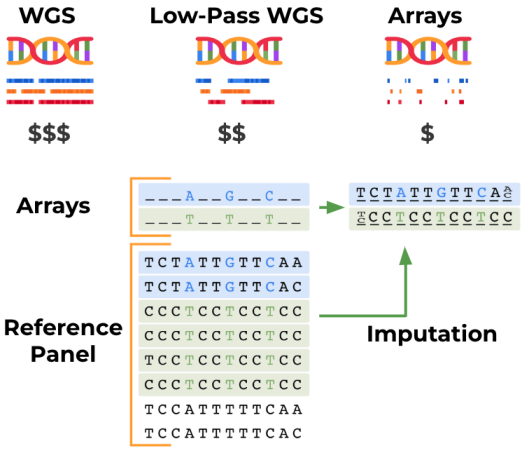
All of Us + AnVIL Imputation Service

BROAD INSTITUTE
DATA SCIENCES PLATFORM

Imputation leverages established reference panels to increase the power of array data.

Arrays are a cost-effective way to increase sample sizes and statistical power for population genetic studies. When paired with **imputation**, it can approximate genome-wide coverage at a fraction of the cost. The quality of imputation is greatly dependent on the **size, accuracy, and diversity** of the reference panel.

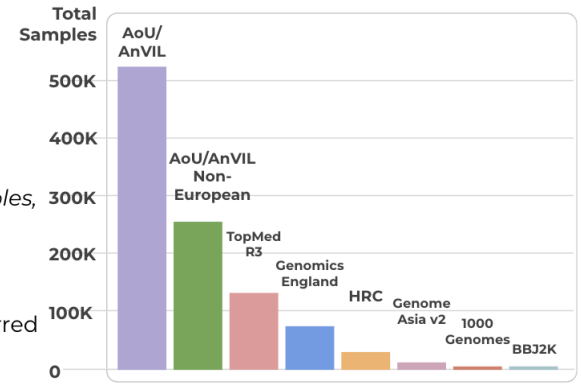


With the world's largest, most diverse reference panel, All of Us + AnVIL Imputation Service delivers superior accuracy for discovery.

All of Us RESEARCH PROGRAM
AnVIL

Over 515,000 *samples, including more rare variants.*

Over 250,000 from non-European inferred genetic ancestries



Combining results from two NIH flagship projects, ***All of Us*** and **AnVIL Centers for Common Disease Genomics**, the reference panel contains over 515,000 high-quality genomes, enabling top-tier imputation accuracy, especially in underrepresented ancestry groups and for rarer variants.

Key Features

Secure Service
FISMA and FedRAMP Moderate. Industry-level infosec best practices.

Scalable sample size
The **cloud-native** service scales to match the size of your genomic research.

Fast turnaround
Turnaround time within **days** (vs. weeks to months using other services).

Versatile interface
Both **CLI** for computational researchers and **GUI** for low-code users.

Try it now and get the first 2500 samples processed for FREE!*

*Limited-time offer sponsored by NIH.