Friends of GST,

A new academic year is about to begin, and with it, please get ready to welcome a new cohort of nine GST students! The new class of 2022 is well prepared to succeed in the program and beyond. To complement your meeting in person, please see the brief vignettes on the back of this newsletter.

Over the past year the GST faculty has also continued to grow. New faculty who have joined the program include cell biologist Amit Joshi (Department of BCMB), geneticist Troy Rowan (Animal Science) and synthetic biologist Carrie Eckert (ORNL). Each is bringing rather new expertise into GST, as exemplified by an article below on cattle genomics with Dr. Rowan. It is not uncommon for new faculty to quickly recruit new students, and this cohort is no exception.

The revised GST II course ‘Biological Data Analytics’ has continued to evolve. The course is taught in four topically separate month-long modules that can be taken individually. This past Spring semester more first-year GST students enrolled. GST II is meant to catalyze the dissemination of computational know-how throughout our community to broaden the foundation of expertise of our trainees. Would it make sense to have senior students join the roster of instructors? Please consider what aspect of your expertise would benefit your fellow students.

Over the past year GST has moved closer into the orbit of the UT Oak Ridge Innovation Institute (UT-ORII). The UT-ORII serves as the umbrella for all of the many channels of interaction between Oak Ridge National Lab and The University of Tennessee. Over this coming year GST will continue its migration from the College of Arts and Sciences to UT-ORII and take its place as the third joint program next to its two sister programs, Energy Science and Engineering and Data Science and Engineering. The three joint programs are overseen by Interim Education Director, Dr. Philip Rack. One benefit of the migration is that first-year students will be financially supported by research assistantships from UT-ORII, similar to the other joint programs. For the time being, graduate teaching assistantships in the Division of Biology will continue to be available for more senior GST students, thanks to an emerging cooperative agreement with the College of Arts and Sciences.

There has probably been no more dynamic and self-evident display of genome evolution in action than the rapid waves of new SARS-CoV-2 virus strains. A punctuated equilibrium? It seems we deserve to cautiously regard the current phase as “post-pandemic”. This summer conferences have finally returned to in-person format. Many of you are taking advantage to present advances accumulated during the hiatus of the past few years. But while the severity of infections has declined a great deal, thanks to bioscience’s warp innovations, vaccinations and even antiviral drugs, we should be wise enough to not become overconfident. Some have been surprised that despite booster shots they produced a positive Covid-19 test! How can that be? The larger the population of virus the more likely that a new and potentially nasty variant will arise. We can expect that we have not seen the last surprise, yet.

Regrettably, GST’s Program Coordinator, Ms. Terrie Yeatts will leave GST to take a new position in UT’s Department of Anthropology. Terrie has served GST with charm and patience and—most of all—expertise for over 16 years, her mission laser-focused on the students’ needs. We will miss Terrie a great deal, including her wall-to-wall artwork in her office! Let’s wish Terrie all the best in her new position!

Best wishes for a successful Fall semester!

Albrecht von Arnim
FAREWELL TO TERRIE YEATTS

Terrie Yeatts has been the administrative staff for GST for over 16 years, and most recently the only one. Much to our regret, Terrie will be leaving GST for a new position at UT. In her position, she has handled a broad portfolio of responsibilities, from payroll and contracting, assisting students every step of their way, to organizing catered events. Terrie’s deep knowledge of who does what well at UT and ORNL has been a key to the program’s success.

Here are a few comments from GST students: “Whenever I did need help, you have always helped me in a kind, quick and effective manner. I wish you all the best in your new position, our loss is their gain” - Ricardo; “...On my first day... Terrie was so calm, kind and patient with me. I was nervous because this was all very new to me but she made it all so easy. She made me feel comfortable and this will always be my first and best memory of meeting her.” - Esha; “Terrie's done a great job of being the glue that helps hold GST together as well as the oil that keeps us running, she'll be hard to replace!” - Matthew.

Many readers of the Newsletter are aware that Terrie is also an accomplished painter. Over the years, we have witnessed her artistic progression through a variety of distinct styles. Visiting Terrie in her office is a trip to the “Yeatts Art Gallery”. Terrie has truly been the heart and soul of GST!

SELECTED RECENT PUBLICATIONS BY GST STUDENTS

Jennifer Schuster and members of the Barrera lab collaborated with the laboratory of Mike Best (Chemistry) in a project that was recently published in the Journal of the American Chemical Society, the world’s preeminent journal in chemistry. https://doi.org/10.1021/jacs.2c00191. Jen demonstrated that changes in cytoplasmic calcium can be used for selective delivery into human cells of cargo encapsulated in ATP-responsive liposomes.

Yang Xu and Priyojit Das are coauthors, along with other members of the McCord lab, on a ‘snapshot’ article in the top journal for molecular biology, Molecular Cell. https://doi.org/10.1016/j.molcel.2022.05.020.

Daniel DeGennaro, Ricardo Andres Urquidi Camacho, Liang Zhang 1, Elena D Shpak. (2022) Initiation of aboveground organ primordia depends on combined action of auxin, ERECTA family genes, and PINOID. Plant Physiology. 10.1093/plphys/kia288

Yang Xu, Priyojit Das, Rachel Patton McCord (2021) SMILE: Mutual Information Learning for Integration of Single-cell Omics Data. 10.1093/bioinformatics/btat706


Rachel Patton McCord, Yang Xu, Heng Li, Priyojit Das, Rebeca San Martin, Matthew. (2022) Snapshot: Chromosome organization. Mol Cell. 10.1016/j.molcel.2022.05.020


Dr. Carrie Eckert is the Synthetic Biology group leader in the Biosciences Division at ORNL. She started her appointment in July 2021. She had previous appointments at the National Renewable Energy Laboratory and the University of Colorado, Boulder under the Renewable and Sustainable Energy Institute (RASEI). Her research is focused on developing tools to enable and accelerate the genetic manipulation and metabolic engineering of a number of eukaryotic and prokaryotic systems. Specifically, she is most interested in the development of high throughput, CRISPR-based methods for genotype-phenotype discovery for applications in metabolic engineering. She serves as the Genetic Tools Team Lead for the Center for Bioenergy Innovation (CBI), with research focused on Clostridium thermocellum and Pseudomonas putida KT2440 engineering. She is also a co-PI for the Secure Ecosystem Engineering and Design (SEED) SFA where she is working on developing CRISPR systems for key soil microbes associating with poplar.

Dr. Amit Joshi is an Assistant Professor in the Department of Biochemistry & Cellular and Molecular Biology at UT. He received his PhD from Dr. Miriam Greenberg’s lab at Wayne State University in Detroit. He obtained post-doctoral training in Dr. William Prinz’s lab at the National Institutes of Health in Bethesda and Dr. Sarah Cohen’s lab at the University of North Carolina in Chapel Hill. During his post-doc he discovered a novel family of ER membrane shaping proteins involved in biogenesis of peroxisomes and lipid droplets. He joined UTK in January 2021.

Dr. Troy Rowan is an Assistant Professor in the Department of Animal Sciences. He grew up on a small Charolais operation in southwest Iowa. He was an active 4-Her, exhibiting home-raised heifers and steers both locally and nationally. He attended college at Creighton University in Omaha, NE where he majored in Biology. Despite his initial desire to pursue a career in the medical field, he was drawn to research, and missed being involved with the beef industry. Following graduation in 2016, he started his Ph.D. in genetics at the University of Missouri. There he performed research on the genomic variants that underlie artificial selection and environmental adaptation in beef cattle. His research interests are detailed in the Faculty Spotlight elsewhere in the newsletter.

Rachel D Johnston — PhD, Perturbing fatty acid metabolism in Enterococcus faecalis disrupts responses to exogenous fatty acids and the antibiotic daptomycin, Fall 2021 (Fozo lab). Subsequent position: NIH National Biosafety and Biosecurity Training Program Postdoctoral Fellow, Rockville, MD.

Kyla Hooker — MS, Ecological Controls on Successional Patterns in Bloom-Forming Cyanobacteria, MS Spring 2022 (Talmy lab). High school math teacher in Atlanta, GA.

Nicholas C Mucci — PhD, Mechanisms by which Xenorhabdus nematophila interacts with hosts using integrated -omics approaches, Spring 2022 (Goodrich-Blair lab). Field application scientist, Seer, Redwood City, CA.

Benjamin Nordick — MS, Computational Analysis of Transcriptional and Post-transcriptional Feedback in Development and Cell Differentiation, Spring 2022 (Hong lab). Software engineer for an education technology company.

Alexandra H Teodor — PhD, Improving the Biocompatibility of the Bio-Inorganic Interface for Enhanced Photosystem I-Based Biophotovoltaic Device Performance, Spring 2022 (Bruce lab). Staff scientist for a photovoltaics company, Los Angeles metro area, CA.

Samantha Peters — PhD, Metaproteomics as a Systems Biology Approach to Characterize Microbiome Functionality and Interactions in the Human Gut, PhD Summer 2022 (Hettich lab). Postdoctoral Research Associate at ORNL.

Stephen Grady — PhD, Efficient Network Domination for Life Science Applications, Summer 2022 (Langston lab).

Yang Xu — PhD, What I talk about when I talk about integration of single-cell data, Summer 2022 (McCord lab). Computational scientist at the Broad Institute, Boston, MA.

Payal Chirania — PhD, Characterization of microbial metabolism at diverse complexity levels: Extending integrated metaproteomics from simple cell-free systems to complex environmental microbiomes, Summer 2022 (Hettich lab). Research Scientist at Vertex Pharmaceuticals, Boston, MA.
Professor Philip Rack is the Leonard G. Penland Chair and Associate Department Head in the Department of Materials Science and Engineering and serves as the Education Director (interim) for UT-ORII. Thank you for answering a few questions for “Growing Trends.”

GT: What is the role of UT-ORII in the UT research infrastructure?

PR: UT-ORII is positioned to help stimulate research collaborations between UT and ORNL. Beyond simply administrating several longstanding programs, like the Governor’s Chair program, the Science Alliance, and the joint PhD programs, we hope to increase meaningful research collaborations between the two places. One aspect of that is the hiring of new joint research faculty that will sit in the Institute and have appointments at both UT and ORNL. We are trying to identify critical areas of science and engineering where we can hire these faculty to work at the interface between ORNL Staff and UT Faculty.

GT: What benefits do you foresee from bringing GST into UT-ORII?

PR: There are three joint UT-ORNL PhD programs - Energy Science and Engineering, Data Science and Engineering, and Genome Science and Technology. We hope with investments from UT-ORII, that all three programs can be stronger and more vital. For GST this will mean competitive first-year research fellowships that will hopefully jump start students into research. We also want to add academic services for the students that have to navigate research across the interface of UT and ORNL. This is critical as many of the joint PhD students will be mentored by ORNL staff who are not as familiar with the academic side of operations. While not as exciting, we also hope we can streamline administrative processes for the 3 joint programs as well as PhD students in regular departments that work with researchers at ORNL. GST is our oldest joint program, and 20 years ago, the name was really an aspirational goal. We are currently strategizing with GST constituents on how to reorganize the program to better serve the UT and ORNL bio-science researchers so the next 20 years are as successful as GST’s first 20 years! We hope that by lowering barriers between researchers at UT and ORNL that graduate students can have a very unique graduate experience.

GT: How is UT-ORII investing into graduate training in the UT-ORNL partnership?

PR: We are supporting first-year fellowships as well as competitive fellowships for senior students (GATE Fellows), new opportunities with research faculty, as well as bolstering and modernizing curricula via coursework development funds.

AWARDS AND RECOGNITIONS WON BY GST STUDENTS

**Matthew Keller** (Hettich lab) won the 2022 Division of Biology Alexander Hollaender Fellowship.

**Payal Chirania** (Hettich lab) won a Cokkinias / Fite Award for Outstanding Scholarly Achievement by a Graduate Student.

**Alex Teodor** (Bruce lab) was recognized by the journal RSC (Royal Society of Chemistry) Advances for the best student-authored paper in the ‘Energy Chemistry’ category.

*Nice going and congratulations!*
Iyanu Oduwole his PhD adviser, Drew Steen, and others took part in an expedition far north into the Arctic to study the microbiomes that inform emerging geochemical models of carbon cycling as climate change keeps thawing the permafrost.

Q: What was the scientific motivation for the trip to Svalbard?

Our lab is interested in the fate of organic carbon in permafrost soils as this environment warms due to global change. How is this carbon being converted into methane and carbon dioxide? And is this carbon reassimilated by microbes in the permafrost environment or is it released into the atmosphere?

Q: What other questions can you address with these samples?

A: Our lab is interested in both the diversity of microbes that exist in the soil and their metabolic capabilities. For this we take soil core samples and extract DNA and RNA to take back home for metagenomic and meta transcriptomic analyses. We are also especially interested in the role of extracellular enzymes, such as peptidases and glycosyltransferases, some of which are actively released by the microbes. Compared to soils in warmer climates that contain more metabolically active microbes, we think that in the permafrost, and especially in marine sediments, the extracellular enzymes play a comparatively larger role in the geochemistry.

We drill for soil samples from the ‘active’ soil layer, which thaws seasonally, and also from the frozen permafrost layers below. This is hard work, because as you can imagine the terrain is very rocky, and if you hit a rock you have to start over. The soils and the microbiomes in them can also be quite diverse – not all permafrosts are alike! You may be surprised to hear that we were based at a large research station with ample equipment. This allowed us to extract DNA and RNA right away, to take with us, and we also analyzed the samples for gas content such as CO2 and methane.

Q: I suppose this type of work really requires a robust research infrastructure.

A: Yes, the research town has stations from many different countries, including Norway, Italy, Great Britain, India, and South Korea. We were hosted by the French/German station, which has a permanent staff, who also take an active interest in the projects being conducted. They guided us to where the better sampling sites are. Also, besides a lot of hard work, there were social events. We happened to be there for the “sunlight party”, to celebrate the reappearance of the sun over the horizon after the polar winter. Meal times were also good to casually meet polar researchers from other countries who are conducting all sorts of other projects around the station.

Q: What other questions can you address with these samples?

A: I am very interested in a side project, namely what kind of viruses exist in these permafrost samples. Could they be relevant for human health, either directly as pathogens or by affecting the human microbiomes? We won’t know until we look.

Q: How was it like to travel so close to the North Pole? Did you see the northern lights?

A: It was quite something. We took four flights to reach Longyearbyen on Svalbard, and then another 16 hour boat ride to the station at Ny-Ålesund at 79ºNorth, where we spent nearly 2 weeks. I got seasick on the ship, which was one of the less pleasant experiences. My adviser has spent 30 days on that boat in similar waters on previous expeditions, and those were absolutely the worst conditions he had ever seen! On the fun side, I learned how to ride a snow scooter. Although it is a safe environment, it is only safe because of the training all visitors go through, which includes training to fend off any polar bears. Thankfully for everyone the bears kept their distance.

Thank you for sharing your unique experience!
Quick! Guess, which animal has the largest number of high-density genotypes (after humans)? The cow! Since 2008, the cattle genomics community has an exceptionally well-assembled reference genome and a trove of genetic resources. They’ve put this to work with extensive genomic testing to catalog genetic variation across populations. The cattle community has ‘genotyped’ over 10 million animals in this manner! This has enabled widespread, genomic selection that has rapidly accelerated genetic gain. Beyond producer applications, this has generated opportunities to use farmer-generated data for biological discovery.

Assistant Professor Troy Rowan (Animal Sciences) in the UTIA Genomics Center for the Advancement of Agriculture is heavily involved in this research and recently joined the GST program, “Cattle are an excellent model system understanding complex traits. We are interested in solutions that allow cattle producers to breed animals that will be genetically superior for important traits, such as feed and water use efficiency, greenhouse gas (methane) emissions, health and longevity, end product (beef) traits, etc. Towards this goal, my group works at the intersection of genomics, quantitative genetics, and animal breeding to improve genetic selection tools for producers.” The wide array of genotypic data, coupled with high-coverage reference sequences and imputation, can be used to map which genetic variants underly phenotypic traits using powerful genome-wide association studies.

Rowan grew up on a cattle operation in Iowa, which has motivated him to make beef production more efficient and sustainable. The genome holds the key for linking genetic variants to specific traits. “The more detailed our data on the behavior of the animals the better the chance to connect these phenotypes to the genetics of the animal and its microbiome. To this end we are using a variety of sensor technologies to measure animal activity, feed and water consumption, and even methane emissions – you know, burping.” In addition, the research community has prioritized generating functional gene annotations using a variety of -omics data through the Functional Annotation of Animal Genomics (FAANG) Project.

The team also measures molecular phenotypes, such as genome-wide mRNA levels and metabolite production, rich and mechanistically relevant, multiscale datasets, which are interpreted with machine learning methods to help predict future animal performance for a variety of traits (e.g., health risk, fertility potential, etc.). Compared to whole transcriptome sequencing, a 3’ RNA-Sequencing approach makes it cost-effective to measure gene expression on huge groups of animals.

Rowan is very intrigued by exploiting the phenomenon of hybrid vigor (heterosis) in cattle. Hybrid vigor is a phenomenon more widely exploited in crop plants such as corn, where individuals that are highly heterozygous across the genome express favorable traits in terms of growth and resilience to stress than their homozygous parents. Because cattle varieties are also highly inbred and thus genetically homozygous, the hybrid vigor phenomenon has great promise. Says Rowan, “We’re very interested in understanding how hybrid vigor manifests itself in cattle at the molecular level, i.e. gene expression, protein, metabolite, etc.). We are working to combine this data with non-additive trait mapping to eventually deliver precision mating decisions for breeders that maximize the benefits of heterosis.”

Rowan’s group uses a diverse array of tools (live animal studies, high-throughput phenotyping, -omics data, statistical methods, in vitro & in silico approaches). This presents great opportunities for GST students to get exposure to cutting-edge agricultural genomics, a growing field with ample employment opportunities. The underlying principles are extremely similar in other eukaryotes, including humans, should a student have any inclination to part ways with their bovine companions in the future. Because Rowan has a part-time extension appointment, he regularly travels throughout Tennessee interacting with cattle producers and breeders. Exposure to ‘extension’ work also adds an irreplaceable applied facet to his students’ research experience.

Should interested students have prior experience with livestock? Not necessarily! “My group is really diverse, from students who are lifelong cattle producers to those that hadn’t ever seen a cow in real life!”

**RECENT CONFERENCES ATTENDED BY GST STUDENTS**

- **Biophysical Society Conference**, San Francisco, CA, February 19-23 2022: Das Priyoyit (Mc Cord Lab) 
- **Experimental Biology**, Pennsylvania, PA, April 2-5, 2022: Barbra Dompreh (Fernandez Lab)
- **American Society for Mass Spectrometry Conference**, Minneapolis, MN, June 5-9, 2022; Samantha Peters, Manasa Appidi, Steven Tavis, Payal Chirania, Him Shrestha, Matthew Keller, Katie Ostrouchov, Megan Elliott, Sameer Mudhbari (all Hettich lab).
- **Center on Membrane Protein Production and Analysis**, New York, New York, June 22—24, 2022: Jennifer Schuster (Barrera lab); Eugene Ageemang (Lamichhane lab)
- **ASPSB**, Portland Oregon July 9—13, 2022, Manasa Appidi, Him Shrestha
What’s nicer than winning some cash prize money, showcasing your skills to potential employers, and networking with biotech startup companies?

The HudsonAlpha Institute for Biotechnology hosted its fifth annual HudsonAlpha Tech Challenge (HATCH) on May 6th-8th in Huntsville, Alabama, where high schoolers, college students, and professionals competed in a genomics hackathon event. This event brought together professionals across the country with a diverse set of skills, including those without computer science or genomics backgrounds, to generate solutions to challenges faced in the field of genomics and biotechnology. Up to $5,000 in prize money was awarded this year.

Teams consisted of up to 5 people, and members could participate remotely, but one team member had to be present at the event to be considered for judging. The night before the hacking began, participants were introduced to the challenges for the event, and they were given the opportunity to mingle and form their own teams. The next day the hacking began. Teams were challenged to stay up 36 hours to create a software product that addressed one of the challenges in the competition. They were judged based upon the impact, creativity, complexity, and usability of their product, as well as the quality of their presentation.

This year a second year GST student, Katherine Ostrouchov, participated in this event - and won!

Which challenge did you choose?

“We chose the ‘More Than Pharm to Table’ Challenge. A common problem prescribing physicians face is deciding which database to rely on for gene variants and their associated drug metabolism to arrive at a recommended patient-specific dosage. Currently, the two largest databases that have this information are CPIC and PharmGKB. These databases have yet to be integrated. Not only are there gaps in coverage across the databases, but standards for arriving at a drug dosage level are different. We were challenged to integrate these databases, and develop a web application that allowed physicians to choose relevant interaction information that matched their uploaded patient gene variant reports.”

How did your team build the software product?

“We integrated CPIC and PharmGKB pharmacogenomic databases using postgresql, Rscripts, and bash. We searched a list of gene variants from a mock patient dataset in bash against the integrated database. We created a python web application through Streamlit that allows providers to upload a patient’s gene variant results, select which drug/gene variant interaction results are relevant from the search, and display a PDF report which could be saved and printed.”

What were some of the challenges your team faced?

“Designing a user interface and integrating PharmGKB and CPIC databases was not an easy task. We were unfamiliar with the structure of pharmacogenomics data as well as how to design and develop an app for an end user.

I am so impressed that your team made first place! Congratulations. Do you recommend the event for other students?

“Absolutely. I have stayed up for longer than 36 hours in the Army, but this event was intense even for me. Besides, the entry fee is affordable, and the organizers provide free food and mentoring during the event. Students with little to no coding experience are encouraged to attend along with students outside of genomics. The goal is to have a team that can specialize in many areas and complete the task efficiently. Watch out for the announcement next March!”

NEW GRADUATE STUDENT SENATE REPRESENTATIVE

GST has a new delegate for the UT Graduate Student Senate (GSS). After Viswanathan Gurumoorthy ably represented GST for several years, the baton is being handed over to Megan Elliott. The GSS can serve as a conduit to the UT administration to discuss vexing issues that need attention. Please make your voices heard.

Hello! My name is Megan and I am the new GST senator. I look forward to continuing getting to know you all and talking about how I can best represent our department!
Mahbuba Ferdous has a B.S. and M.S. in Biochemistry and Molecular Biology from University of Dhaka, Bangladesh. Her MS research was focused on endophytes, their interaction with plants, and purification of novel antibiotics. For the last two years she is working as a scientist at a government research institute in her country where most of her work is focused on plant molecular biology. She has also been worked as a faculty at a university for quite a long time. Her research interest includes plant-microbe interaction, plant regulatory pathways, genetic factors, human genomics and bioinformatics. She is looking forward to joining GST in order to expand her knowledge and experience and gather new expertise in research.

Sam Cothron has a B.S. in agronomy from Mississippi State University in 2022. While at MSU, Sam worked as a lab technician for a USDA-ARS unit focused on host plant resistance in maize. Later, he worked as an assistant in the lab of Dr. Ling Li, which is focused on plant starch metabolism. Sam used physiological experiments and generated overexpression mutants to identify key transcriptional regulators in the starch biosynthesis pathway. He is passionate about the potential of plant genetics to address issues facing global food security and bioenergy production.

Gayle Purdy has a Master’s degree from the University of Arizona in Applied Biosciences, and a B.S. degree from Arizona State University dual majoring in Molecular Biosciences/Biotechnology and Sustainability. Her thesis work explored the effect of mine soil remediation strategies on extra cellular enzyme activity as part of an environmental study for a proposed mining site. She has experience in the protein crystallization workflow, particularly in DNA extraction and the transformation of polykedtide synthesis into E. coli. She is interested in applied research problems related to furthering sustainability through understanding sequence-structure-function relationships.

Andrew Amburn graduated with a B.A. in Biology from Maryville College in 2020. His senior thesis focused on the chemical and biological molecular interactions that govern bacterial disinfection and inactivation for specific viruses. He has previously worked with Dr. Jennifer Morell-Falvey, and Dr. John Cahill to co-write a python script which automated the peak-picking process for mass spectrometry data used in determining metabolite profiles of interacting rhizosphere bacteria. As a graduate student with interests in bioenergy production, synthetic biology, and computational biology, he is excited to further his skillset in these and related disciplines.

Emine Berfu Ozmen graduated with a BS in Biology from Ankara University, Turkey, in 2022. Emine explored her passion in science in a variety of research settings. Starting in a plant molecular biology laboratory at Ankara University she studied the transcriptome of plants under abiotic stresses. She continued with an internship at the center for stem cell research and development, at Hacettepe University, participating in a project about circadian clock genes in human bone marrow mesenchymal stem cells. In her final year in Leiden, The Netherlands, she learned molecular techniques such as gene editing with CRISPR-Cas9 as well as metabolomics.

Brynn Biddle, from Clinton, TN, graduated with her B.S. in 2021 from UT Knoxville, where she majored in biology with a concentration in biochemistry and cellular and molecular biology (BCMB) and minored in chemistry. Her undergraduate research was primarily conducted at the Oak Ridge National Laboratory under the mentorship of Dr. Sindhu Bhowmik. She applied machine learning and deep learning algorithms to molecular dynamics data to better understand the structure of certain proteins under specific conditions. Brynn is extremely excited to return to both UT and ORNL for her doctoral training. She is interested in regenerative medicine and computational biology.

Mitchell Long graduated with a BS in Biology and Chemistry in 2020, then an MS in Biology in 2022, from East Tennessee State University. Through a previous research focus on spider behavioral ecology with Dr. Thomas C. Jones at ETSU, Mitchell fostered an interest in genetic optimization in natural systems and looks forward to applying similar concepts in model organisms of industrial interest. He hopes to learn programming and modeling techniques to efficiently identify genetic targets and the gene editing techniques necessary to make further optimizations a reality for a career in the biotechnology industry.

Alvaro Rodriguez graduated with a B.S. in nanotechnology engineering with a focus on material science before earning an M.Sc. in the same field with a specialization in biophysics in an Erasmus Mundus program sponsored by the Katholieke Universiteit (KU) Leuven in Belgium. His interests took a turn into bioinformatics after a brief time at the University of Montreal, and he is looking forward to expanding his knowledge in the fields of genomic and proteomic data analysis.

Alaa Ahmed has a B.S. in Biomedical Sciences and a concentration in Computational Biology and Genomics from the university of science and technology known as Zewail City, Egypt. She has co-authored two different research projects in which bioinformatics was utilized to get better insights into applying personalized medicine. For graduate school, Alaa is looking forward to honing both her computational and wet-lab skills. Alaa has worked as a scientific reviewer and even as a children’s books curator and editor! Outside of academia, Alaa enjoys reading, taking care of her indoor plants, and creating new recipes.