

Zetta Genomics

Unleash the power of genomic data

Zetta Genomics - A history of innovation in Genomic analysis...

Developed during a seven-year collaboration with:



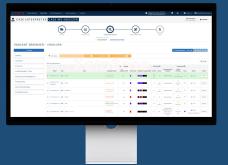




Our future proof solution is designed specifically to deal with the challenges of managing genomic data at massive scale



World leading genomic data management solution including tertiary analysis - enabling research and clinical use from the same platform.





Xetabase has 4 Customer segments



National Genomic Database projects



Clinical Genomic services



Pharmaceutical / CRO research



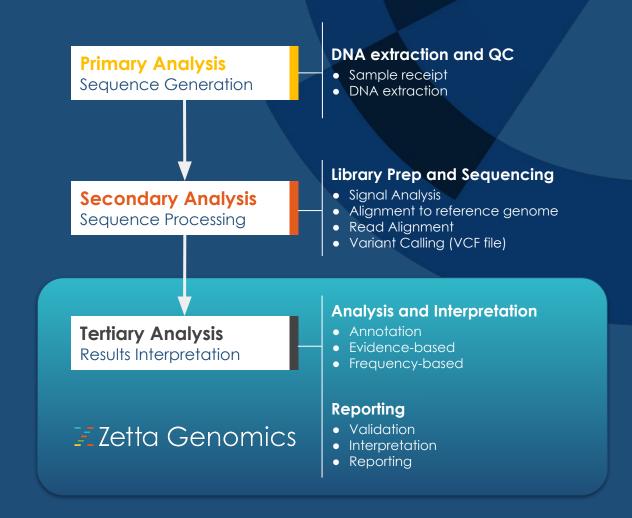
Academic research



Where does Zetta fit into the sequencing pipeline?

We store and enrich the data from secondary analysis in a unique way, enabling our users to complete **tertiary analysis** quicker and with a higher chance of successful diagnosis.

- An integrated Knowledge base annotates and enrichs variants with biological information from over 40 sources including ClinVar and COSMIC
- The variant data store allows rapid re-interpretation in clinical use (important for neonatal care).





Existing data storage technologies limit the usability of Whole Genome Sequence data



Genomic data is difficult to manage

VCF file storage systems are cumbersome to organize and difficult to control access. Apache Spark immutable data files have long lead times to refresh data - unsuitable for clinical use



Phenotype and Reference data is not static

New pathogenic variants are identified continuously patients miss out on diagnosis when their genomic data is not held in a variant store which enables easy re-analysis



Solutions built for panels not WGS

Solutions for gene panels and exomes are not designed for whole genome sequences and will not cope with the increasing number of WGS as costs decrease.

1 Exome = 15000 variants , 1 Genome = 3M variants



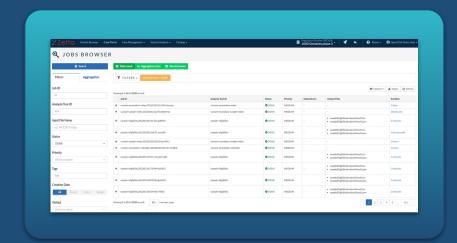
Time-consuming

Interpretation and analysis pipelines can be clunky and inefficient. Bioinformaticians are a scarce resource, reducing their workload is a priority



Our Solution: ==etaBase

A genomic-native tertiary analysis tool powered by world leading genomic data management solutions.





Real-time, self service access - no cold storage of data



Simple and customisable UI



High speed upload and annotation



Automatic reanalysis



One platform integrating clinical and variant data



Pioneering dual-indexed database

Real-time

A single, highly automated platform which cuts processing times, reduces workload and accelerates speed to discovery.

Scale

Capable of processing whole genome, whole exome or gene panel samples without impacting performance.

Confidence

Compliant - Cloud and on-premise hosting options developed under ISO27001 and ISO13485.



Zetta Genomics

What do our customers think?



"With the ability to rapidly access, interpret and interrogate genomic data, there is real potential to identify disease more accurately, intervene earlier and deliver more effective and less invasive treatments"

"There is no software system like it anywhere in the world"

Xiaowu Gai

Director of Bioinformatics, Center for Personalized Medicine, Children's Hospital Los Angeles



"This is a game-changer for our clinical services, and we are excited to see where these new data capabilities will lead"

"My team will be able to look efficiently at unparalleled data volumes from the largest genomic tests"

Joo Wook Ahn

Bioinformatics Lead, East Genomic Laboratory Hub



"XetaBase is a data management system **developed specifically for the genomic age**.

It addresses both research and clinical needs – allowing us to store, analyse and constantly re-interrogate genomic data at scale and speed."

Alison Meynert

Senior Research Fellow & Bioinformatics Analysis Core Manager, MRC Human Genetics Unit, University of Edinburgh

Zetta Genomics Thank you