ROSABIO

Enhanced measurement of genetic complexity to drive clinical breakthroughs

Non-Confidential

December 2025

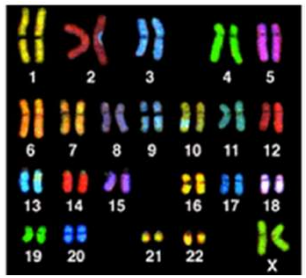
Old paradigm, new reality

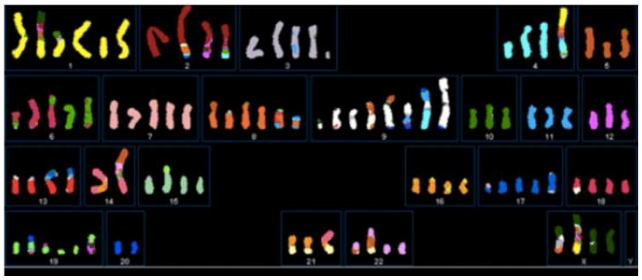
- NGS technologies generating massive amounts of genomic data
- Increasing importance of precision medicine and genetic screening
- Advances in ML and AI create new opportunities
- Current reference and alignment-based approach has inherent limitations

Reference genome-to-phenotype associations are based on a paradigm developed in a different era

Reference genomes poorly represent biology

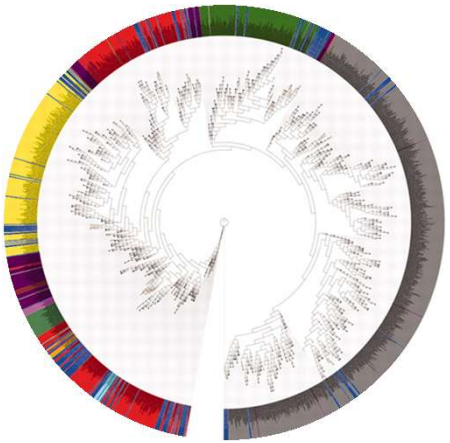
Normal (reference) vs. Cancer





https://bscb.org/learning-resources/softcell-e-learning/what-causes-cancer-more-details/

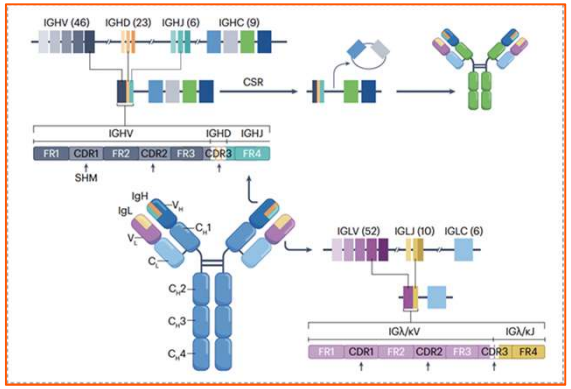
Human Microbiome



DOI: 10.1126/science.1183605

Immunology

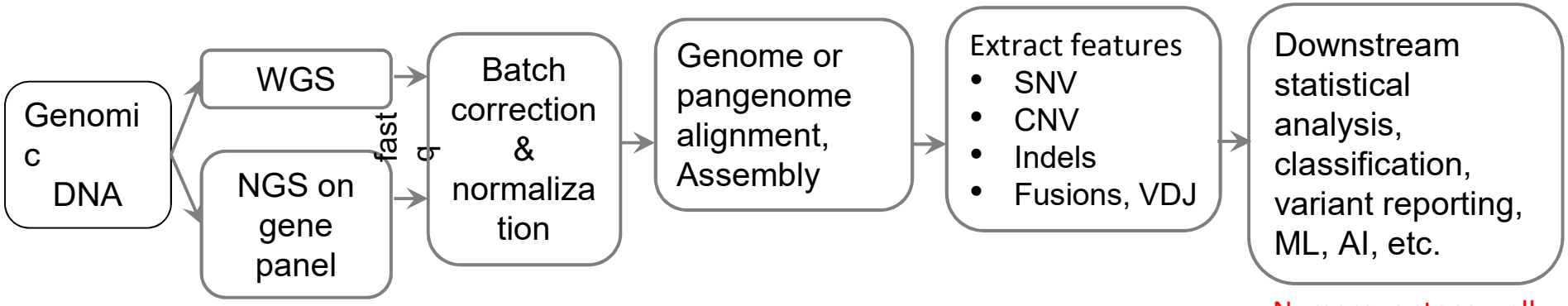
Adaptive Immune Receptor Repertoire



https://doi.org/10.1038/s43586-023-00284-1

YET, current methods are dependent on comparisons to reference genomes

Legacy genomics workflows are complex, time and resource intensive, and have unavoidable data loss



Many workflows need deep NGS to see signal - $$$
-
Upfront loss of data when using gene panels

Computationally intensive - $$$
-
Many hours to run
-
Degree of data loss depends on the reference

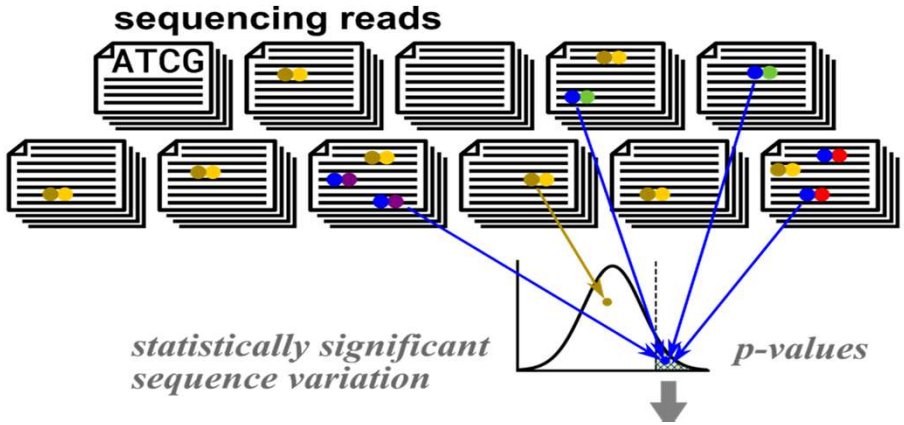
Numerous steps – all with data loss- are required prior to AI

A separate analysis workflow is required for other sample types – RNA, single cell, etc.

ROSA changes the paradigm with a “statistics first” approach

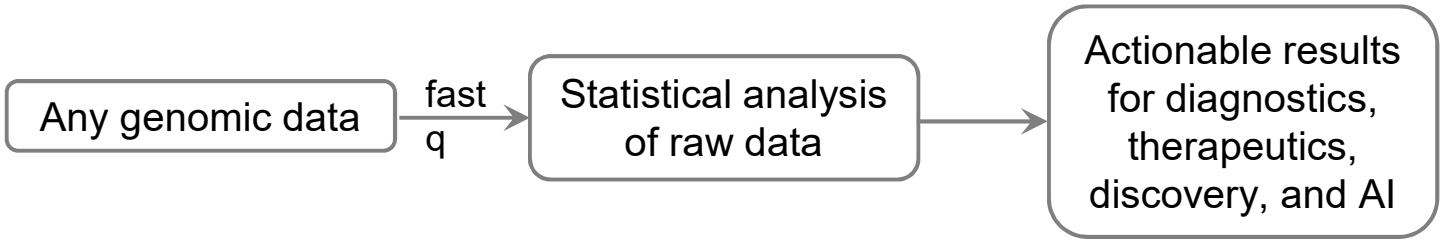
- Completely reference-free – uses all the data, eliminating the need for alignment.
- Robust statistical analysis for upfront extraction of signal from noise to generate AI-ready data.
- Can find signals that are missed by reference methods.

SPLASH: A statistical, reference-free genomic algorithm unifies biological discovery



Cell Volume 186, Issue 25 P5440-5456.

ROSA's Semore genetic analysis software platform: smarter, faster, cheaper



SMARTER: All raw data is analyzed statistically, minimizing loses

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FASTER: >10X

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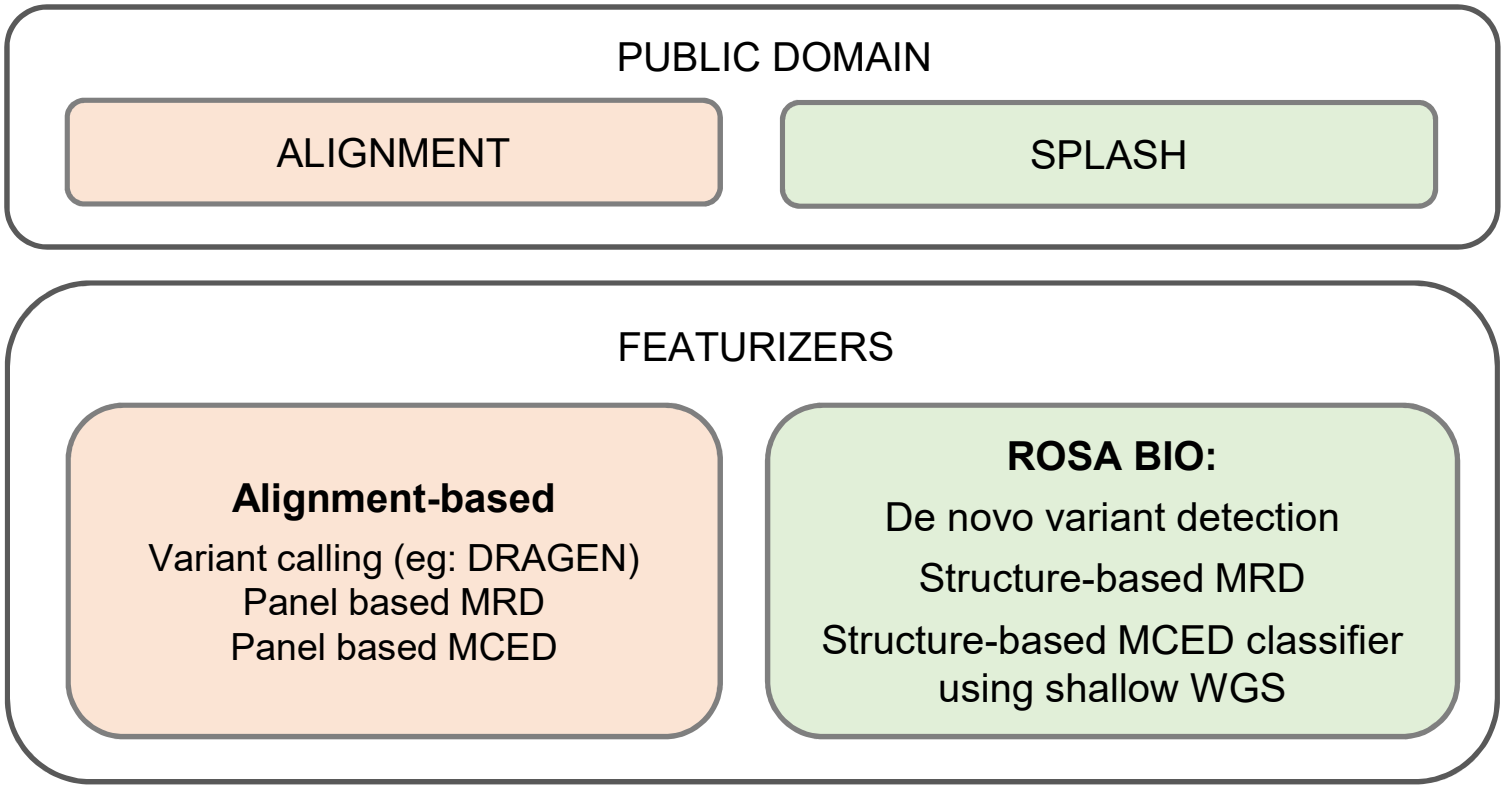
CHEAPER:
Computationally light - $

Comparison of Approaches to Genomic Analysis



ROSA Semore software ability to detect all genetic features leads to increased accuracy

Alignment pipelines:

- Miss critical hallmarks of cancer
- Repeat instability (2/3 of the *normal* genome are repeats[1,2])
- Chromosomal instability (CIN)
- Telomere instability
- Indels and structural variation
- Fusions

ROSA:

- **All genomic complexity can be detected**
- Many more “shots on goal” -- ~10x more markers than point variants
- Statistical weighting of features– not just presence/absence
- Plasma queries with much richer signature

1. https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1002384
2. https://www.nature.com/articles/s41588-024-02051-8

ROSA Semore Software Overview

- ROSA's "statistics first" Semore platform allows detection of genomic complexity missed by other methods
- Allows faster, cheaper, smarter genomics analysis
- Readily scalable
- Agnostic to nucleic acid type: DNA (WGS and targeted), RNA, short and long read, exome, non-coding regions, ctDNA, bisulfite, etc.
- Detects structure-based changes, not based on gene panels
- Can be used with tissue sample or liquid biopsy
- Semore software output = AI-ready
- Diverse applications: Dx, Tx, other

ROSA BIO Intellectual Property

- ROSA statistics-first approach is differentiated and protectable
- Foundational patent applications filed; solely owned by Rosa
- Additional patentable tools in development
- Proprietary platform software developed and solely owned by Rosa Bio