OAK RIDGE National Laboratory

Artificial Intelligence Enabled Multiscale Molecular Simulations

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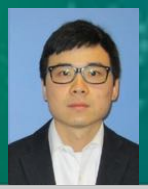

Heng Ma
CSED

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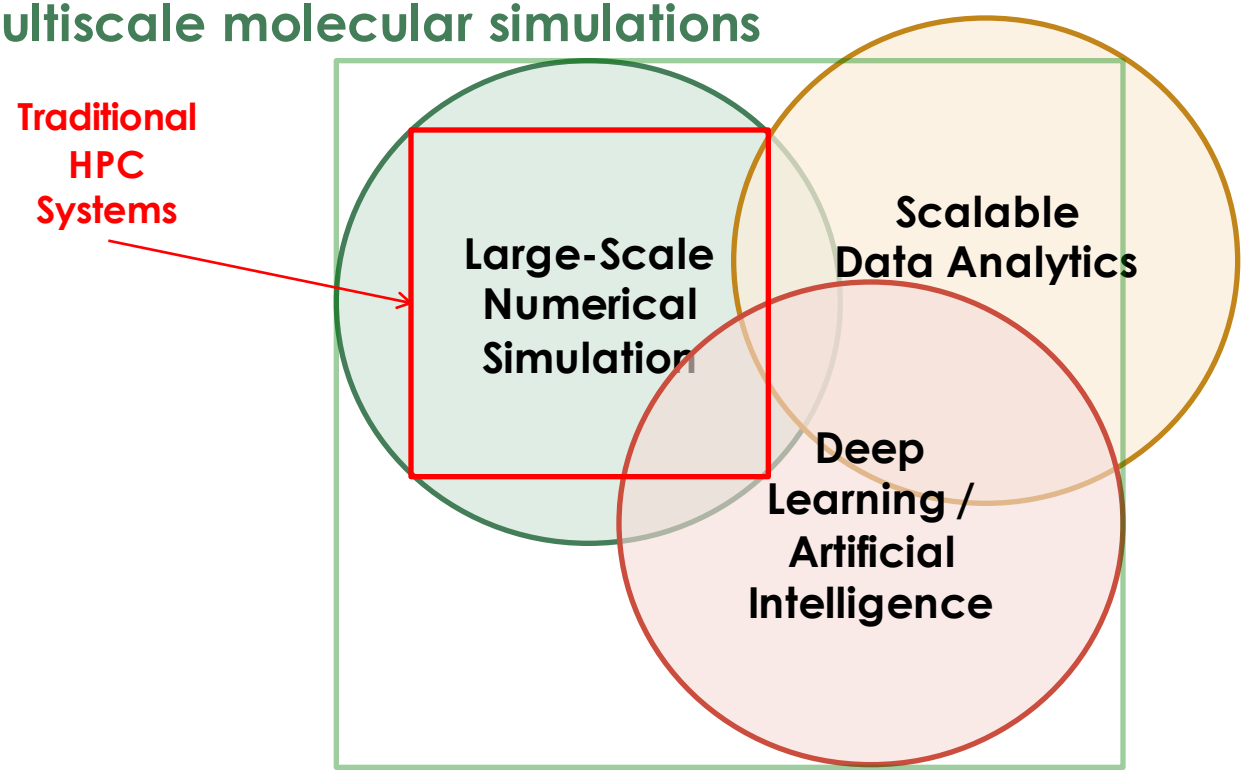
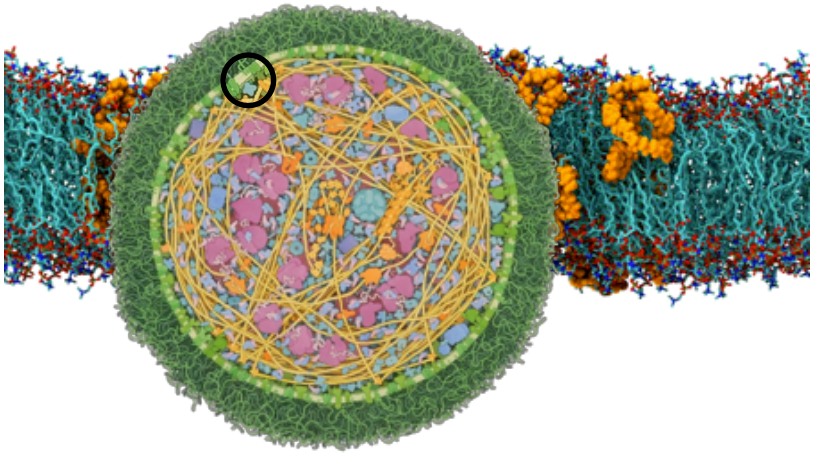
U.S. DEPARTMENT OF ENERGY

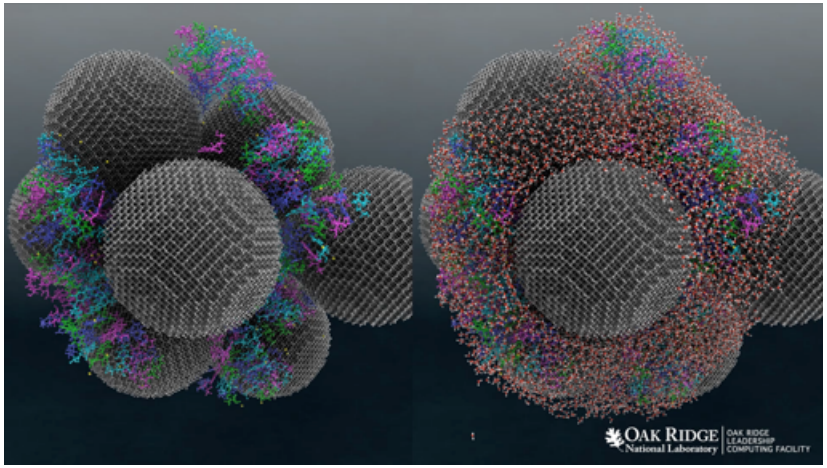
Drive Integration of Simulation, Data Analytics and Machine Learning

Molecules Library: AI-driven multiscale molecular simulations

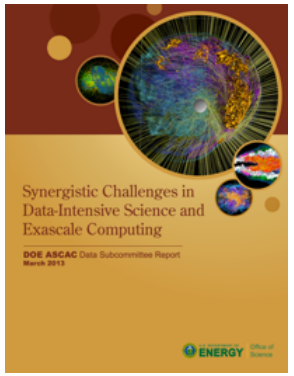


Multi-scale phenomena in biological systems pose challenges for modeling/ simulations @ Exascale



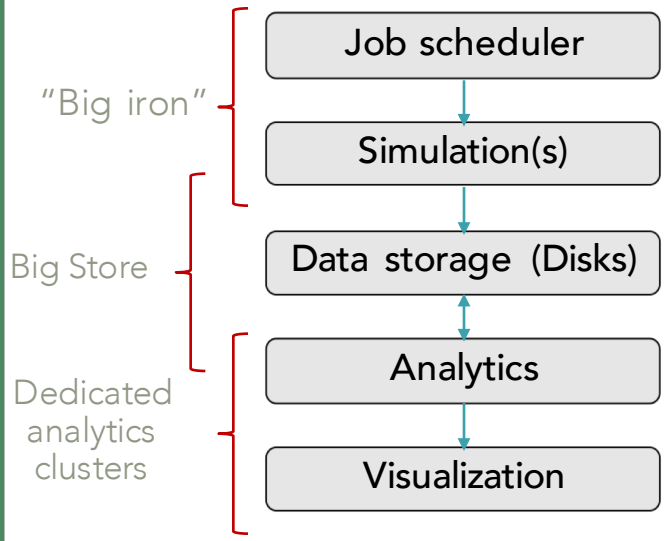


- Simulations of physical phenomena take 45-60% of supercomputing time
  - Coupled to experimental data such as Spallation Neutron Source, X-ray scattering/ diffraction facilities, etc.
- "Exascale simulations will require some analyses… be performed while data is still resident in memory…"



Towards AI-driven simulations: Interleaving data analytics + simulations

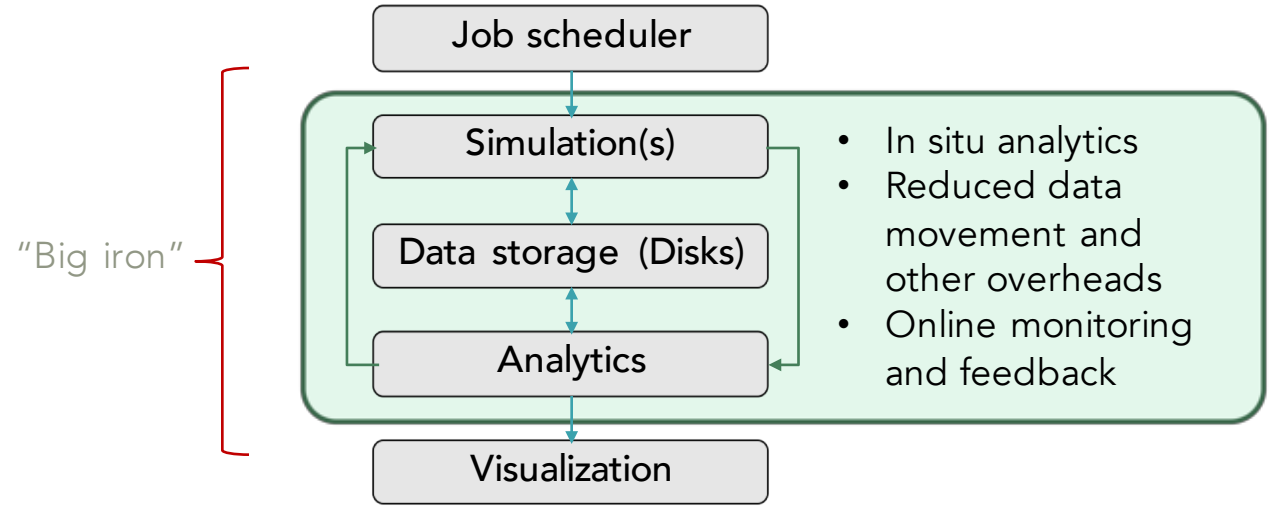
Traditional Compute + Simulations



Unsustainable at Exascale

- Data movement bottlenecks
- Parallel analytics bottlenecks

Interleaving Analytics + Simulations

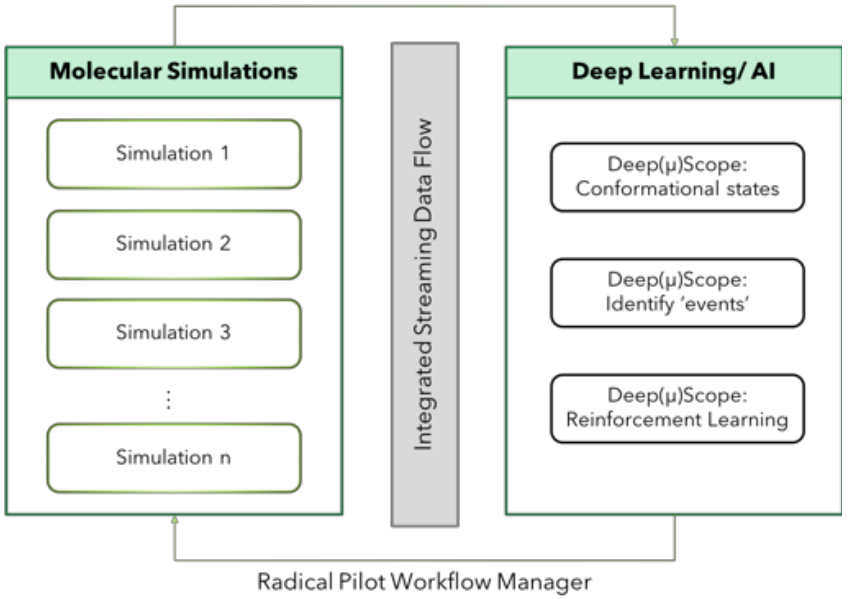


Iterative forward/backward loop

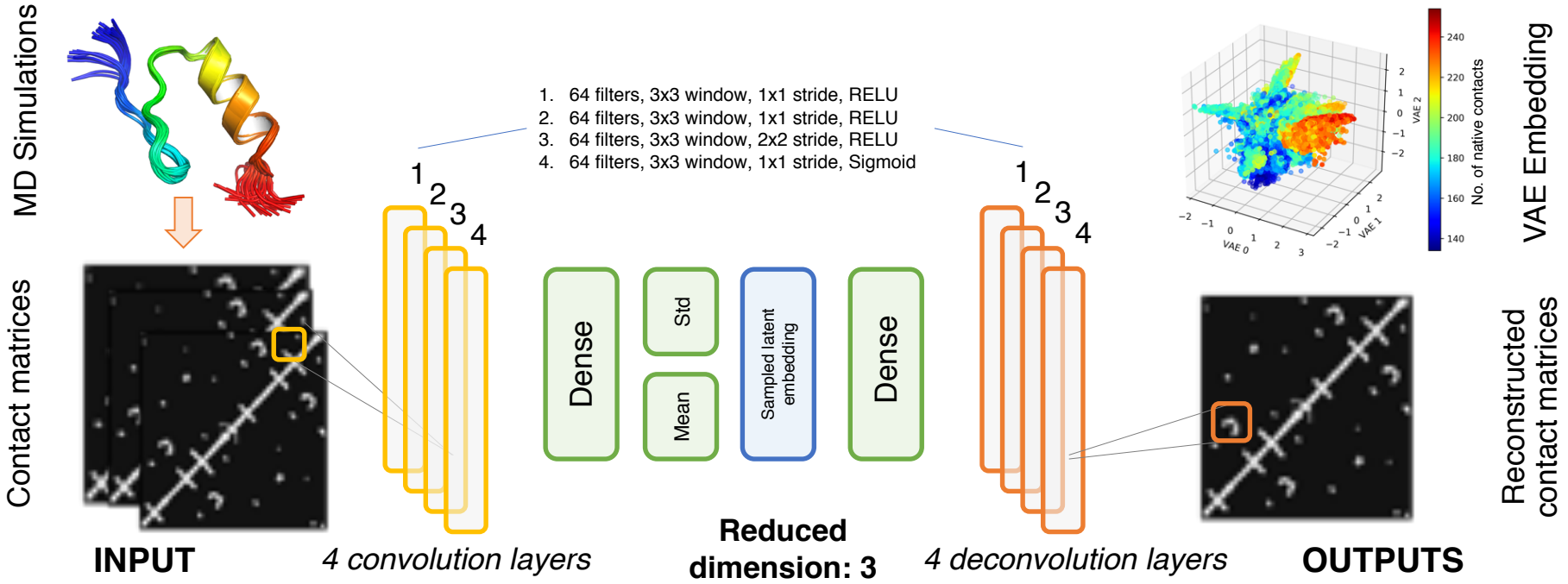
- **High performance framework** to monitor & analyze simulations as they are running with little/ no modification to simulation software
- **Demonstrate on molecular dynamics simulations**, but generalize framework for broad applicability

Outline: Can artificial intelligence (AI) techniques be leveraged for accelerating molecular simulations?

- Building effective (low-dimensional) latent representations of simulation datasets:
  - Using deep learning approaches for molecular dynamics (MD) data
  - Scaling convolutional variational autoencoder for MD
- Predicting where we should go next in MD simulations:
  - Building a recurrent autoencoder to predict future steps
- Preliminary work on a reinforcement learning approach for protein folding/ docking



A variational approach to encode protein folding with convolutional auto-encoders



Related work:
Hernandez 17 arXiv,
Doerr 17 arXiv

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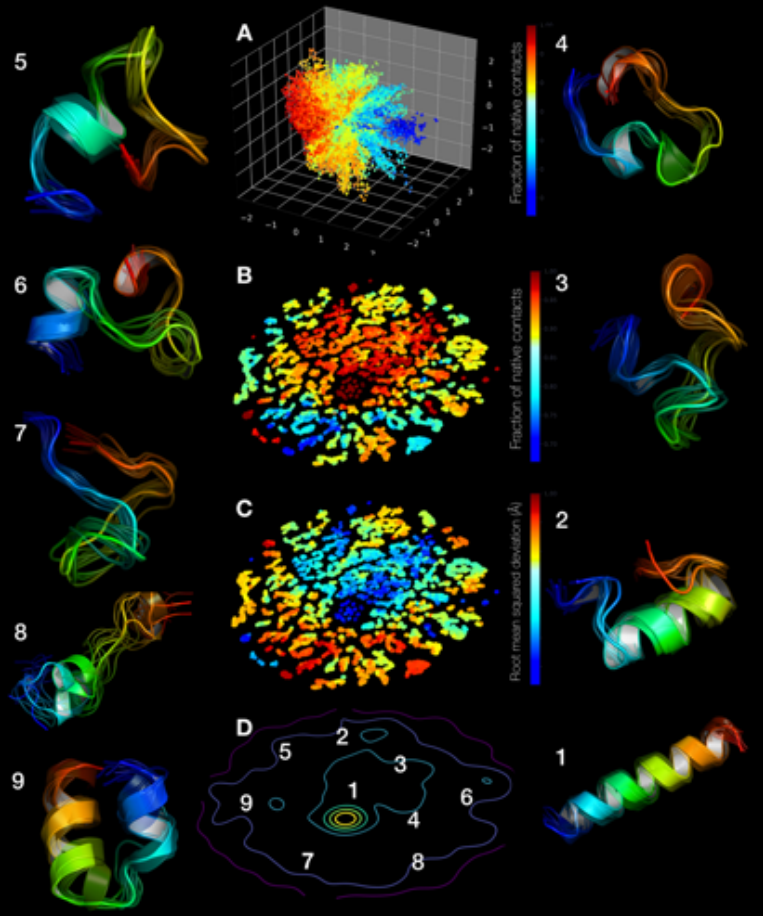
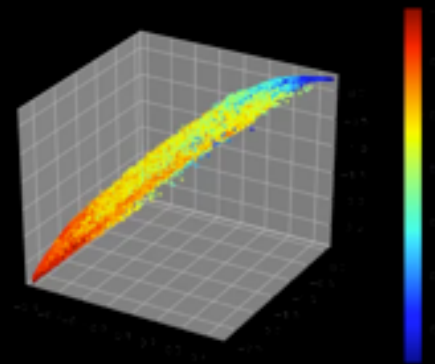
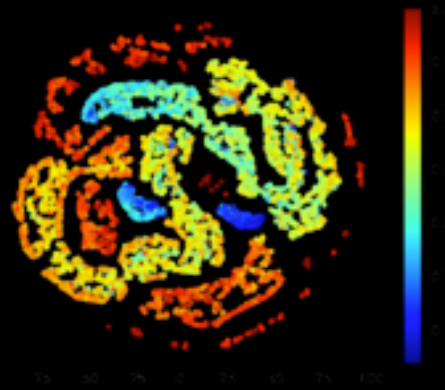
D. Bhowmik, M.T. Young, S. Gao, A. Ramanathan, BMC Bioinformatics (accepted)

Deep Learning reveals "metastable states" in protein folding…



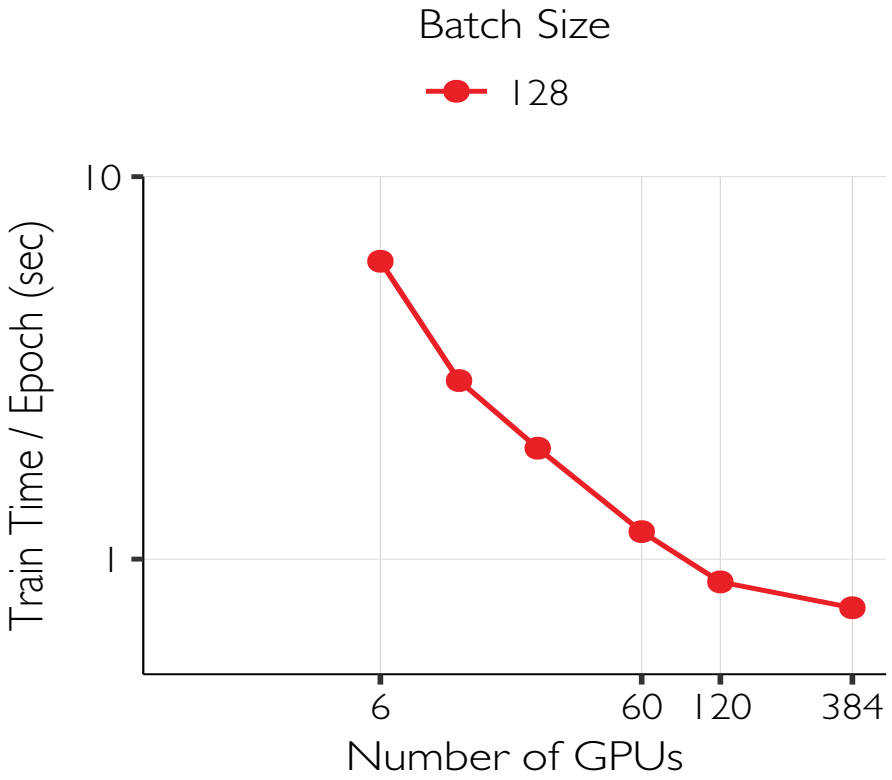




MSM Builder Datasets, Pande group

Scaling & Performance: Enabling DL approaches to achieve near real-time training/prediction

- Scaling deep learning on Summit to facilitate online training
  - DeepEx: a custom-built deep learning stack for Summit
- Exploiting low rank structure of scientific data:
  - Accelerate training
  - Scale to larger datasets
- Performance on Resnet like convolutional nets



S. Yoginath , M. Alam, K. Perumalla, R. Kannan, D. Bhowmik, A. Ramanathan, ORNL Tech Report

Current platforms for hyperparameter optimization rely on sequential optimization techniques

- Bayesian optimization, Bandit
  usually sequential search proc
- Exponential scaling:
  - The number of samples required
    optimization procedure is scales
    search dimensions, as in 2^D, wher
  - Forgotten in the recent exciteme

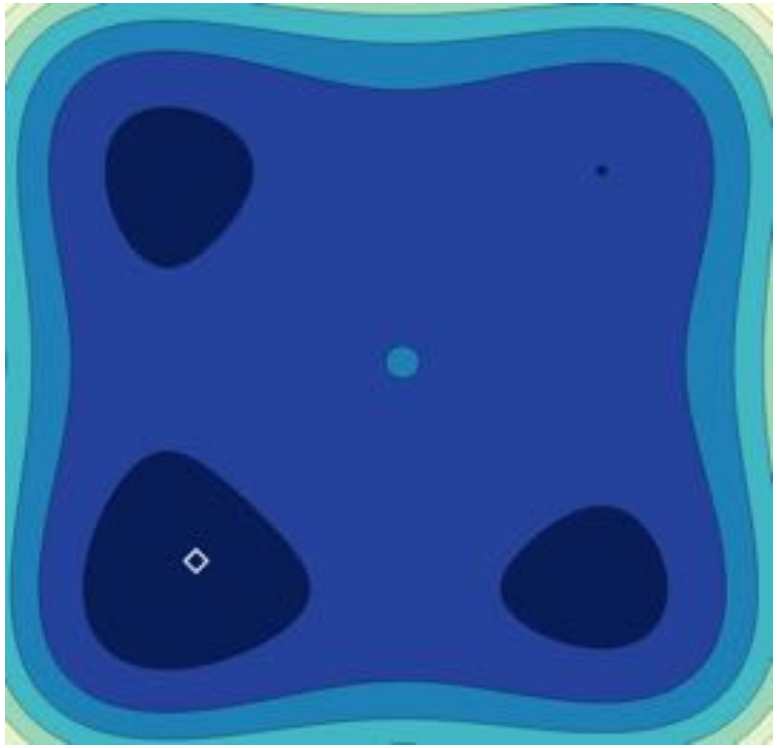
HyperSpace: Distributed Parallel Bayesian Optimization

- Hyperspace, instead seeks to focus on the search space:
  - Parallelism to exploit the statistical structure of the search space
  - Reveal partial dependencies across parameter spaces
- Build many surrogate functions in parallel
- {Prayer}!

N. Srinivas, A. Krause, S. M. Kakade, and M. W. Seeger. Gaussian pr
abs/0912.3995, 2009.

S. Grunewalder, J.-Y. Audibert, M. Opper, and J. Shawe-Taylor. Regre
Thirteenth International Conference on Artificial Intelligence and Statis
2010.

HyperSpace: Parallel exploration of large search spaces



https://github.com/yngtodd/hyperspace

1. Define the bounds of each hyperparameter search space.

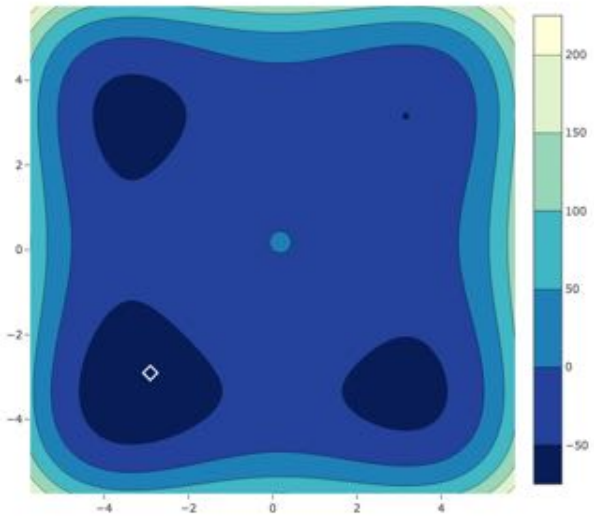
2. Divide each search space bound into two nearly equal sub-bounds with overlap ϕ, where $\{\phi \in \mathbb{R} \mid 0 \leq \phi \leq 1\}$.

3. Create all possible combinations of hyperparameter sub-bounds to form 2^D search spaces (hyperspaces) where D is the number of model hyperparameters.

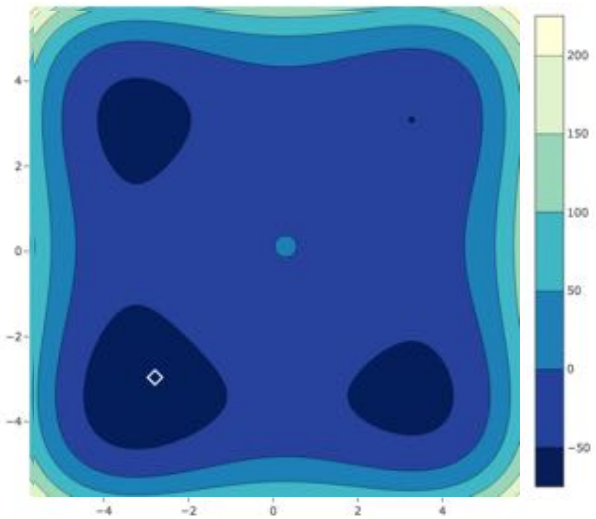
4. Run Bayesian optimization over each hyperspace in parallel

M. Todd Young, J. D. Hinkle, R. Kannan, A. Ramanathan, HyperSpace: Massively Parallel Bayesian Optimization, Workshop on High Performance Machine Learning, 2018, Lyon, France

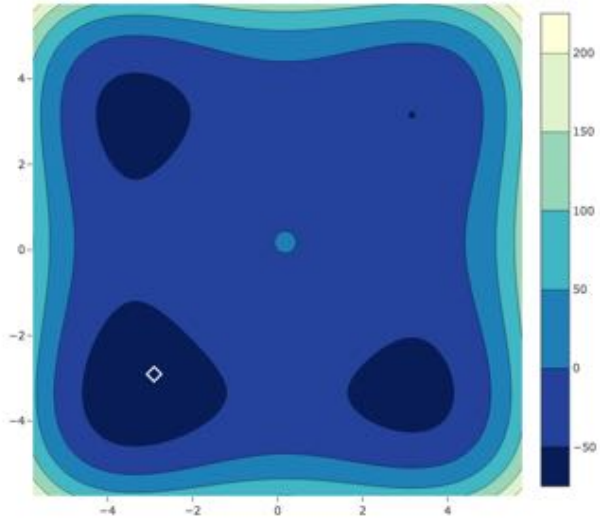
Parallel exploration of large search spaces works better than random/ sequential based optimization



HyperSpace



Random search



SMBO

- Exploiting statistical dependencies in the hyperparameter dimensions leads to better set of parameters for ML models

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https://hpml2018.github.io/HPML2018_7/index.html#/

Outline: Can AI techniques be leveraged for biological experimental design?

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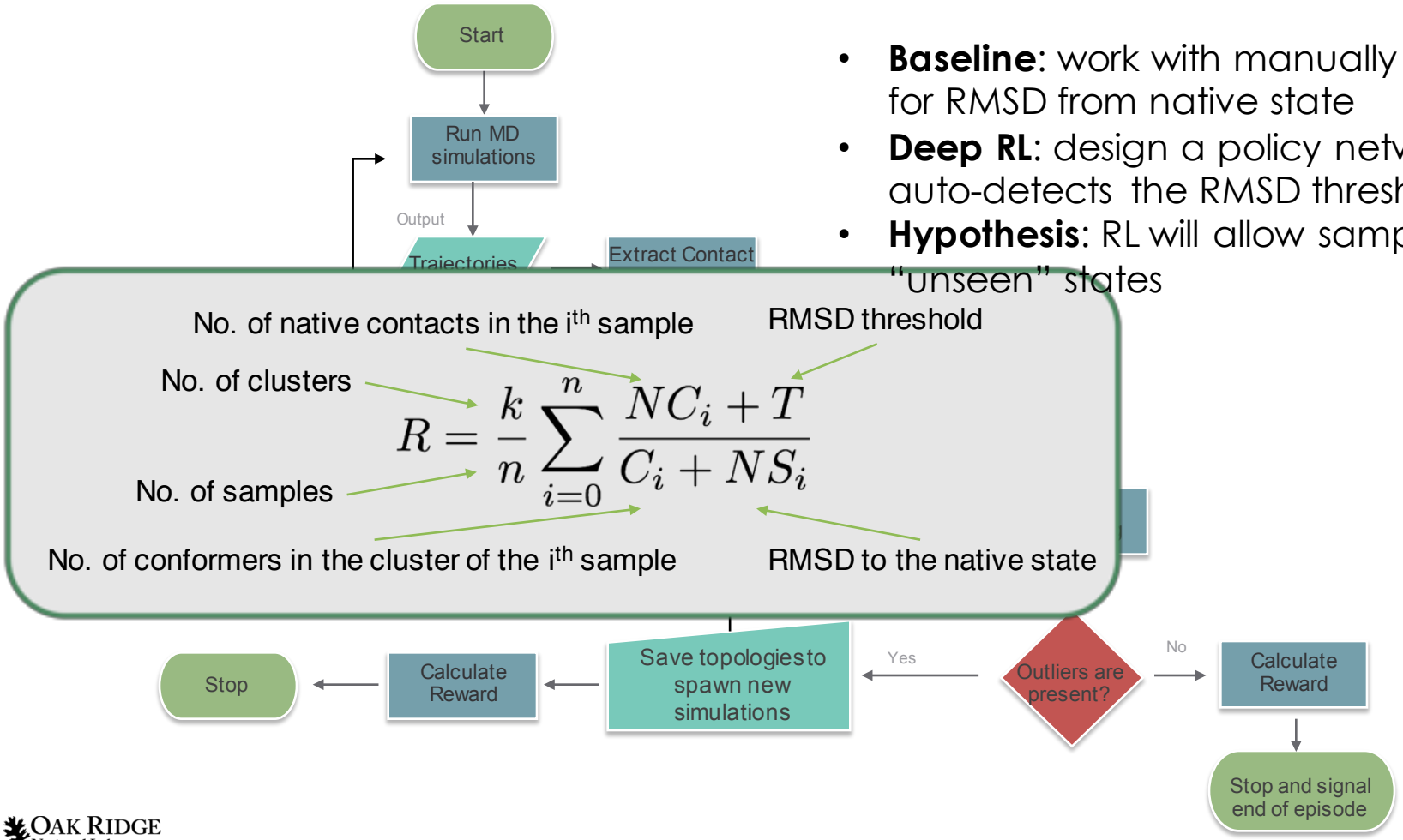
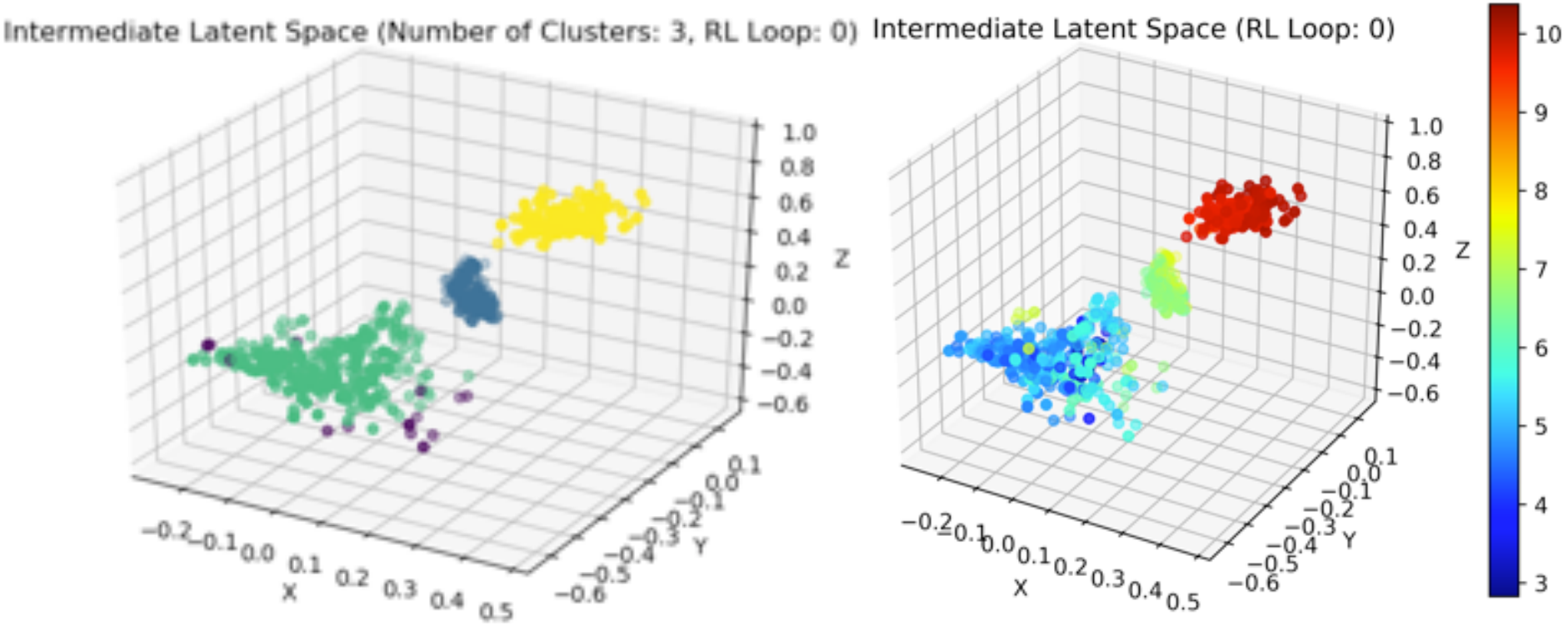
RL-Fold: a naïve design based on native structure



- **Baseline**: work with manually set threshold for RMSD from native state
- **Deep RL**: design a policy network that auto-detects the RMSD threshold
- **Hypothesis**: RL will allow sampling of "unseen" states

Pre-trained deep learning model allows RL explores possible states in protein folding



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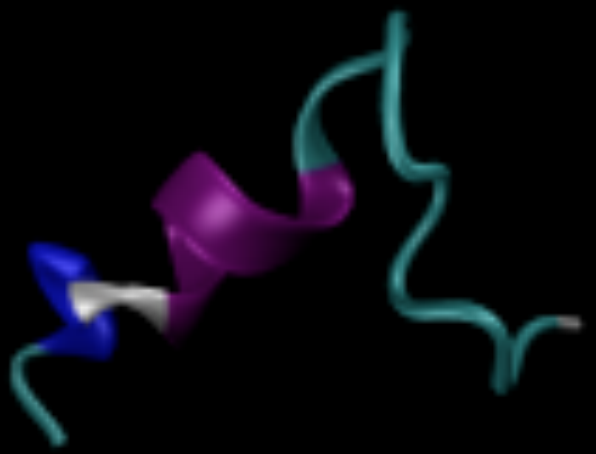
How does the folding look?



- Within 3-4 iterations, RL reaches near native state RMSD
- Further cycles explore misfolded states:
  - Unfold within a few steps of MD simulations
  - Sampling allows exploration of more intermediate states
- Builds on all-atom simulations + RL in a loop

Summary

- *Deep learning / AI techniques show promise*: learning biophysical characteristics that can be used to guide simulations
- *Reinforcement learning:* Preliminary evidence suggests the approach is feasible to speed up protein folding simulations!
  - How to integrate with physics-based models?
  - How to build scalable approaches beyond RL?
  - How to integrate with sparse experimental observables?
- Enabling iterative, active, and optimal experimental design
- *Extensible library:* Molecules to enable analysis of MD simulations at scale with Deep(μ)scope supporting AI-driven MD simulations

Some emerging challenges in HPC for multi-scale simulations…

- Design of coupled data analytic and simulation workflows on OLCF - Summit and ALCF – A21/Theta
  - In situ analytics approaches are required
  - Streaming applications of ML are different from post-processing of data

- Scaling DL/ AI approaches for biomolecular simulations
  - Faster and more efficient training for deep learning / AI approaches
  - Tensor based approaches to build deep learning algorithms

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THANK YOU !!!

- ORNL LDRD – Exascale computing initiative
- DOE-NCI Joint Design of Advanced Computing Solutions for Cancer (JDAS4C)
- DOE Exascale Computing Project Cancer Deep Learning Environment (CANDLE)
- OLCF Early Science Access (Summit)

Questions/ Comments: ramanathana@ornl.gov