Accelerated Genomics and AI for Advanced Precision Breeding

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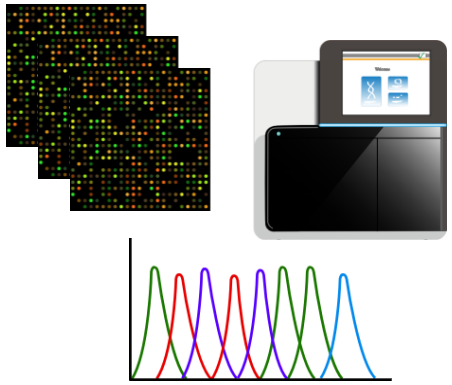
Senior Scientist, Genomics and AI @ NVIDIA

Precision breeding is a resource-intensive process

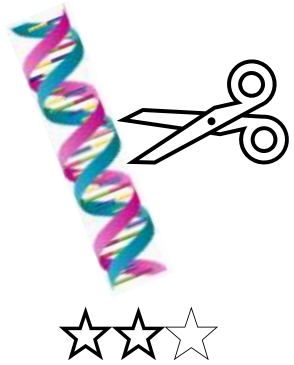
Identifying genetic components to edit requires significant time, sequencing, and compute resources

Phenotyping



Sequencing

Bioinformatics + Association Testing



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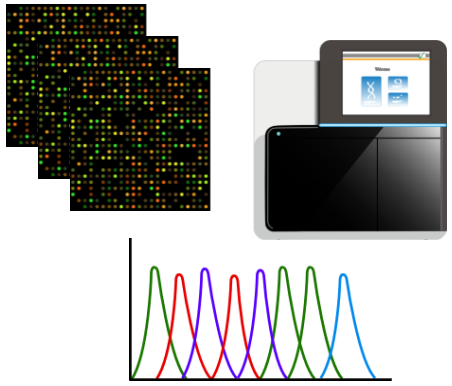
Precision breeding is a resource-intensive process

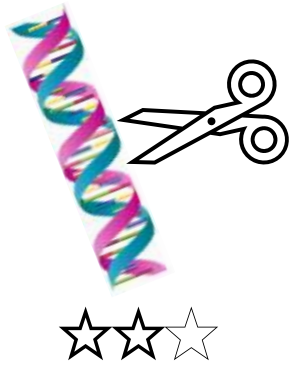
NVIDIA's tools can help make this process faster, cheaper, and more accurate, facilitating discovery.

Phenotyping



Sequencing

Bioinformatics + Association Testing



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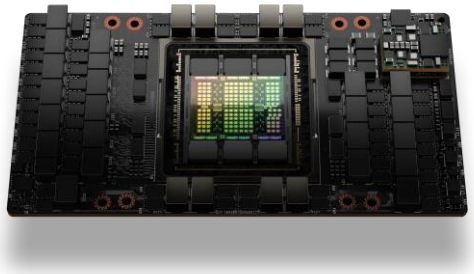
MONAI
MEDICAL OPEN NETWORK FOR AI

TensorRT

PyTorch

NVIDIA
CLARA PARABRICKS



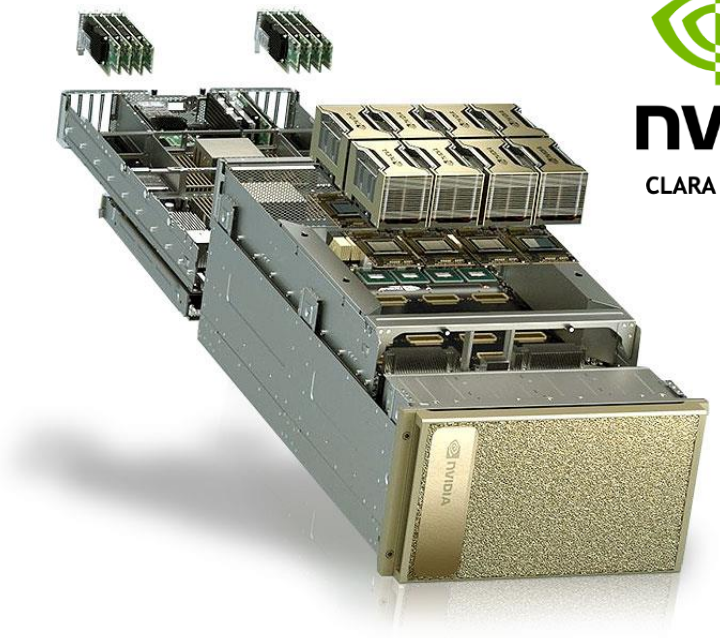
NVIDIA
TAO

TensorFlow

RAPIDS

Accelerating genomics with NVIDIA GPUs

Support and solutions across major short- and long-read sequencing and analysis platforms



NVIDIA CLARA PARABRICKS

PacBio

Oxford NANOPORE Technologies

ULTIMA GENOMICS

SINGULAR GENOMICS

Terra

DNAnexus

lifebit

aws

Google Cloud

BAIDU AI CLOUD

ORACLE CLOUD

Alibaba Cloud

NAVER CLOUD PLATFORM

Across the Computational Genomics Workflow

From sequencing sensor to biological insights

TACGTG

DNA Basecalling

TACATG

Basecall polishing

ATTCATGG
TACATG

Alignment / assembly

ATTCATGG
TACATG

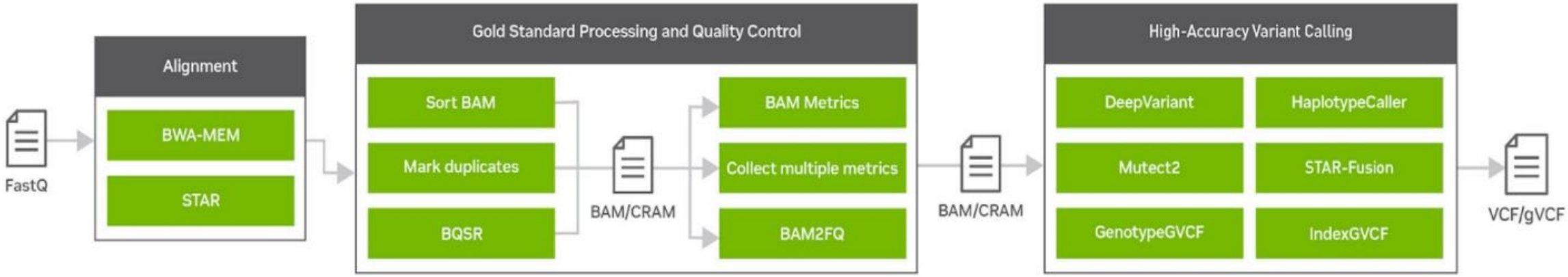
Variant calling

Interpretation / modelling

Primary — Secondary — Tertiary

NVIDIA Clara Parabricks

Accelerated genomics powered by NVIDIA GPUs



Key Applications

Industry-standard germline, somatic and RNA tools

Up to 80x Acceleration

Up to 80x faster & 50% cheaper for WGS than CPU-only

Flexible Workflows

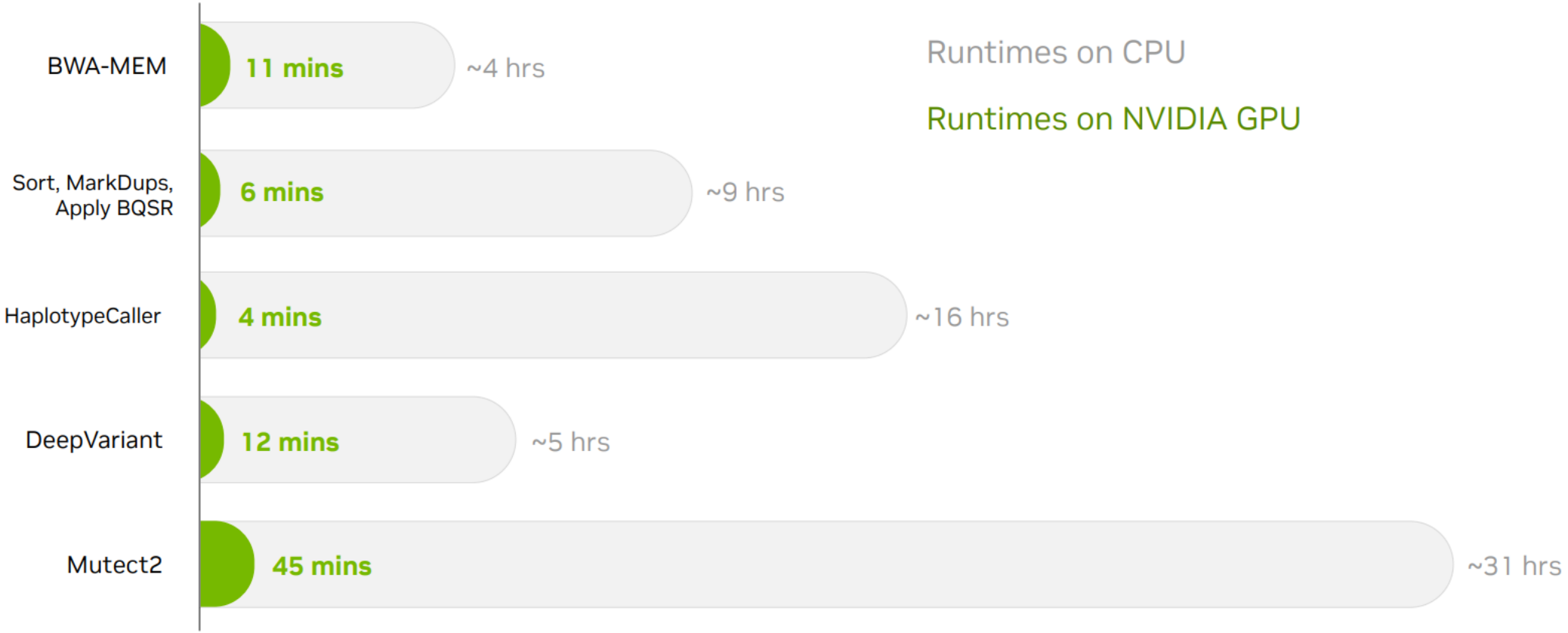
Customizable & scalable workflows for high throughput analysis

Better Accuracy

The power of deep learning for high accuracy analysis

Parabricks Acceleration

High Speed Option: Up to 80x faster on the NVIDIA DGX



v3.8 Benchmarks
Dataset: HG002 30x WGS, except Mutect2 on SEQC2 50x WGS
CPU: m5.24xlarge; GPU: 8xA100, except DeepVariant & Mutect2 on 8xV100

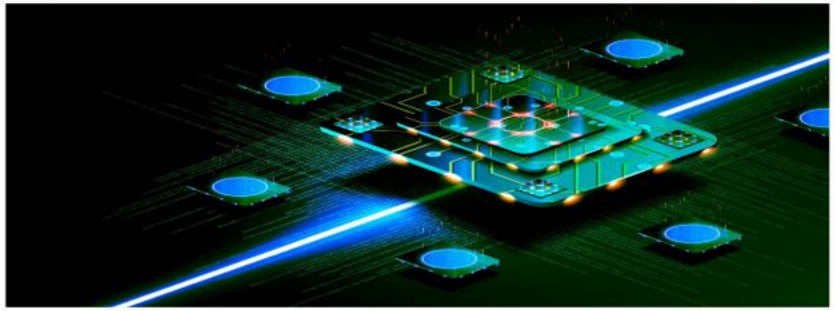
NVIDIA

Parabricks Scale & Cost

Cost Effective Option: 50% cheaper

Terra

MENU



NVIDIA's Clara Parabricks workflows in Terra bring GPU acceleration to genomic analysis

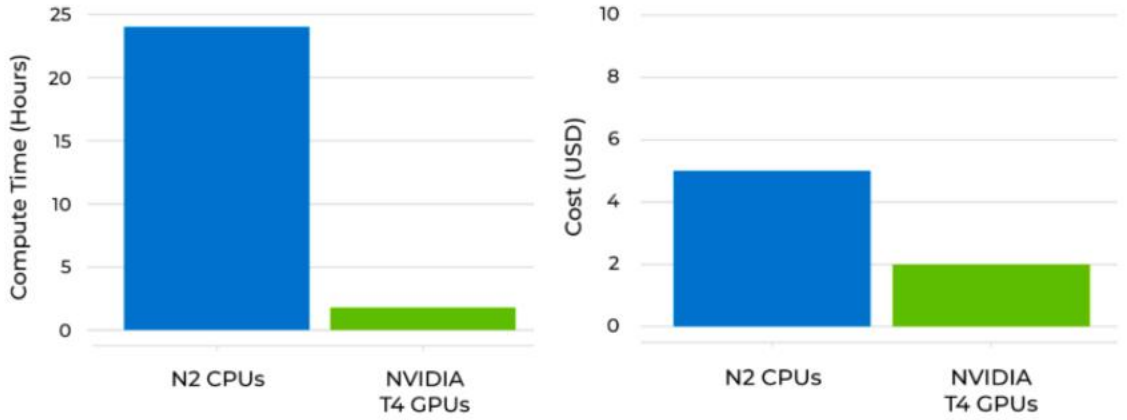
Geraldine Van der Auwera

September 20, 2022

The past few years have seen a massive surge in the development of advanced analytical methods for biomedical research, fueled in part by technological innovations that allow computational scientists to crunch data at ever-increasing speed and scale. A growing number of technology companies have joined the effort to help researchers tackle emerging challenges, ranging from large-scale genomics to multi-modal analysis of the myriad data types associated with medical records — including doctors' notes, which are famously easy to read and interpret.

Today NVIDIA, a pioneer in AI and accelerated computing, announced a new partnership with the Broad Institute that will pool the two organizations' respective expertise in deep learning, accelerated compute, and biomedical research. This partnership builds on an existing collaboration between NVIDIA and the Broad's GATK team, who have already been working together to improve some of the deep learning algorithms in GATK. (Keep an eye on the GATK blog for an upcoming release announcement.)

The NVIDIA team released a Clara Parabricks workspace in Terra that makes their GPU-accelerated genomic analysis toolkit available on the cloud at the click of a button. As



NVIDIA

Enabling Genomics at Industrial Scale

Over 1 Million Whole Exomes Analyzed

HIGH THROUGHPUT LABS

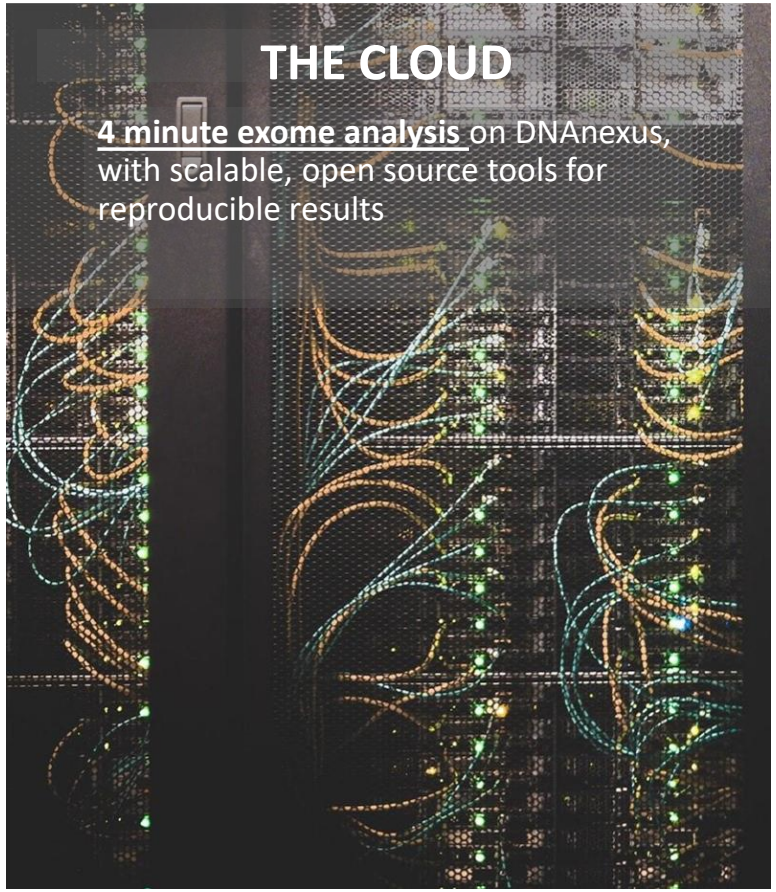
Regeneron Genetics Center using Google's DeepVariant:

Processing 20,000 exomes/week, with >1 million exomes to date

BIOBANKS

UK BioBank: ~500,000 UK genomes

A foundation for breakthroughs in prevention, diagnosis & treatment.

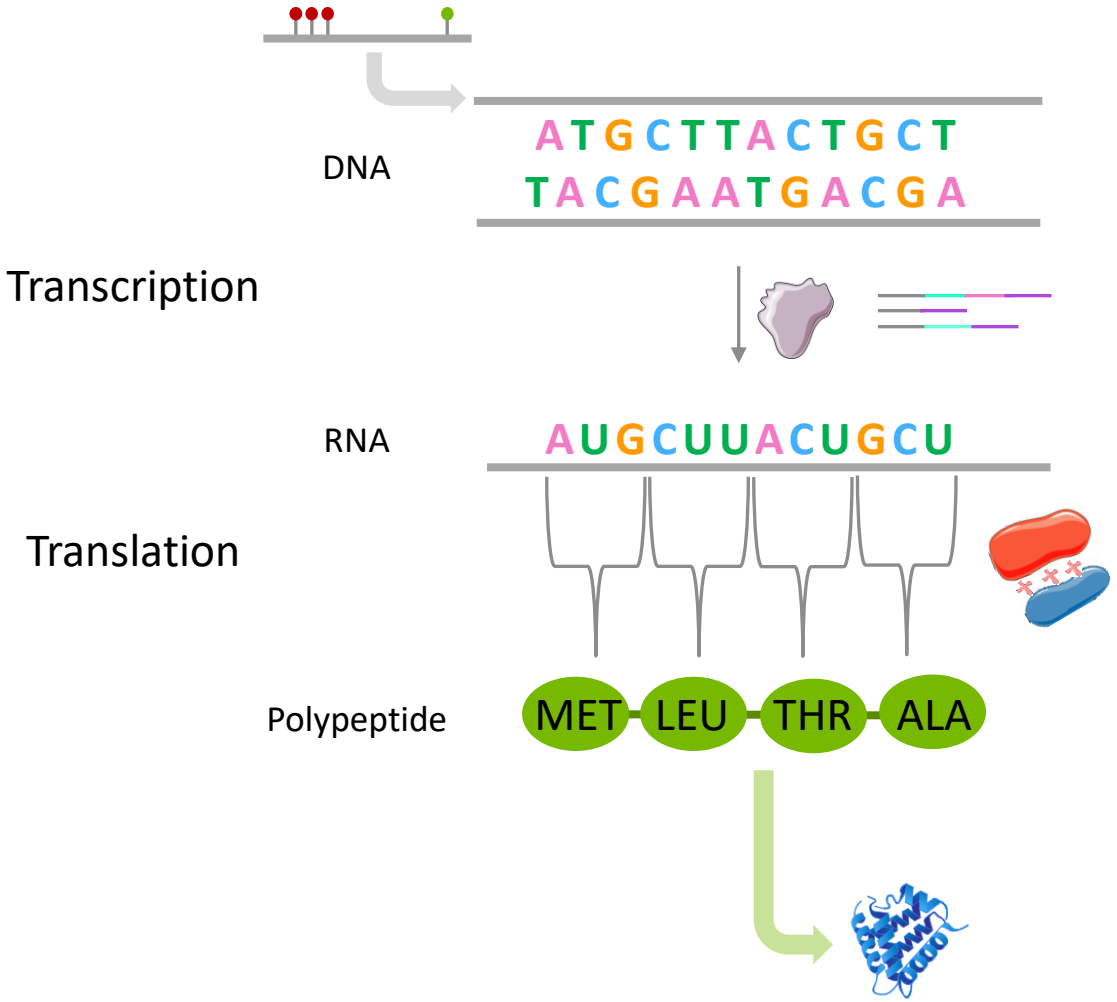


THE CLOUD

4 minute exome analysis on DNAnexus, with scalable, open source tools for reproducible results

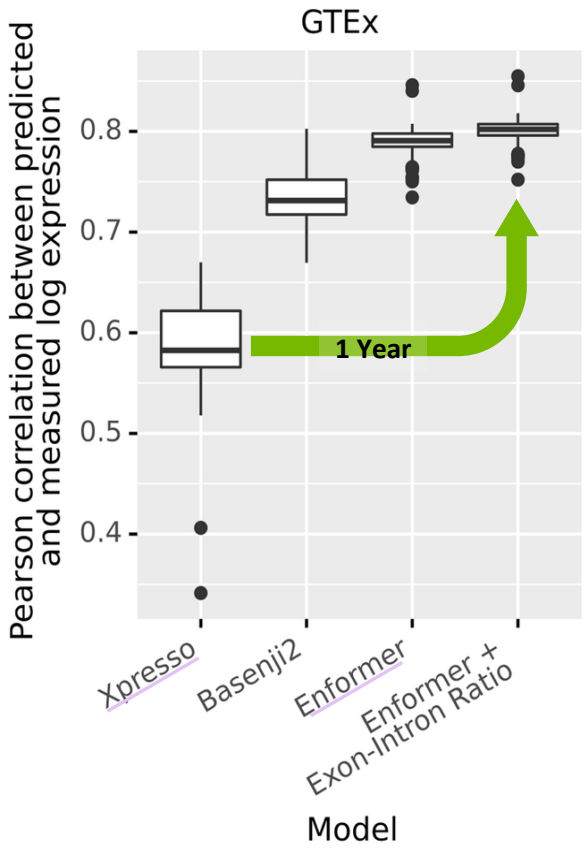
Genotypes alone do not fully explain function

A more complete picture of the Central Dogma includes epigenetic marks; RNA splicing and modifications; protein structure, folding, and binding

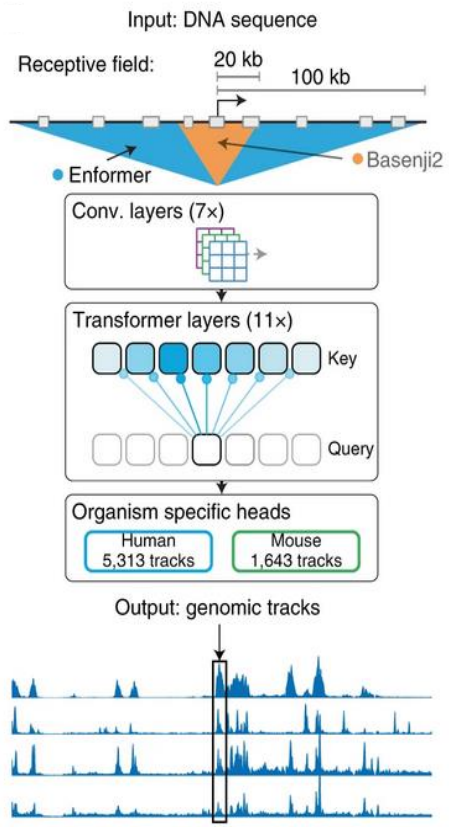


AI models are learning the complexity of the Central Dogma

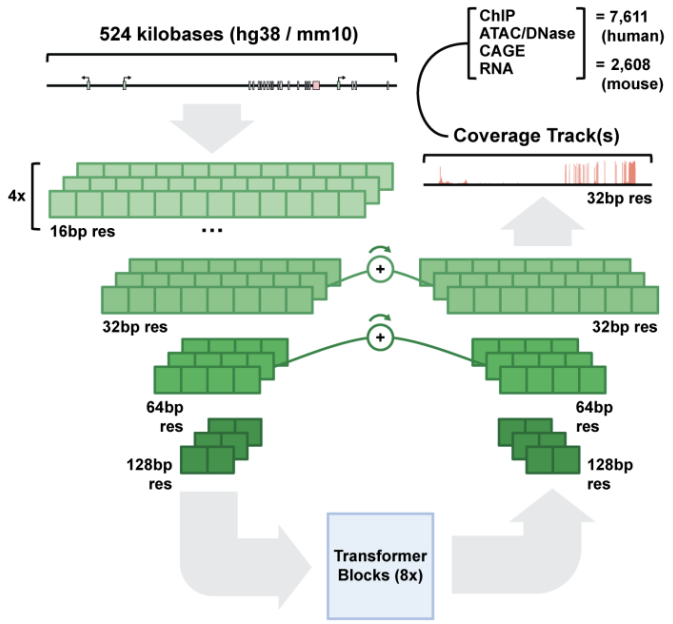
Transformer models (such as Enformer), for example, are rapidly improving at predicting gene expression from sequence data



Enformer (2021)

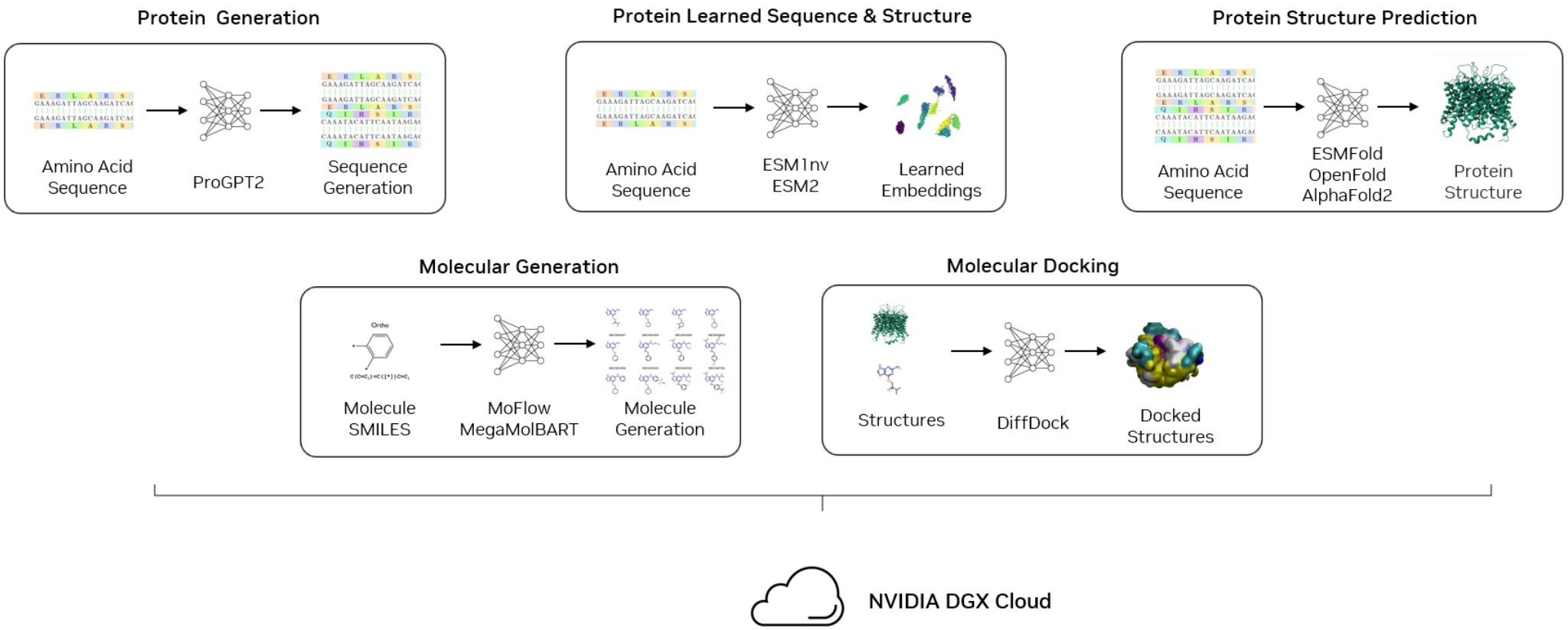


Borzoi (2023)



BioNeMo accelerates AI-driven generative biology

Nine state-of-the-art models and growing, all running on NVIDIA DGX Cloud



How can we use this technology to address challenges in meeting global food demand?

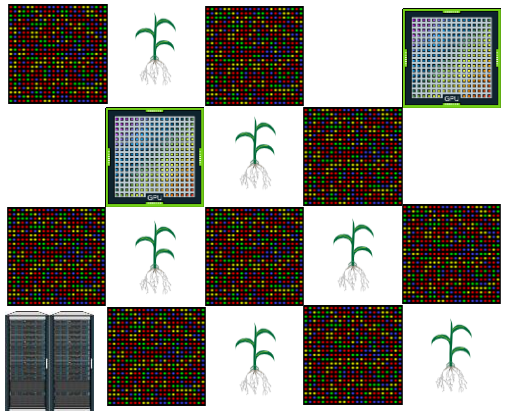
Make analysis more accessible

Reduce time and resources required

Enable labs without significant infrastructure to contribute

Cloud-ready; run anywhere there are GPUs

Expand AI training availability to more organizations and non-model organisms

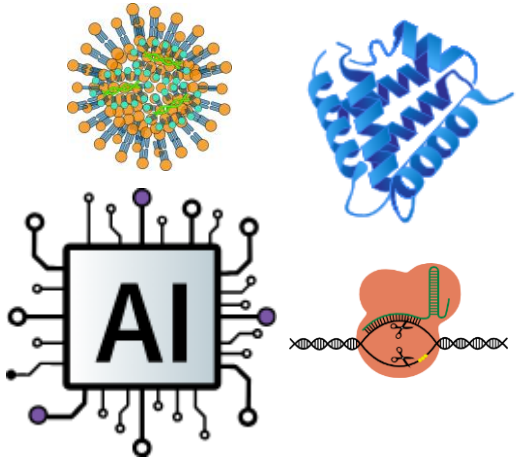


Scale the size of experiments by 10-100X *today*

Analyze 10-20X the number of samples for same runtime

Utilize accelerated tools for image analysis, data science, etc. to automate the entire pipeline

Discover more rare candidate variants by increasing sample size



Discover more candidates using Generative / Predictive Biology

Guide experiments using predictive AI

Predict off-target effects before running expensive experiments

Discover candidate variants hidden in complexity

Develop models that can generate strong candidates


NVIDIA