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Highlights

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Highlight: Community Tournament GHIST Fuels Advances in Computational Genetics

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In recent decades, computational biology has raced to keep pace with advances in data generation. Approaches have proliferated, particularly methods to infer population histories based on genomic data, which include those based on the site frequency spectrum (SFS), linkage disequilibrium, coalescent models, or ancestral recombination graphs. Amid this methodological diversity, it is challenging to determine the most suitable approach for testing a given evolutionary scenario. While new software tools are commonly benchmarked against existing tools, these comparisons are not standardized, preventing direct comparison of the relative performance of different approaches.

Collaborative competitions present an intriguing solution to this benchmarking problem. These initiatives enlist a large number of researchers to solve analytical challenges designed by the organizers (Meyer et al. 2011). The specific answer to each challenge is hidden from the competitors. Since different participants may use alternative methods to solve the same challenge, this facilitates direct comparisons between approaches.

While organizing bioinformatic competitions may seem like computational biologists' idea of a good time, these "crowdsourcing" initiatives have a long history of innovation in our field and have led to important advances. A prominent example is the biannual CASP competition ("Critical Assessment of protein Structure Prediction"), which served as the test bed for AlphaFold, the deep learning program for protein structure modeling that became one of the most consequential advances in protein biology in the last century (Jumper et al. 2021).

Ryan N. Gutenkunst, Professor at the University of Arizona (USA), was inspired by the success of CASP. In a new article now published in *Molecular Biology and Evolution* (Struck et al. 2025), Gutenkunst and colleagues report on the conception and first edition of *GHIST: The Genomic History Inference Strategies Tournament*, an initiative to overcome benchmarking challenges in genomic history inference. "The idea of GHIST and the related stdpopsim project actually began long ago in a Twitter conversation between myself, Adam Siepel, and Dmitri Petrov," Gutenkunst explains, referring to the community-driven stdpopsim initiative, which has developed a framework for standardized population genetics simulations (Adrion et al. 2020). He adds that "Adam Siepel hosted the first meeting at Cold Spring Harbor Laboratory, which led to stdpopsim starting, and from there, we developed GHIST."

So, how was GHIST implemented? The organizing team was led by Gutenkunst and Travis J. Struck, the first author of the article, in close collaboration with a "design team" that devised the challenges. The team generated genetic polymorphism data for four hypothetical species, each representative of distinct demographic scenarios involving combinations of bottlenecks, admixture events, or migration. Competitors could analyze the simulated data using their method of choice to infer key demographic parameters (eg estimates of population sizes, divergence times, or admixture proportions). Entries were scored based on how closely the contestant's estimates matched the simulated parameter values.

The first competition ran from July to November of 2024—kicking off with a workshop at the SMBE2024 annual meeting in Mexico—and attracted approximately 60 participants, from graduate students to senior faculty. Across the different challenges, methods based on the SFS generally exhibited the best performance, as they were both highly accurate and widely used. On the other hand, promising methods based on machine learning or ancestral recombination graphs were underused. "Although I knew SFS-based methods would be popular, I was surprised they held their own in the face of the many inference methods developed since then," Gutenkunst says. The four challenges varied in complexity, and it was not surprising that analyses of the more complex scenarios involving admixture were comparatively less successful in estimating the true parameter values. Validating expectations is what makes initiatives such as GHIST exceptionally valuable for refining future approaches in the field.

Since competitors with differing expertise faced the same challenges, awareness of the need to shorten the learning curve of computational tools was one of the most important outcomes of this first edition. Several junior participants reported poor documentation for popular software tools such as *dadi*, requiring video tutorials or mentorship. Underuse of more recently developed inference methods suggests that these approaches still require development to decrease their technical complexity before broad acceptance by the community.

Will GHIST succeed in fostering breakthroughs in genomic inference, mirroring the success of CASP for protein biology? As we publish this Highlight, the second edition of GHIST is already nearing its end (Fig. 1), featuring even more complex demographic scenarios. Gutenkunst explains that "in addition

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Fig. 1. GHIST workshop led by Ryan N. Gutenkunst during the Evolution 2025 meeting in Athens, Georgia (USA). The logo of the initiative is shown at the bottom. Photo by Katie Lotterhos.

to demographic history inference, GHIST now includes challenges for the detection of selective sweeps, devised in collaboration with Andrew Kern's group." This is just an example of how collaboration can increase the diversity of challenges and the overall scope of the initiative. "The competition only succeeds if the community engages and participates," ends Gutenkunst, adding that "we've worked hard to reduce barriers to competing, so everyone in the community should join in!"

Want to learn more? You can visit the GHIST website to learn how to contribute at https://ghist.bio; you can also check out other articles on bioinformatic tools for historical demography recently published in *Molecular Biology and Evolution*:

- "Comparison of Bayesian coalescent skyline plot models for inferring demographic histories" (Billenstein and Höhna 2024)
- "Computationally efficient demographic history inference from allele frequencies with supervised machine learning" (Tran et al. 2024)
- "Modeling biases from low-pass genome sequencing to enable accurate population genetic inferences" (Fonseca et al. 2025)

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