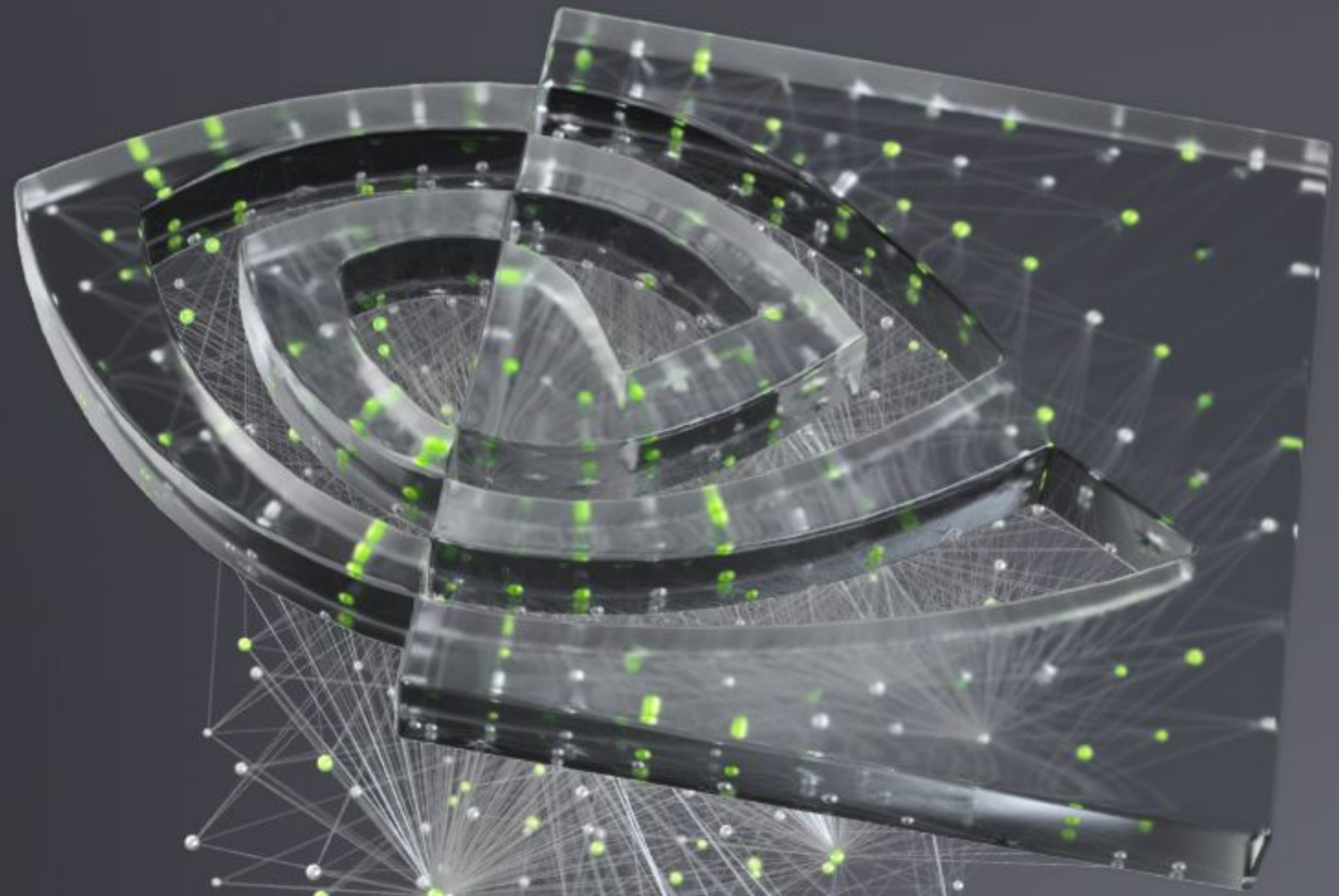


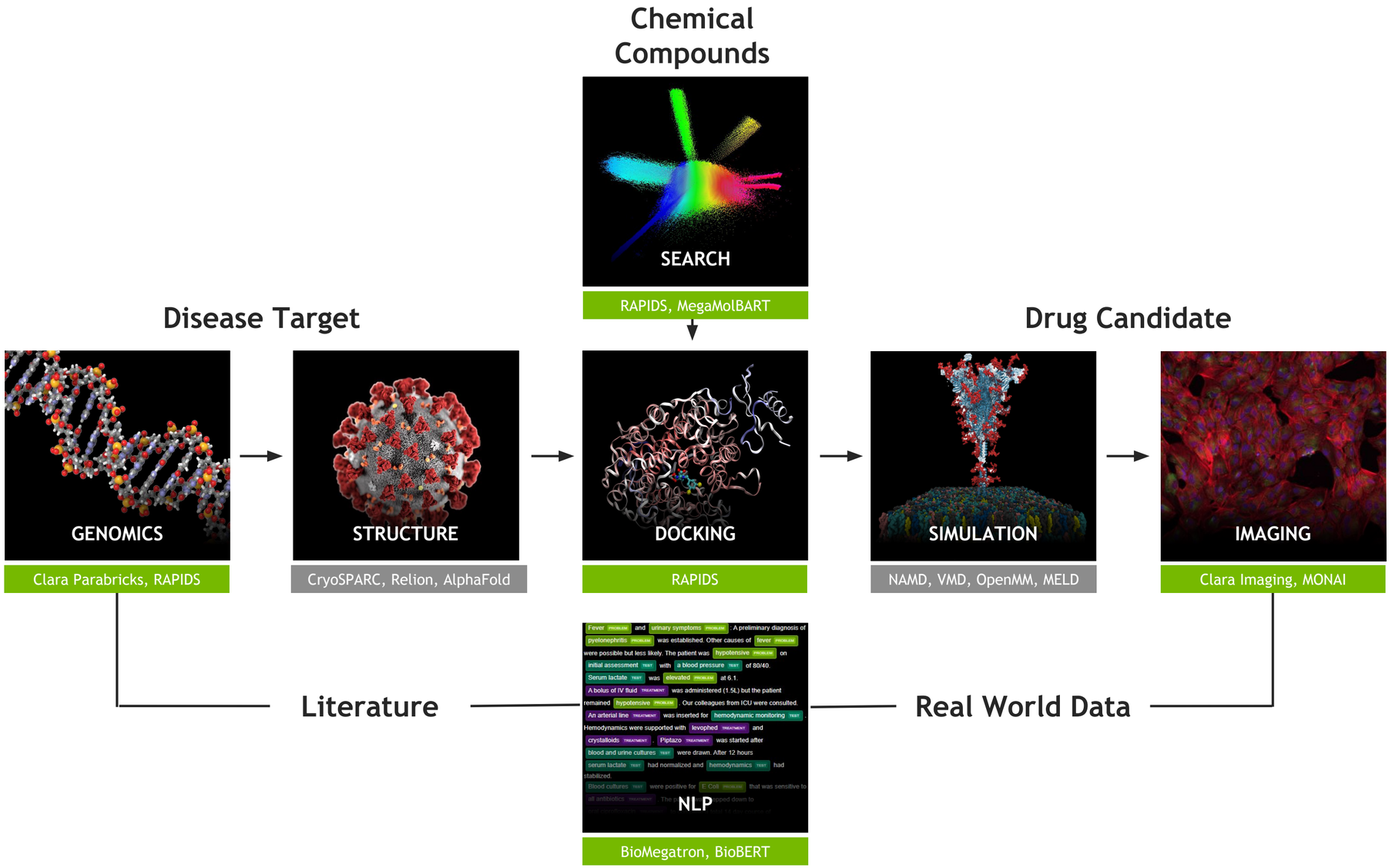
Exploring Molecular Space and Accelerating Drug Discovery with Clara Discovery and MegaMolBART

Michelle L. Gill, Ph.D.

4th RSC-BMCS / RSC-CICAG Artificial Intelligence in Chemistry Symposium

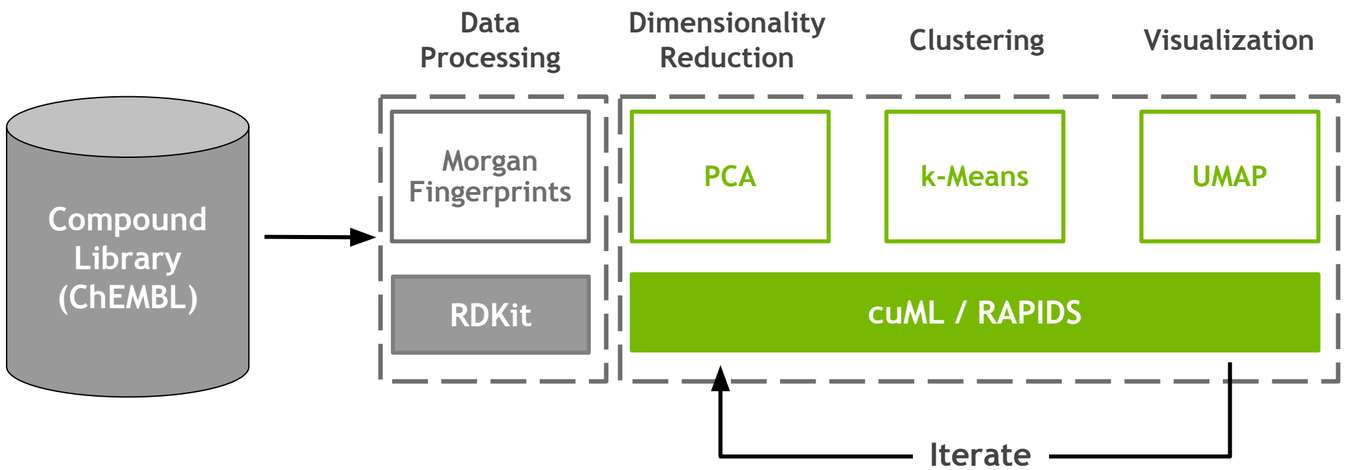
September 27, 2021

NVIDIA Clara Discovery

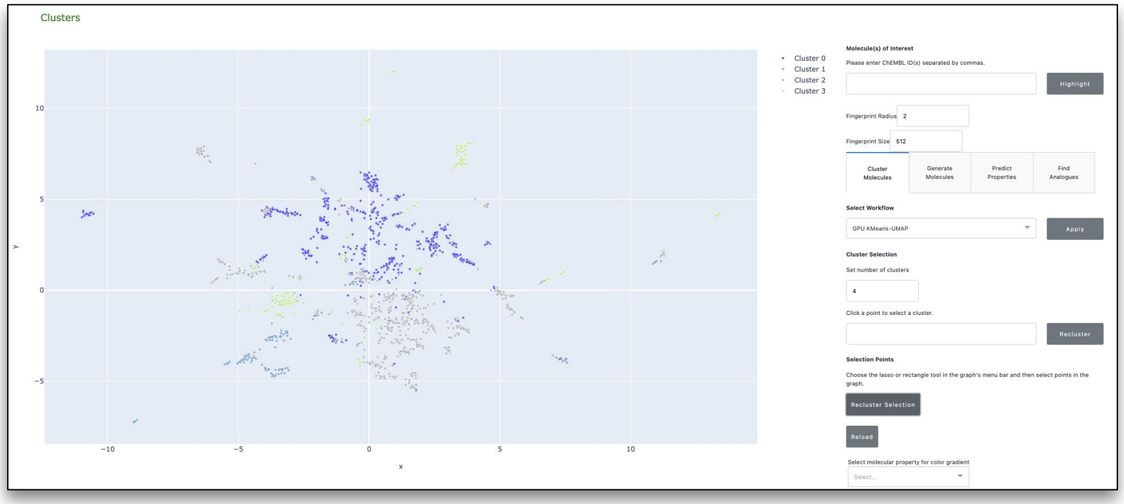


Interactive Clustering and Visualization

Workflow



Interface



plotly | Dash

NVIDIA

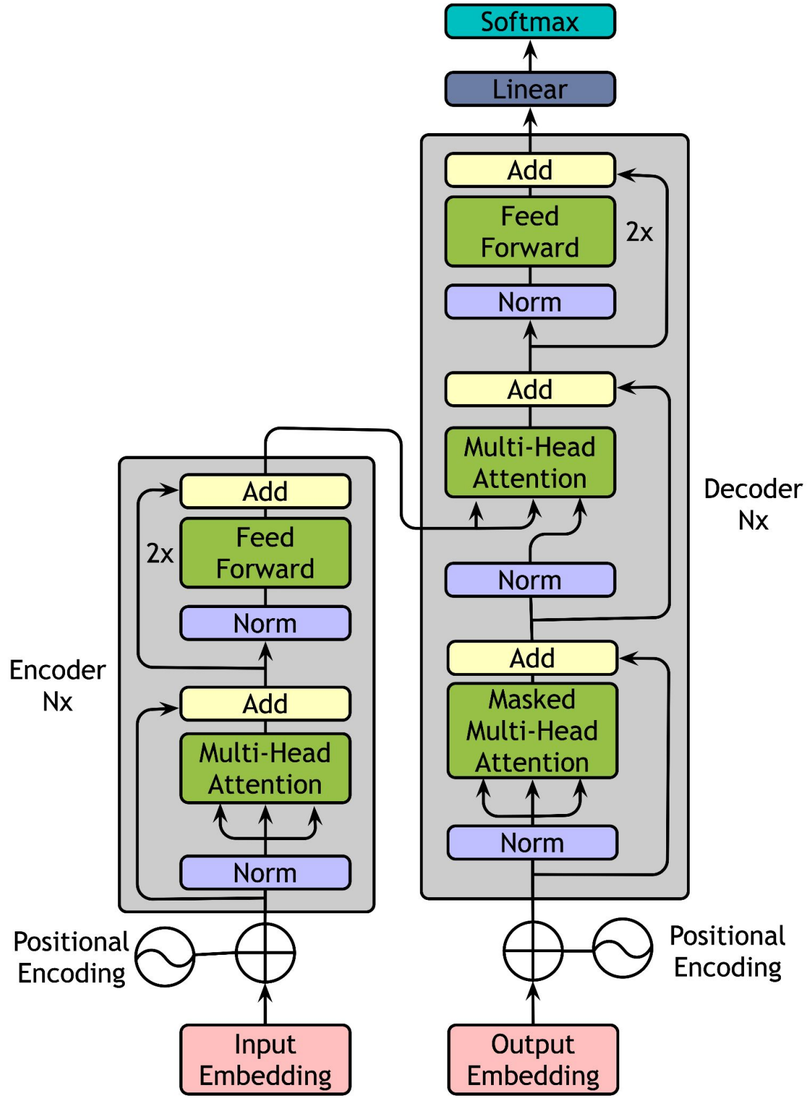
MegaMolBART Architecture

MegaMolBART is a transformer-based model for small molecule drug discovery

MegaMolBART is based on a BART (seq2seq) transformer -- bidirectional encoder and autoregressive decoder

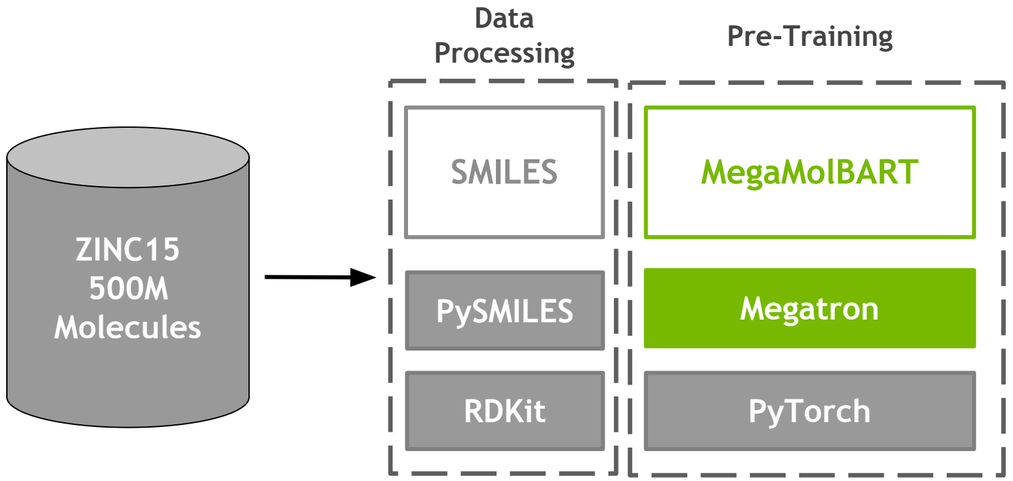
Developed in collaboration with AstraZeneca

Built on NVIDIA's Megatron framework to enable training and inference at scale



Ross, I., Spyridon, D., Jiazhen, H. & Esben, B. Chemformer: A Pre-Trained Transformer for Computational Chemistry. ChemRxiv (2021) doi:10.33774/chemrxiv-2021-v2pnn.

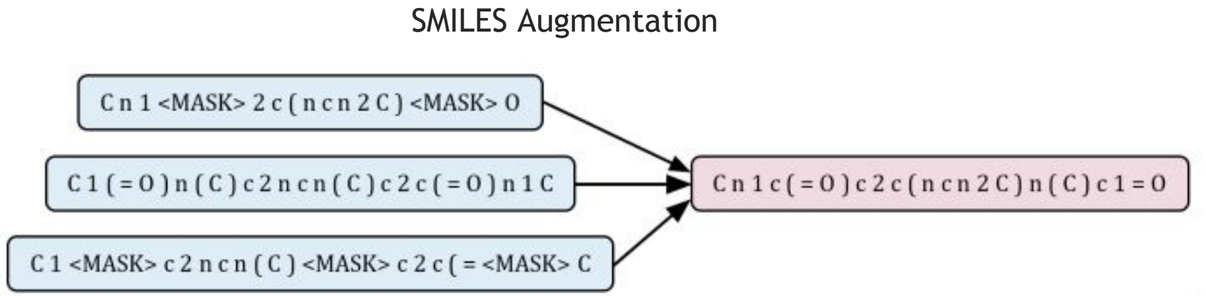
Pre-Training of MegaMolBART



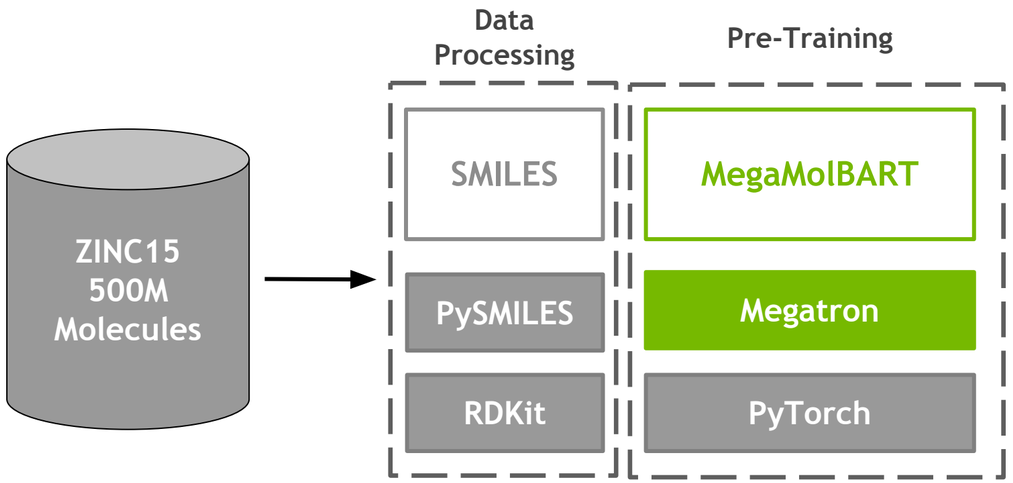
Pre-training performed on ZINC15 -- tranche from reactive, annotated molecules with molecular weight ≤ 500Da, and LogP ≤ 5

Train, validation, and test splits were 99% / 0.5% / 0.5%

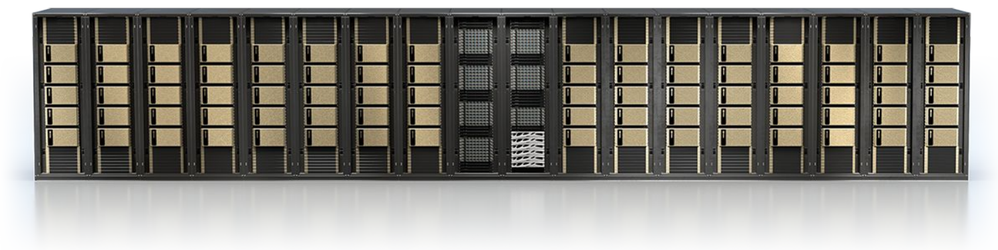
SMILES molecules were masked and enumerated (randomized) during training



Pre-Training of MegaMolBART



DGX SuperPOD / Cambridge-1



Pre-training performed on ZINC15 -- tranche from reactive, annotated molecules with molecular weight ≤ 500Da, and LogP ≤ 5

Train, validation, and test splits were 99% / 0.5% / 0.5%

SMILES molecules were masked and enumerated (randomized) during training

Trained on DGX SuperPOD -- upto 8 nodes x 8 A100 GPUs

AstraZeneca concurrently developing on Cambridge-1

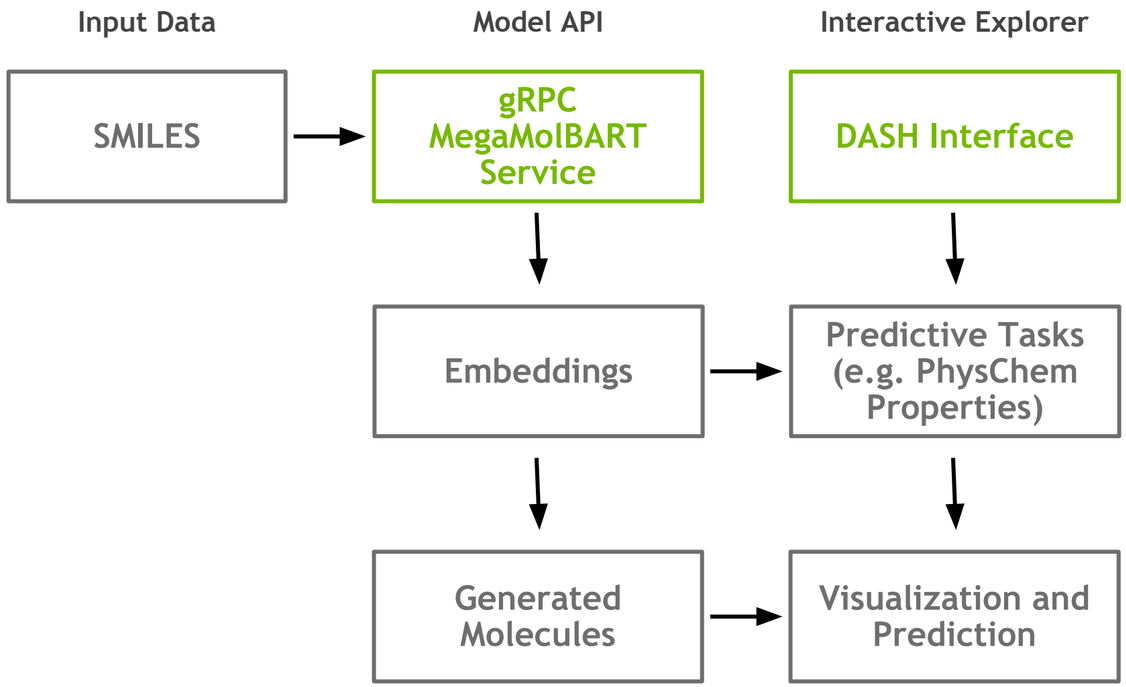
MegaMolBART Model Service

Model inference tasks available via gRPC API:

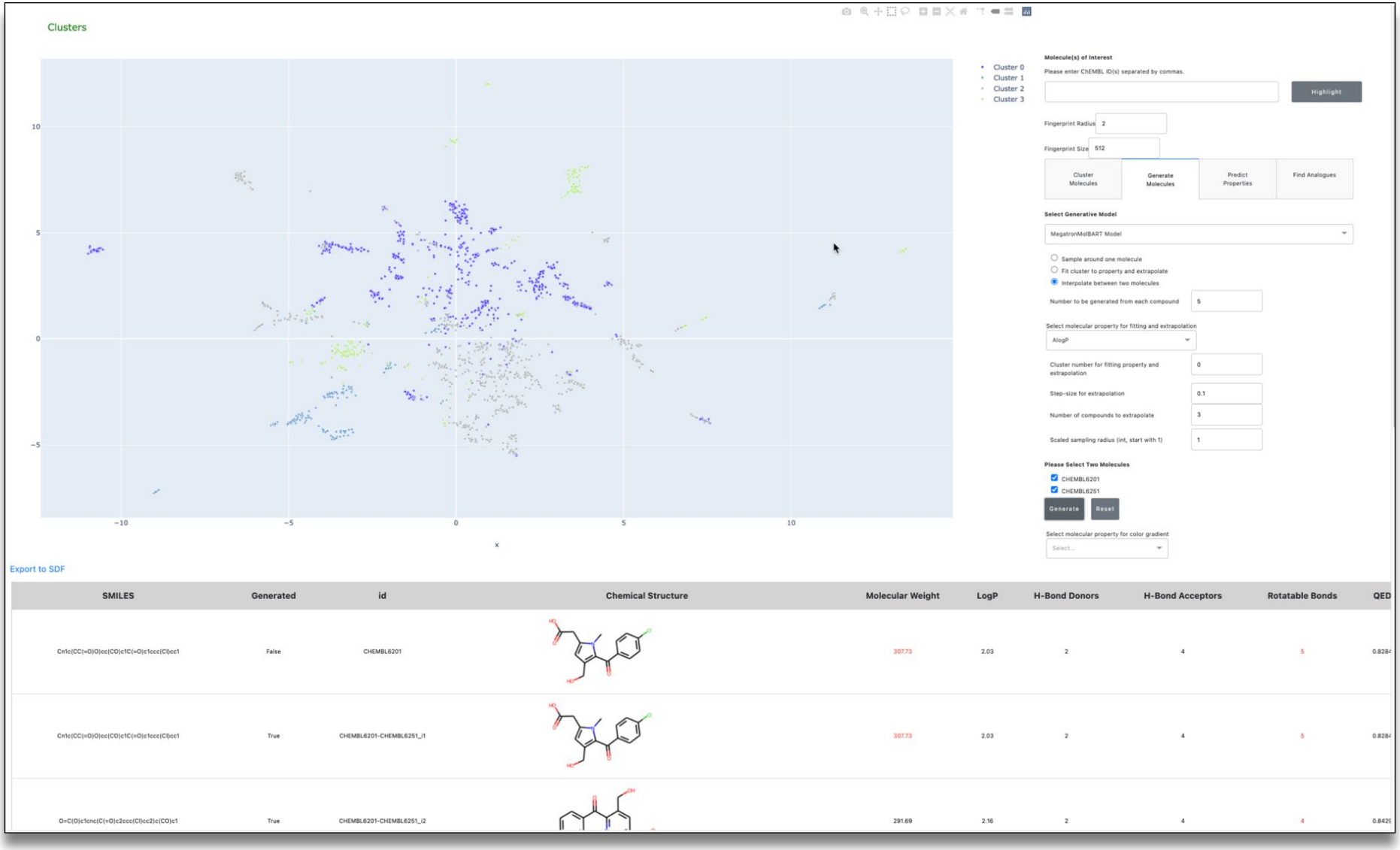
- Learned embeddings from SMILES molecule(s)
- Molecule generation from SMILES molecule(s)

Workflows and outputs are integrated into the interactive explorer

Designed for user customization -- predictive tasks incorporated into workflow



Demo of Interactive Explorer and Molecule Generation

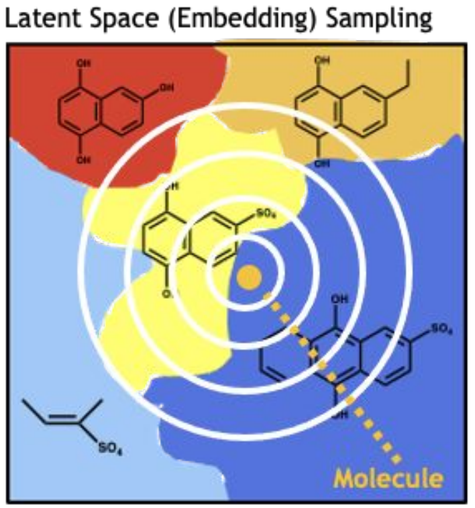


What's Next?

Scaling MegaMolBART -- what are the limits to larger models?

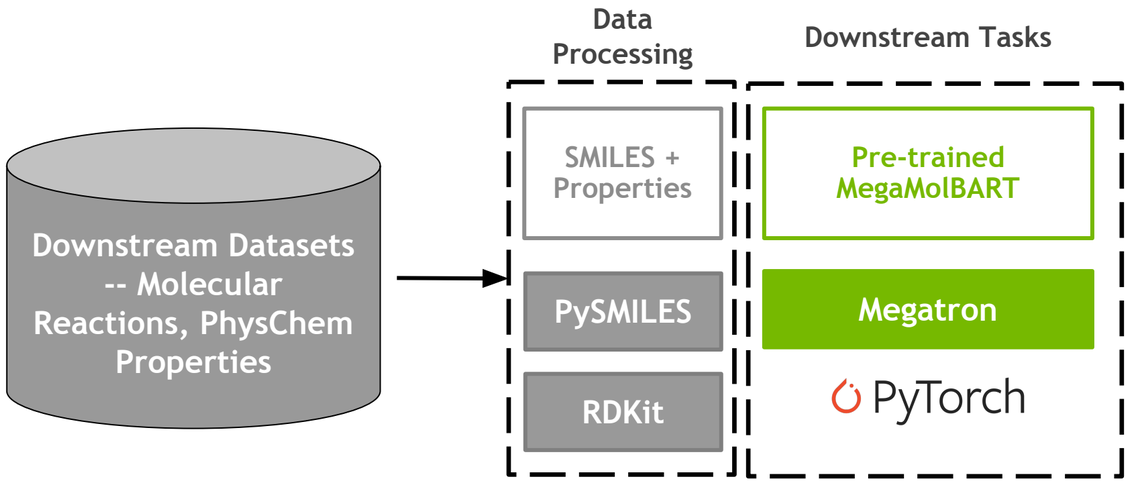
Attention Heads	Layers	Hidden Size	Feed Forward	Parameters
8	4	256	1024	10M
8	6	512	2048	45M
16	8	1024	4096	230M
...	...	...	...	...

Improved molecule generation -- development of novel model architectures

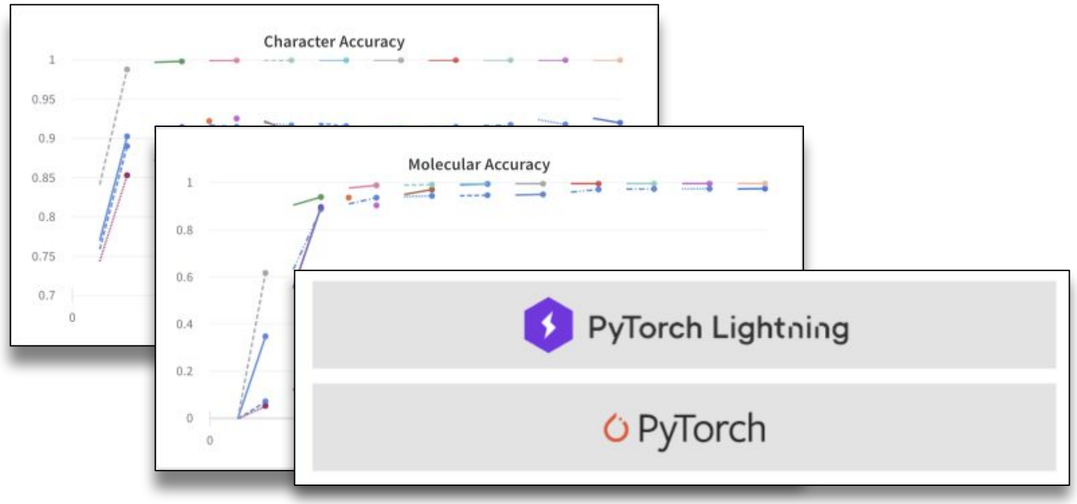


What's Next?

Predictive tasks based on model embeddings -- physchem properties, reaction prediction, retrosynthetic synthesis



Improved user experience -- automation of data processing, pre-training and downstream tasks



Where to Get It:
Clara Discovery Release V0.1.3

Resource	
MegaMolBART Weights	https://ngc.nvidia.com/catalog/resources/nvidia:clara:cheminformatics
Featurizer Service	https://ngc.nvidia.com/models/nvidia:clara:megamolbart
Interactive Explorer	https://ngc.nvidia.com/containers/nvidia:clara:megamolbart
Tutorials	https://ngc.nvidia.com/containers/nvidia:clara:cheminformatics_demo
	https://github.com/NVIDIA/cheminformatics

Conclusions

Clara Discovery is a collection of tools and frameworks that accelerate drug discovery

The interactive explorer provides a framework for visualizing and customizing workflows

MegaMolBART is a seq2seq transformer model developed in collaboration with AstraZeneca and trained at scale

All tools are open source and freely available

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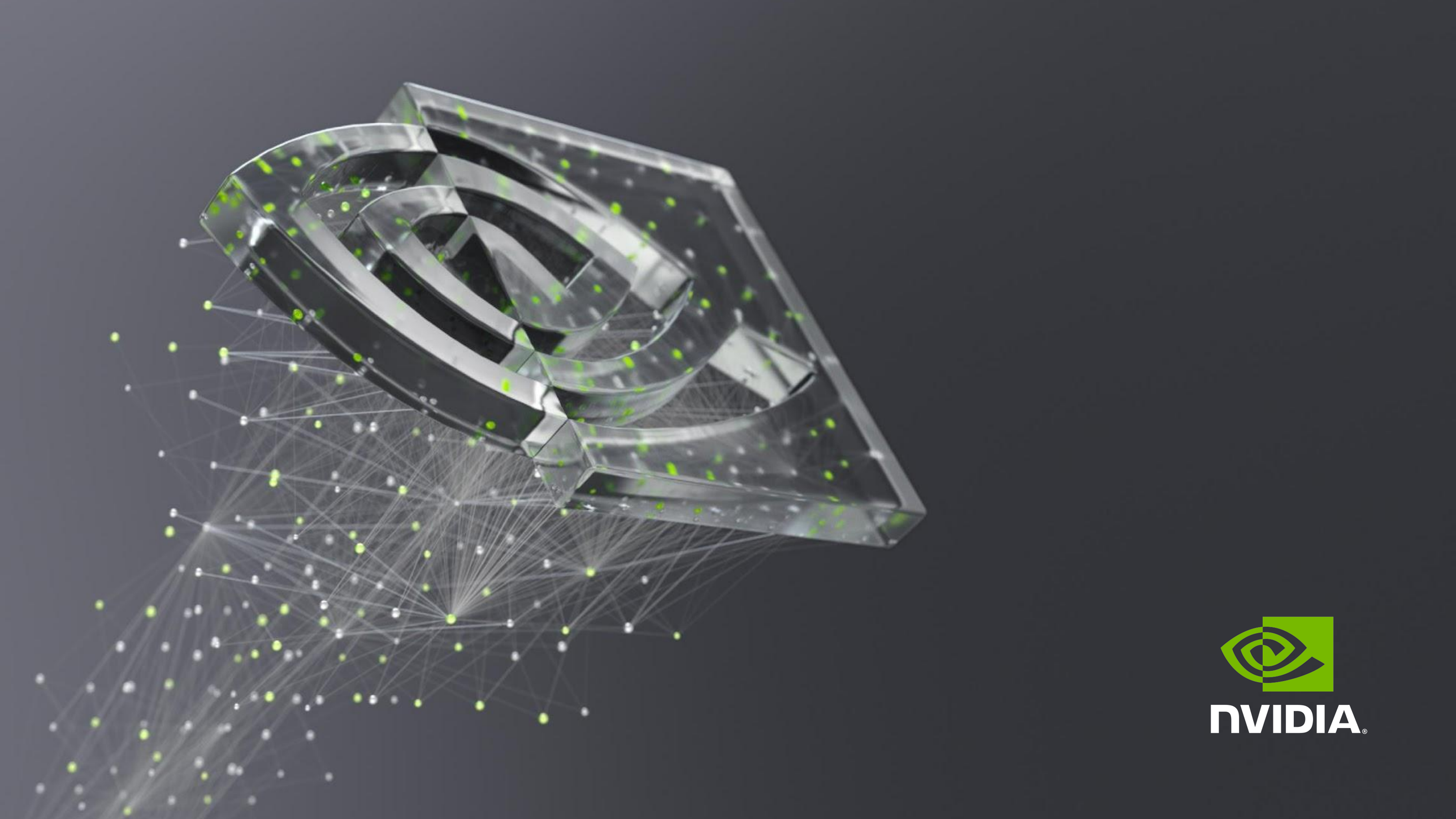
Ross Irwin

Jiazhen He, PhD

Ola Engkvist, PhD


NVIDIA