

To the International Society for Computational Biology,

The RADCamp workshop series hosted its third full-stack, all-inclusive wet lab, sequencing, and bioinformatics workshop from July 20–27th, 2026, in association with CoreLab Genomics at Tecnológico de Monterrey, in Monterrey, Mexico. The workshop aimed to provide much-needed training in high-throughput library prep and bioinformatics methods, specifically for colleagues from Latin American countries. Given limited funding for scientific research throughout Latin America, an additional goal of this workshop was to raise sufficient funds to offset participant support costs for lab materials, sequencing, travel, and lodging. We are happy to report that the workshop was an outstanding success through a huge effort from everyone involved, from organizers to support staff to participants to numerous administrators and sales reps, and through outstanding financial contributions from numerous societies, most notably from the International Society for Computational Biology through the Advancing Computational Biology and Bioinformatics Grant.

Our goal for this workshop was to support and lead sixteen Latin American participants through a full pilot RADseq project, from genomic library preparation to high-throughput sequencing, bioinformatics, and downstream analysis. RADseq is a reduced-representation library preparation protocol for short-read sequencing that selects reads from regions adjacent to restriction enzyme recognition sites, providing a cost-effective alternative to whole-genome sequencing. Although RADseq requires little specialized equipment, detailed knowledge of library preparation protocols can present a significant barrier to entry. Therefore, in the first part of the workshop, we aimed to provide complete instruction on implementing 3RAD (a RADseq variant developed by workshop co-organizers and co-instructors) using participants' own set of 24 DNA samples. This included introducing the necessary reagents and equipment, where and how to obtain them, challenges and troubleshooting in Latin America, and hands-on experience implementing the protocol. Following this first part, all participant libraries were pooled and sequenced in-house on the Illumina NovaSeq 6000 platform, thanks to the state-of-the-art facilities and resources provided by CoreLab Genomics at Tecnológico de Monterrey, where the workshop took place. With a turnaround time of 18 hours to generate all sequence data, our goal was then to introduce *ipyrad2*, the recently updated, powerful, and user-friendly RADSeq assembly tool, also developed by the co-organizers and co-instructors, as well as Linux command-line utilities, Jupyter notebooks, and the *ipyrad2analysis* tools, which enable reproducible bioinformatic analysis. The CoreLab also made this bioinformatics portion possible, in collaboration with the Data Science Hub team at Tecnológico de Monterrey, which provided servers to enable efficient data analysis. With support from the societies and CoreLab, we covered the full cost of reagents and sequencing, participants' and instructors' travel and accommodations, coffee and snacks each morning of the workshop, and a mid-week social bowling activity to encourage networking among participants and instructors.

RADCamp Latin America 2026 received 92 applications from candidates in Argentina, Brazil, Chile, Colombia, Mexico, Panama, Paraguay, Peru, Puerto Rico (and elsewhere in the United States), Slovenia, Spain, and Uruguay, representing scientists at different career stages and from diverse socioeconomic backgrounds. We hosted 16 participants from Argentina, Brazil, México, Uruguay, and Paraguay (5 male- and 11 female-identified, as self-reported in response to the prompt: "What is your gender identity?"). The pool of participants included four faculty/professors, one early-career scientist, one research fellow, five postdocs, one lab technician/manager, three PhD students, and one master's student. We focused on researchers at leadership stages so they could share their knowledge with other researchers. Participants came from universities and institutions from all over these countries in Latin America, with 3 different institutions from Argentina (Universidad de Buenos Aires, Universidad de Rosario, and Centro Austral de Investigaciones Científicas Ushuaia), two different institutions from Brazil (Instituto Nacional de Pesquisas da Amazônia and Universidade Federal do Paraná), one from Paraguay (Instituto de Investigación Biológica del Paraguay), one from Uruguay (Universidad de la

República), and four from Mexico (Universidad Nacional Autónoma de México, El Colegio de la Frontera Sur, Universidad Autónoma de Baja California, Universidad del Mar, and Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias). Study organisms investigated during the workshop were similarly diverse, sampled broadly across the eukaryote tree of life, and included quebracho trees, ghost spiders, birds of prey, flamingos, Amazonian mushrooms, endophytic fungi, cacao trees and relatives, mygalomorph endemic spiders, neotropical ants, Western screech-owls, Northern rainfrogs, bottlenose dolphins, paradoxical frogs (*Craugastor*), vesper mice, neotropical cichlid fishes from Nicaraguan lakes, and tarantulas.

In total, we sequenced 10 of the 16 3RAD projects, as library preparations were unsuccessful for 6 participants due to insufficient DNA. Nine of these ten projects produced sufficient reads for further analysis. The sequencing run generated 261.36 Gbp of 151-cycle paired reads, which translated to 800,585,572 reads that passed quality filtering. Of these, 95.01% of reads had a quality score equal to or greater than Q30 on the Phred scale. Each of the nine successful participants' projects obtained from 6.27 to 20.77 Gbp of data. Altogether, these metrics indicate the success, high quality, and abundance of the data generated.

To give everyone access to assembling and analyzing real data, participants who could not generate data from their own organisms were mentored to download publicly available RADSeq datasets for organisms of interest, if they did not already have one. The bioinformatics portion of the workshop introduced the *ipyrad2* RADSeq assembly and analysis tools. We first led participants through quality-control steps and a mock assembly of simulated data, then gave them time to assemble their real data. CoreLab generously provided computational resources for this part of the workshop. Participants also learned standard population genetic (principal component analysis) and phylogenetic (RAxML maximum-likelihood phylogenetic inference) analyses.

On the final day of the workshop, we held a symposium in which all participants were asked to create a few slides presenting their focal system, key research questions, and workshop results. All sixteen attendees, regardless of whether library prep and sequencing worked for them, so we could learn and discuss any challenges that may be present and how to troubleshoot them.

Overall, the workshop was highly successful. Collectively, the instructors had led numerous prior RADCamp workshops, including two previous all-inclusive workshops: RADCampNYC-2019 and RADCampNYC-2023. Building on lessons learned and experience from these previous workshops, and facing new challenges in bringing these technologies to Latin America, we effectively planned and managed the significant advance preparation and on-site execution required for a successful workshop.

We circulated an anonymous post-workshop survey for participants to express their insights regarding 1) workshop impact, 2) future impact, 3) genomics in Latin America, 4) workshop organization, 5) workshop instruction, 6) wet-lab component, 7) dry-lab component, 8) facilities, 9) demographics, and 10) afterthoughts, which we are sharing as an Appendix below. Overall satisfaction, on a scale of 1 (very low) to 5 (very high), was 4.87. The average likelihood of recommending the workshop was 5 (very likely), and 93.3% of survey respondents categorized our workshop as "Among the best I have attended." All these metrics reflect participants' positive experience. We also want to highlight some of the participants' comments that underscore the value of this type of initiative in Latin America, as 40% of survey respondents replied "Definitely not" and "Probably not" to the question of whether they would have attended a similar workshop elsewhere if it had not been offered in Latin America. 93% of survey respondents selected "Rarely" or "Never" to the question of how frequently this kind of workshop is available in your country.

“Thank you to everyone who made this workshop possible. One of the aspects I appreciated most was that the workshop went far beyond teaching a protocol. We learned how to think critically, troubleshoot unexpected results, and understand the reasoning behind each step, which is far more valuable than simply learning a technique. I also leave with a valuable network of colleagues from different countries, and I hope we will continue exchanging ideas and collaborating in the future.

I would also like to acknowledge how important it was to hold a RADCamp edition in Latin America. For researchers like me, it provided access to hands-on training and methodologies that are not always easy to access locally. I hope this initiative continues to create opportunities for researchers across the region.”

We invested significant time organizing reagents, materials, sample shipments, and laboratory manuals for the wet-lab portion, and the exit survey showed this effort was worth it, as 93% of respondents agreed that the laboratory component increased their understanding of RADseq library preparation (5 on a Likert scale), answered they are very likely (80%) or likely (20%) to use the lab skills learned in the future, 93% answered they feel confident or very confident preparing 3RAD libraries after the workshop, and 100% of them are planning to teach these lab skills to others.

Similarly, we prepared the computational resources and planned all the bioinformatics material needed to assemble and analyze empirical datasets in real time over three days, including brand-new resources from *ipyrad2*. These instructions and resources were also a major benefit to participants. 93% of respondents said the bioinformatics component increased their understanding of genomic and data analyses (5 and 4 on a Likert scale), 67% said they felt confident or very confident using *ipyrad* after the workshop, and 100% rated all the resources provided in the bioinformatics portion highly.

Some of the long-term impacts we detected from the exit survey are that half of the participants feel very confident (5 on the Likert scale) that they can now implement these advanced genomic methods in their home institutions. Importantly, 20% of survey respondents may train more than 20 people at their home institutions, while about 50% of the rest may be able to train between 6 and 20 more people, showing high expected dissemination rates for these protocols. Finally, 93% of survey respondents affirmed that the workshop will contribute to new research projects and collaborations, whereas 67% also mentioned new grant proposals, new scientific publications, and the establishment of genomic methods at their home institutions.

The [RADCamp Latin America 2026](#) workshop received generous support from the American Genetics Association (AGA) through the Special Event Awards program, the Society for the Study of Evolution (SSE) through the International Event Grants, the American Society of Naturalists (ASN) through the Workshop and Regional Society Committee, the International Society for Computational Biology (ISCB) through the Advancing Computational Biology and Bioinformatics Grant, the British Ecological Society (BES) through their Research Equity Fund, CoreLab Genomics from Tecnológico de Monterrey, and the National Science Foundation through award #DEB-2046813 to Deren Eaton. During this workshop, we provided a diverse group of Latin American participants with hands-on training in a broad array of techniques, from lab work to bioinformatics processing and statistical inference. We are happy to report that the workshop was an overwhelming success, and this success was in no small measure due to the generosity of our sponsors, as indicated by 100% of participants who replied in the exit survey that the financial support was very helpful (5 on the Likert scale) in allowing them to participate.

With thanks on behalf of the RADCamp Latin America 2026 Organizing Committee,

Isaac Overcast

Natalia Bayona Vásquez
Deren Eaton
Erika Magallón Gayón
Sandra Hoffberg
Todd Pierson
Silvia Hinojosa Álvarez
Jesús Hernández Pérez
Andrea Félix Cenicerós