A quantitative-genetic decomposition of a neural network

We tested equivalent linear mapping (ELM) on a neural network trained to predict phenotypes from genotypes in simulated data. We show that ELM successfully recapitulates additive and epistatic effects learned by the model, even in data with substantial environmental noise.

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Purpose

Understanding the behaviour of deep learning (DL) models when applied to genotype–phenotype mapping has been a recent focus at Arcadia **[1][2]**. To date, our efforts have largely focused on exploring the predictive performance of various types of models (but see **[3]**). In this notebook, however, we extend our work to trying to understand how we might extract functional information from trained DL models. We apply a recently described method for obtaining equivalent linear representations of DL models to assess feature importance per input sample. We show that under certain conditions, the distribution of feature importance values across samples can be used to infer familiar quantitative genetic parameters such as additive effect sizes, epistatic interactions, and genetic variance components, allowing for the use of DL models in tasks such as genomic target identification and interaction mapping.

View the notebook

The **full pub** is available here.

The **source code** to generate it is available in this GitHub repo (DOI: 10.5281/zenodo.17458438).

In the future, we hope to host notebook pubs directly on our publishing platform. Until that's possible, we'll create stubs like this with key metadata like the DOI, author roles, citation information, and an external link to the pub itself.

Contributors (A–Z)

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References

1. Sandler G, York R. (2025). Epistasis and deep learning in quantitative genetics. https://doi.org/10.57844/arcadia-25nt-guw3
2. Bigge BM, Kiefl E, McGeever E, York R. (2025). Cross-trait learning with a canonical transformer tops custom attention in genotype–phenotype mapping. https://doi.org/10.57844/arcadia-bmb9-fzxd
3. Mets DG, York R. (2025). G–P Atlas: A neural network framework for mapping genotypes to many phenotypes. https://doi.org/10.57844/arcadia-d316-721f