Post Doctoral Position: Imputation for Database-Wide GWAS USDA-ARS on Cornell University campus

The position is with the USDA-ARS Plant Soil and Nutrition Research Unit and the Jannink lab is co-located in the Plant Breeding and Genetics Section at Cornell University. The Jannink lab maintains the largest publicly available data resource on field and genotyping trials for wheat, barley, and oat: the Triticeae Toolbox (T3, triticeaetoolbox.org). The postdoc will leverage *de novo* assembled genomes in these species to create an imputation engine, which, combined with T3 data, will enable more powerful association analyses than ever before in these species.

The USDA-ARS Plant Soil and Nutrition Research Unit and the Cornell Plant Breeding & Genetics Section train interdisciplinary scientists in the elaboration of new breeding methods, the discovery of genetic mechanisms important for economically important traits, and the creation of genetic stocks, germplasm, and varieties. We promote a collaborative and interactive workspace to improve learning, cross connectivity, and mutual support between basic and applied researchers. We are world leaders in innovative plant breeding research, teaching, and extension, and we collaborate globally.

The Jannink lab works with several crop species (wheat, oat, barley, cassava, and the brown algae sugar kelp) to develop genomic prediction methods and integrate them optimally into breeding schemes. We work together to discover, build on, and share new ideas and tools from across computational disciplines that lead to successful applied breeding outcomes.

The valuable phenotypic data resource that we have compiled over more than ten years in T3 contains lines that have been genotyped on a number of different platforms, preventing a powerful joint analysis. Recent decreases in the cost of long-read sequencing have facilitated the *de novo* assembly of small but diverse panels in our target species. These panels sample a high percentage of the haplotypes segregating across the genome in domesticated populations and thus enable whole-genome sequence imputation for any line that is genotyped at sufficient density. Imputation, in turn, creates a uniform, high density marker set across lines as needed by many genotype-to-phenotype mapping analyses. The postdoc will work in this computational genetics space and collaborate with software developers to make analyses available to public-sector breeders globally.

We seek a candidate with computational biology expertise and interest in large-scale genotype-to-phenotype analyses as well as in software development. Primary tools for the analyses exist. The postdoc will implement them in robust code deployable in the cloud or local servers, apply them to data in T3, and publish methodology and discovery articles. In addition to T3, the campus hosts much relevant software development: Breedbase (breedbase.org), GOBii (gobiiproject.org), Breeding Insight (breedinginsight.org), and BrAPI (brapi.org). The postdoc will collaborate whenever fruitful with these efforts to extend functionality to broader audiences.

Term is two years.

Anticipated Division of Time

Imputation and GWAS model building and implementation	35%
Software development / collaboration	20%
Writing	30%
Training of lab members and collaborators in computational biology	15%

Position Requirements
PhD in bioinformatics or computational biology with knowledge of quantitative or population genetics, or PhD in plant or animal breeding, quantitative or population genetics with emphasis on computational and statistical methods. Strong programming skills, ability to collaborate on software development projects. Proficiency in R. Demonstrated communication skills, both written and verbal. Management and leadership soft skills a plus.

How to Apply
For further information, contact Jean-Luc Jannink (jeanluc.jannink@usda.gov). Applications should include a statement of interest relative to the research proposed here, a CV, and a list of three references. References will only be contacted if you give permission. We will review applications holistically, seeking to understand your relevant skills, your motivation for creating knowledge and problem solving, your contribution to our group's diversity and its organizational capacity. Review of applications will begin immediately and continue until the position is filled.

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