Grace Coppinger Application Responses

# 2024 Application Questions and Answers to WashU DBBS EEB Program:

**Essay 1:** Please upload each essay as either a PDF or Word document. Submit no more than two (2) single-spaced pages per essay (or approximately 8000 characters, including spaces).
For one or more of your research experiences, a) describe your research project(s) and specific contributions to the work in the most comprehensive way possible, including the question, the approach, the results, and the interpretation; b) discuss your motivations for graduate study; and c) relate a fundamental biological, biomedical, or data science question that most intrigues you, highlighting potential Washington University DBBS faculty mentors.

**Essay 1 Answer:**

**Research projects:** Did you know Garter Snakes are venomous? As a freshman, I was very surprised to learn this and would go on to study these unique rear-fanged snakes for over three years. I joined the Snakes, Spiders, Scorpions, INformatics, and Genomics (SSSTING) Laboratory working with Dr. Jason Strickland at the end of the fall semester of my freshman year. When I first met with Dr. Strickland, he described three different projects, and I chose the most biologically interesting project that would need to be built from the ground up, starting with specimen collection all the way to bioinformatic analysis. Rear-fanged snakes account for two-thirds of snake biodiversity, however, they have been overlooked due to their small size, low venom yield, and non-medically significant bites, leaving little known about their venom. After learning that garter snakes are venomous rear-fanged snakes, I could not wait to learn more. I began my honors thesis during my freshman year, focusing on identifying intraspecific differences in venom phenotypes between male and female garter snakes. The objective was to investigate sex-based phenotypic venom variation among *Thamnophis sirtalis* specimens while considering that male and female genomes are fundamentally alike, with differences arising from distinct gene expression levels. During the summer of 2021, I spent over 100 hours in the field to catch my target species. The bycatch records of mammals, reptiles, and amphibians I found in
the field contributed to a 13-year longitudinal biodiversity study on my campus. Through this fieldwork, I earned co-authorship on a publication in September 2023 in the journal Herpetological Review.

My second year of research was spent milking snakes, dissecting specimens, and learning the molecular techniques needed to generate next-generation sequencing data. The part of research that has been the most exciting is bioinformatics and coding. DNA is life's blueprint, and bioinformatics allows me to conceptualize the blueprint and determine how changes in the genomic architecture result in variation. By the end of fall 2022, all samples I collected were sequenced on an Illumina NovaSeq6000 and I was able to see my hard work pay off when I began processing my transcriptomic data. I have determined that three-finger toxins (3FTxs), snake venom metalloproteinases (SVMPs), and cysteine-rich secretory proteins (CRISPs) make up the majority of garter snake venom. The presence of 3FTxs, which are neurotoxins, is unique for the genus and suggests that *T. sirtalis*' diet has led to a unique venom profile. My thesis will be submitted for publication early next year. My research has enabled me to network with many people and I have presented posters at two symposia for undergraduates and given oral presentations at two conferences: Alabama Chapter of Partners in Amphibian and Reptile

Conservation and Southeast Partners in Amphibian and Reptile Conservation 2021. My involvement in undergraduate research has provided many opportunities for me to grow as a researcher and person.

However, being one of the only students at the University of South Alabama working on bioinformatics drove me to apply for an REU at Cornell University to further my experience. I was so excited to meet other students with similar interests and learn from some of the leading bioinformaticians in the country. I worked under Dr. Zhangjun Fei at the Boyce Thompson Institute to identify structural variants (SVs) in wild and cultivated Watermelon crops. Because of the challenges associated with polyploid genomes, I needed to learn how to write my own Python and R scripts. I also practiced using genome alignment and gene annotation software, including altering the software to fit my needs. I successfully identified 111,738 SVs which affected 19,482 and 19,096 genes in the cultivated and wild genomes, respectively. By integrating SVs and differential gene expression information, I identified candidate disease-resistant genes. The genome alignments I generated are being used in a pan-genome paper to continue the work I started on disease-resistance genes impacted by SVs. The SVs I identified also serve as a resource to inform watermelon breeding efforts. While the REU project was intellectually invigorating, I faced challenges that motivated me to become a more independent scientist. Unfortunately, my PI had to spend the majority of the REU out of the country and we had little communication. Thus, I was required to work more independently than most of my cohort at Cornell. I quickly learned problem-solving techniques and reached out to other scientists for direction on my project. My peers were always surprised with how much solo work I was completing for my project. I pushed to expand the original project objective allowing me to take more ownership of my project than I otherwise would have. I am very proud of the work I was able to put in and share the results that I generated. Although there were challenges, I became a better researcher and communicator because of them.

**Motivations:** My challenging experience at Cornell made me reflect and question if I am performing well as a mentor for underclassmen. I have always been very active in outreach, and mentoring undergraduates. However, I did not truly understand the positive impact I could have on them until I reflected on my own mentoring experiences. My mentorship has included training them on literature review, RNA extraction, cDNA library prep, bioinformatic pipelines, and tutoring them for classes. I began to think about how proud I am of my mentees and how exciting it is when they succeed. I love to hear about when they pass an exam, when they get a line of new code to run, and generally share their excitement for science. I have also been able to work with them in outreach and our lab enjoys being able to show others how exciting science can be, especially when they are at a young age.

My most impactful experiences have been working with K-12 students. The mother of 8-year-old Erin emailed me after I talked with her about snakes and turtles and said, “Our daughter couldn’t stop talking about how cool it was for a ‘big girl’ to love science as much as she does”. I will be part of the generation that prioritizes supporting anyone excited about learning and being involved in research. I want to help the science community continue to thrive and improve, and get more students to be excited about science, like I am. My reflection led me to realize how much I value teaching others. My excitement to answer difficult questions, and see that excitement spread through the people around me are the reason I am writing this essay and applying for PhD programs. I have developed and contributed to a fantastic community, and I can not wait to see it grow at Washington University in St. Louis.

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**The intriguing question:** After deciding to pursue a PhD, I began searching for a project to pique my curiosity for new ways to use bioinformatic tools to answer difficult questions. When I first read about Dr. Landis' work on the coronavirus and the groundbreaking computational tools he was developing, I quickly emailed him to learn more. After talking with him about his work and research program, I want to focus my dissertation on studying the causes and consequences of disease evolution and improve the tools scientists use to predict disease evolution. Getting to read about an AI tool predicting disease evolution, made me reflect on all the evolutionary studies I have worked on since I began my research journey. This project would allow me to contribute to something greater than myself. I can not see a future where I am not working on this challenging but crucial research. Overall, several faculty at Washington University, including Dr. Ben-Shahar, Dr. Lawson, and Dr. Kellogg, are conducting research projects that are interesting to me and would be great to have as potential advisors and mentors.

**Essay 2:** Please upload each essay as either a PDF or Word document. Submit no more than two (2) single-spaced pages per essay (or approximately 8000 characters, including spaces). Drawing on your life experiences (personal and/or professional), please provide a statement showcasing examples of core strengths (e.g., courage, creativity, perseverance, determination) that forged your leadership characteristics and resolve. How will these traits enrich the biosciences training community?

**Essay 2 Answer:**

I feel that we are best described by those we associate ourselves with. I had a difficult time describing my core characteristics in two pages, so I reached out to those who know me best, and asked them to describe me as if they were talking to a stranger. My closest family, friends, and faculty mentors described me as courageous, dependable, and intellectually curious. After hearing the testimonies that I will share with you, I also want to add honesty to the list. I don't know many people who would trust their graduate school application with the people who have seen them at their worst, but honesty is a core value that I apply to all aspects of my life.

After asking my mom, dad, and sister for their testimonies, I had a hard time seeing myself the way they do. “I have been calling you brave since you could walk. I would always find you making new friends and catching animals in our backyard. You were always the first to step up and try something new” said my mother. Of course our parents want us to be brave, and mine have always been encouraging. So, when I decided to work with venomous snakes, I think she might have regretted being so encouraging. Understanding poorly understood and, in some cases, loathed, creatures is a passion for me, and I had a hard time seeing myself as brave, but my sister explained it to me perfectly. “You would not see yourself like that because those are decisions that you think are necessary, but most people are too scared of your commitment. When you set your mind on something you see it through.” It took me a while to realize not everyone commits to goals the way I do. But to me, starting something is always the hardest step, and every project started deserves to be completed. Once I start an application, or paper, or grant application, I want to make sure I represent myself, and those around me to the high level I hold myself accountable for. Today, I am making commitments that will direct my future career. I grew up in the St. Louis area, and committed myself to moving away for college. I knew distance would help me grow as a student and person. I was one of three people in my highschool class of

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200 that moved away for college. To give myself a chance to return to my St. Louis roots is another commitment I have made. Going away for college had a very influential impact on me, and I am ready to make that same impact on others from my home community.

My closest friends called me dependable. “You are always there for people, and willing to help,” said my friend Nicole. “You are the most dependable person I have met,” said my roommate Maddie. I care very much about the people around me, and always want to see them succeed. The best way I can do this is by being there for the people around me. I also reached out to the undergraduate students I have mentored, as I consider them both my colleagues and friends. Sara Beth, a student I mentored during her sophomore year and have worked closely with since said “ Grace is a natural team leader and values conciseness and organization. Not only does she prioritize her own success, she is determined to encourage others to reach their highest potential”. I am so proud of Sara Beth, and have watched her succeed in both research and academics since joining the lab. She is now also starting to apply for graduate school. Adrianna, a student I began mentoring this semester said “In the short time that I’ve known Grace for, she has been a kind, caring, and incredibly helpful mentor and leader. She always keeps the research lab moving in the same direction and maintains a positive and supportive learning environment”. I am currently assisting Adriana with designing a research project, and can not wait to see what she will accomplish in the future. If someone is going to put in effort and care for something, I will match that effort every time. My friends and mentees are very high on my list of priorities, and I always make time to help them reach their goals, and be their best selves.

The faculty who have mentored me during my undergraduate degree called me intellectually curious, intrinsically motivated and an asset in research, the Biology Department, and on campus. Growing up in Missouri I was always digging in the mud and searching for new discoveries from a young age. My elementary teachers quickly realized I was different from my peers, because I was always asking questions and searching to learn more. I loved school, and was lucky to grow up in a supportive environment that encouraged me to ask questions and explore. My professors saw this deep rooted curiosity in me as well. “I don't see many students like Grace. She is very motivated to learn more about how the world functions” said my professor and thesis committee member, Dr. Jonathon Pérez. He and others have kindly supported me and helped me achieve the high level of success I am at. My mentor Dr. Strickland, who has been there for me every step said “Grace is truly exceptional - whether it's her thoughtful approach to research or mentoring peers, her unwavering motivation, her creative problem-solving, or her trustworthy and dependable nature, she consistently exceeds expectations". I am very thankful for the faculty I have been able to work with, and for their encouraging words that pushed me to apply to Washington University and reach my full potential.

After hearing the testimonies from my family, friends, and mentors I would like to add one more descriptor, Honesty. Each decision I have made for my academic career has stemmed from an honest desire, that I want to contribute to something greater than myself. Knowing this has allowed me to have endless motivation, and the ability to complete this goal. By being honest with those around me, I have excelled as a student and mentor. I have developed many trusting connections with students and faculty alike. Having an ability to create relationships where I am trusted as a friend, mentee, and mentor will serve me and those around me well in the future. I have also been able to perform better as a researcher by being honest about my availability and ability. Being naturally curious about the world generates a lot of questions, and not all of those

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questions have time to be answered. I always am honest with those around me and myself to generate the best outcome of the projects I do choose to take on. This has allowed me to be a better leader and contributor to the questions I do ask and answer. Being honest, courageous, determined, and intellectually curious will continue to contribute to my success as a researcher. It is these traits that I will bring to Washington University in St. Louis if I am accepted as a Ph.D. student.

Description of scientific contributions:

**Please provide a 200 word description of your research experience and your specific contribution.**

T. sirt

The Common Garter Snake (*Thamnophis sirtalis*) is a rear-fanged snake and is venomous. Only 23% of all rear-fanged snake species have published transcriptomes, and even genera and species with rich ecology and evolution literature, such as the Common Garter Snake, are data deficient. My work focused on characterizing the transcripts produced in the venom gland and determining if there is sexual dimorphism in venom gene expression between males and females. Within my mentor's research program on venom evolution, I developed the idea, wrote and defended my project proposal, and submitted grant applications to support it. I led fieldwork and trained incoming students in field biodiversity surveys and animal husbandry. After practicing on rattlesnakes, I sampled, processed, and generated venom gland transcriptomes for eighteen Garter Snakes. I used publicly available data in other species to learn the bioinformatic pipeline and processed the data I generated to test for sexual dimorphism. I am the first to characterize the species' venom which can be used by other researchers studying rear-fanged snakes and potentially for identifying novel biological compounds.

Watermelon

Watermelon, *Citrullus lanatus*, domestication has led to significant changes in fruit quality traits, including higher sugar content compared to its wild relatives such as *Citrullus amarus*. Structural variants (SVs) have been reported to contribute to these domestication traits but are understudied due to their complex genomic structure. To address the lack of understanding on SV's effect, I conducted a comparative study between the cultivated representative genome of *C. lanatus* subsp. *vulgaris* and a wild representative genome of *C. amarus*. I aligned the cultivated and wild genomes, identified SV's, and annotated the affected genes using different software and coding platforms. I identified 111,738 SVs, which affected 19,482 and 19,096 genes in the cultivated and wild genomes, respectively. SV's affected 1,107 genes directly linked to fruit development in the cultivated genome and 838 genes in the wild, these genes were differentially expressed. By integrating SV and differential gene expression information, I identified candidate genes crucial