interviewers will ask questions related to those keywords. I also reviewed the theoretical concepts related to the job that I learned as a student before each interview, especially for technical interviews.

Q: How did your graduate research training help your job search or current work?

The knowledge and experience I gained during my graduate research training helped me find a position in the industry. I gained first-hand experience developing statistical and machine learning models using real-world data during my Ph.D. As a research student, I also got exposure to other important tasks like data preprocessing, feature engineering, and model validation. The value added by these opportunities attracted multiple job interviews in my direction, and in the end, I got some really good job offers.

Emileigh Willems
Graduation year: 2020
Biostatistician, Amgen Inc.

Q: How did you learn about the different available career paths? How did you decide what area to apply in (e.g., academia vs. industry)?

I learned the most by attending conferences and events and hearing people from diverse careers and backgrounds discuss their various paths and perspectives. I found participating in job interviews at JSM to be very eye-opening. I did not receive a job offer from these interviews, but found that learning a little more about what was "out there" helped me refine my interests and feel more informed once it was time to start a formal job search.

Q: What is the general timeline of job applications and interviews?

I took a different approach than what is usually recommended here. I finished my PhD in Summer 2020 and found that I just didn't have the energy to add job hunting to my to-do list during the madness of Spring 2020. I also wanted to take a few months off after my PhD to "de-stress," so I did not begin my job search until late Fall 2020. So I would say that the general timeline is whatever feels right for you. Don't be afraid to make your own path or be
discouraged if you're finding that your timeline doesn't align with what is usually recommended or that of your peers.

Q: How did you prepare for the interviews?

I find general interview questions like, "What is your biggest weakness?" to be the most intimidating. They are so open-ended! I like to talk through responses to these types of questions to get my jitters out, but the best strategy I found was thinking about general scenarios, projects, what I learned from them, etc., since these can then be reframed to answer any version of the open-ended questions. There are a lot of resources online that give great advice about this strategy or other interview prep approaches. Find an approach that makes you feel prepared but also lets your personality shine through.

Q: What else do you think people currently on the job market should know?

Having the appropriate technical skills is very important for a successful interview, but it's more important to be able to communicate those technical skills and how they could be an asset in the new position. Don't discount the value of the soft skills developed during graduate school - project management, leadership, communication. Make sure to also highlight your strengths in these areas, since most interviewers value well-rounded candidates.

Q: Anything else you like to share?

Remember that you are in charge of interviewing if the job would be a good fit for you! Take some time to think about the goals and expectations you have for your next job, what might be a dealbreaker for you, etc. Being prepared with questions to ask the interviewer can help you gain insight about these important factors and decide if the role will meet your needs.

Haoyu Zhang
Division of Cancer Epidemiology and Genetics
National Cancer Institute
Job search year: 2022

Q: How did you learn about the different available career paths? How did you decide what area to apply in (e.g., academia vs. industry)?

Friends, particularly senior students who have recently graduated, teach me about various available job routes. They will talk about their life and how they feel about their current circumstances. Attending academic conferences such as JSM or ENAR is a great way to learn about other career possibilities. The conferences will draw attendees from both academics and industry. You can speak with them and learn about the many job options. I decided to pursue a career in academia because I enjoy conducting research and interacting with students. It feels fantastic to be able to make a small contribution to science.

Q: What is the general timeline of job applications and interviews?

In September, I prepared the application materials. The majority of applications are submitted between October and November. Several of the first round of phone/zoom interviews were set in December. The majority of official interviews were arranged between January and late February. In late February or early March, job offers were made.
Q: How did you decide on your current position?

I chose to be an investigator at the National Institute of Health. I have collaborations with some of the investigators for a long time. By joining NIH, I will be able to continue existing collaborations while also expanding them. NIH has a wealth of data resources, which is critical for statistical research. The position is one of hard money. I can focus on my research without having to worry about funding.

Q: How did you prepare for the interviews?

I practiced the job talks multiple times. I presented the job talk in front of different audiences and constantly revised the talks based on their feedback. I also talked to friends who just become assistant professors about the potential interview questions. I prepared a five-minute summary of my research, which was frequently asked during the interview. As the interview season continues, you feel more at ease since you have answered similar questions several times.

Q: How did your graduate research training help your job search or current work?

During my Ph.D. and postdoctoral studies, I received extensive research training. Meanwhile, the schools offer numerous seminars/workshops on job search and tenure track preparation, such as preparing a research/teaching statement, job talk preparation, and grant writing. Attending these workshops was quite beneficial to me.

Future Webinar

Dr. Kim-Anh Lê Cao
Multivariate Integration of Multi-Omics Data
10/24/2022 | 5-6 PM
(EASTERN)

REGISTRATION:
HTTPS://US02WEB.ZOOM.US/WEBINAR/REGISTER/WN_MATDL
DN7RNU4RD4OJOV5TG

Abstract: Technological improvements have allowed for the collection of data from different molecular compartments (e.g. gene expression, protein abundance) resulting in multiple ‘omics data from the same set of biospecimens or individuals (e.g. transcriptomics, proteomics). We propose to adopt a systems biology holistic approach using Projection to Latent Structures (PLS) methods to integrate these multi-omics data. Our goal is to improve biological insights compared with traditional single omics analyses, as it allows to take into account interactions between omics layers.

Data integration includes numerous challenges – data are complex and large, each with few samples (< 50) and many molecules (> 10,000), and generated using different technologies. We have developed a comprehensive dimension reduction multivariate framework to address some of these challenges in the R package mixOmics. I will give a broad overview of the different methods implemented in the package, and how we define statistical data integration in this context. I will then illustrate how we applied these approaches for the analyses of different multi-omics studies, ranging from a human newborns study to multi-omics microbiomes as well as some work in single cell multi-omics. Across all these studies, our main goal is perform variable selection and signature of omics markers to characterise a specific phenotype or
disease status, and thus better understand the underlying molecular mechanisms of a biological system.


**Bio:** Associate Professor Kim-Anh Lê Cao develops computational methods, software and tools to interpret big biological data and answer research questions efficiently. Kim-Anh has a mathematical engineering background and graduated with a PhD in statistics from the Université de Toulouse, France. She then moved to Australia to forge her own non-linear career path, first working as a biostatistician consultant at QFAB Bioinformatics, then as a research group leader at the biomedical University of Queensland Diamantina Institute. She currently continues her strong research focus at the University of Melbourne. Kim-Anh has secured two consecutive NHMRC fellowships from 2014. In 2019 she received the Australian Academy of Science’s Moran Medal for her contributions to Applied Statistics. She was selected to the international HomewardBound leadership program for women in STEMM, culminating to a trip to Antarctica in 2019, and the superstars of STEM program from Science Technology Australia.

Questions? Contact Anna at amp9@williams.edu

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**Student Paper Award Competition**

The Section on Statistics in Genomics and Genetics (SSGG) of the American Statistical Association is pleased to announce the 2023 Distinguished Student Paper Award Competition. Papers considered in this competition should contain methodological innovations and/or novel applications of statistical and computational methods to problems arising in genetics and genomics. Three to six awards will be given.

**Applicants for the SSGG Student Paper Award must meet all the following criteria at the time of submission:**

- Be a current undergraduate or graduate student at any level, or have received their degree in statistics, biostatistics, or related quantitative field in 2022.
- Be a current member of SSGG. The applicant can join SSGG at the time of submission. Instructions on how to join are provided below. Note that ASA membership does not automatically confer SSGG membership; ASA members must join individual sections in addition to generic membership.
- Be first author of the paper and scheduled to present the same paper submitted for the award at the 2022 JSM (current scheduled to be held in Washington, DC) as either a talk, SPEED, or poster.
- Have submitted the paper to no more than one other ASA section 2023 student or early-stage investigator competition. (Note that in the event a paper wins two awards, the author may only accept one of the two awards)
- Have not previously won an SSGG student paper award.

**Applications should include:**

1. A cover letter including name, current affiliation and status including actual or intended date of graduation, and contact information (address, telephone, e-mail) of the applicant.
2. The paper submitted for the competition which should be up to 25 pages (double-spaced, 1-inch margins) including an abstract and references, but not including figures and tables. Figures and tables should be placed at the end of the manuscript. No supplemental materials and appendices beyond the 25-page limit will be accepted. Papers do not need to be anonymized.

3. A letter from the advisor who should certify student status (or completion of degree within the past year), and in the case of joint first-authorship, should indicate the fraction of the applicant's contribution to the paper.

All materials must be received by the Section by 11:59 PM (Pacific Time) December 15, 2022. Winners will be notified by January 15, 2023. Applications must be submitted by email (as separate PDF files). For further information or to apply, please contact Ni Zhao, Chair of the SSGG Distinguished Student Paper Award Committee nzhao10@jhu.edu with “SSGG Distinguished Student Paper Award” in the subject line.

For section members who are faculty or mentors, we would like to encourage you to become a section member, and please bring this to the attention of your students and encourage them to apply. Section members and friends are welcome to contribute funds towards the endowment for future student awards.

**Call for Topic-contributed Session Proposals**

It is time to plan for your 2023 JSM, which will take place in Toronto, Ontario, Canada, August 5-10, 2023.

**We support your submission!**

The Section of Statistics in Genomics and Genetics (SSGG) is a community of individuals interested in Statistical Genomics and Genetics within the American Statistical Association. The goals of the SSGG are to foster research, education and influence of statisticians on genomics and genetics and associated applications. We are now calling for topic-contributed session proposals. The theme for JSM 2023 is “**One Community: Informing Decisions and Driving Discovery**,” but not all sessions have to adhere to this theme. Topic-contributed sessions include papers, panels, and posters:

- Topic-contributed paper sessions consist of five speakers, made up of at least three presenters and, at most, two discussants; each speaker has 20 minutes to present.
- Topic-contributed panels consist of three to six members providing commentary or a point of view on the panel topic.
- Topic-contributed poster sessions have 10–15 participants with posters addressing a common topic.

A topic-contributed session proposal includes a session title, general description of the session, list of participants, and tentative talk titles.

To propose a topic-contributed session:
- Develop your idea and a list of speakers who agree to present on a common topic.
- Submit your idea online from November 15 to December 8, 2022.
- Await approval from a member of the JSM Program Committee.
- Ensure all speakers submit individual abstracts by February 1, 2023, using the six-digit session ID. Note: **All speakers will be required to register for JSM prior to abstract submission.**
- Talk to potential authors early, as no participant can serve as a presenting author in more than one session.

We are supporting proposals broadly related to statistical genomics and genetics, computational biology, and relevant topics. To submit a session proposal to be considered for 2023 JSM, please read the instructions and guidelines at [https://ww2.amstat.org/meetings/jsm/2023/](https://ww2.amstat.org/meetings/jsm/2023/). Be sure to check the SSGG as your first choice of sponsor. Submissions are open Nov 15 to Dec 8, 2022.
Join US
To become a SSGG section member, please first become an ASA member by signing up at http://www.amstat.org/membership/becomeamember.cfm. If you are already an ASA member, there are two ways you can become an SSGG section member: (1) call the ASA Headquarters at (703) 684-1221 and request the SSGG section be added to your membership or (2) renew your ASA membership online via ASA member only website https://www.amstat.org/membersonly/index.cfm and add the “Section on Statistics in Genomics and Genetics” when you are asked to “verify your Publications, Chapters, and Sections, making any necessary additions or removals.”

Executive Committee

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Contact Us

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If you have something to share with our section or would like to contribute to our newsletters, please contact Ching-Ti Liu (ctliu@bu.edu).

Keep Connected

LinkedIn: https://bit.ly/3AOZBWy