

AlphaGenome Atlas

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Why in News?

Google DeepMind officially launched AlphaGenome Atlas, a searchable interactive map predicting the functional and molecular impacts of all single-letter DNA changes across the entire human genetic sequence.

AlphaGenome Atlas

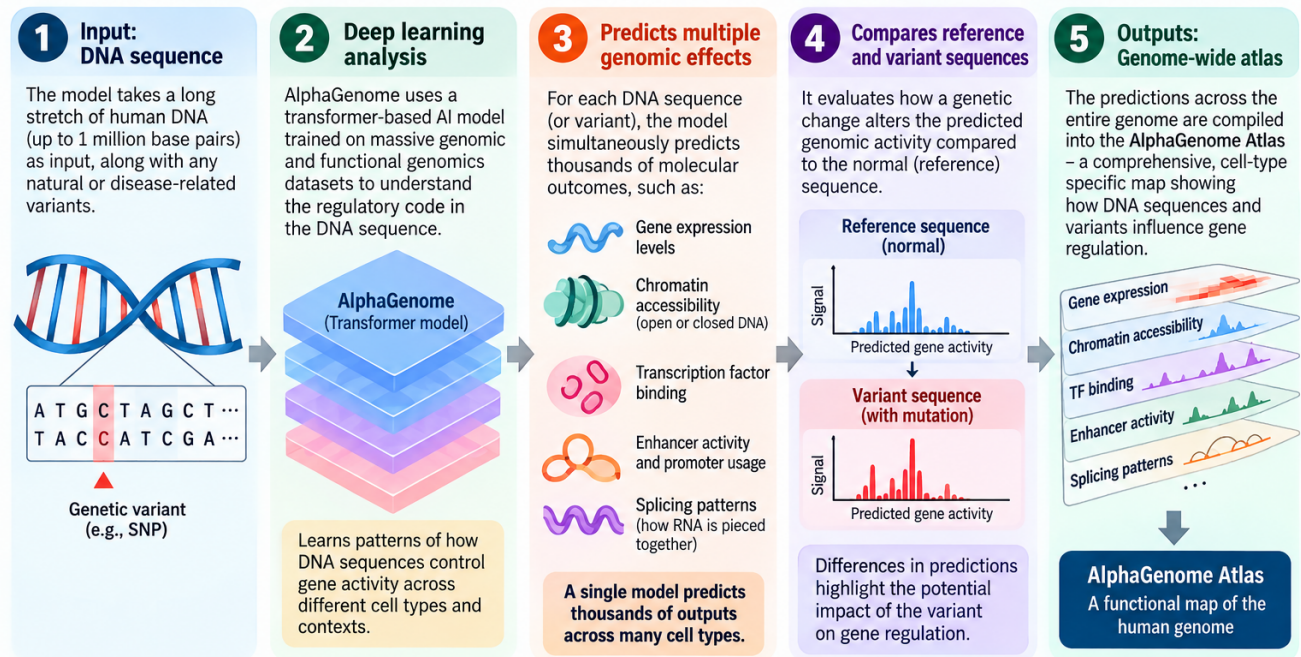
- **Comprehensive Precomputed Database** - A ~1-petabyte digital repository powered by DeepMind's *AlphaGenome* AI architecture.
- **Predictive Mapping** - The Atlas precomputes and maps all 9 billion single-nucleotide variants (SNVs) across coding and non-coding regions.
- **No-Code Academic Access** - Made freely accessible to academic researchers through a web-based portal and API requiring no specialized coding or local high-performance computing infrastructure.

Key Technical Capabilities

- **Unlocking the "Dark Genome"**
 - Protein-coding genes account for only ~2% of human DNA.
 - It maps remaining **98% (non-coding DNA)**, evaluating regulatory elements such as promoters, enhancers, and chromatin accessibility that govern when and where genes switch on or off.
- **AlphaGenome Variant Impact (AVI) Score**
 - Introduces a single unified scoring metric that combines functional regulatory forecasts from *AlphaGenome* with protein-altering predictions from *AlphaMissense*.
 - Enables scientists to instantly rank and prioritize candidate mutations for downstream laboratory validation.
- **Feature Attribution & Motifs** - Catalogs over 2,500 recurring functional DNA sequence motifs and provides detailed attribution breakdowns (e.g., highlighting errors in RNA splicing or altered gene expression).

Working of AlphaGenome Atlas

An AI-powered map that predicts how DNA changes affect gene activity across the entire human genome



Key Idea

AlphaGenome translates the “language of the genome” into functional predictions, helping researchers understand how genetic changes can impact human health and disease.

Significance

- **Accelerating Rare Disease Diagnostics**- Helps pinpoint disease-causing non-coding variants hidden among thousands of harmless background mutations in patients with unsolved genetic disorders.
- **Prioritizing Drug Targets** - Speeds up early-stage pharmaceutical discovery by mapping how point mutations impact cellular function across hundreds of human and mouse cell types and tissue models.
- **Hypothesis Generation Tool** - Serves as an expressive, high-throughput predictive engine rather than a direct clinical diagnostic tool, providing researchers with a structured starting point before committing laboratory time and capital.

Reference

[Times of India | Google launches Alpha Genome Atlas](#)



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