

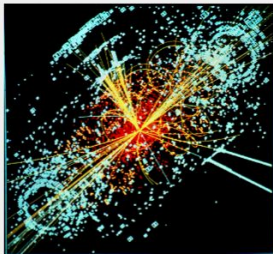
# Towards Exascale Across Scales!

**Shantenu Jha**

**Rutgers Advanced Distributed Cyberinfrastructure &  
Applications Laboratory (RADICAL)**

<http://radical.rutgers.edu>

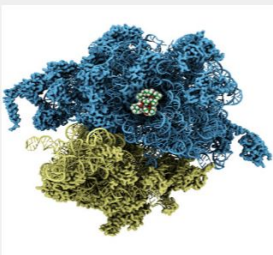
# “Big Science” to the Long Tail of Science



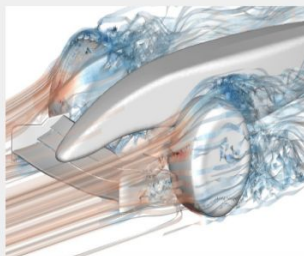
The ATLAS experiment at the Large Hadron Collider in Switzerland uses SAGA in conjunction with PanDA as a workload management system.



The Super-Kamiokande project searches for neutrinos to understand the creation of matter in the universe. It uses SAGA to simulate collisions on HPC clusters.



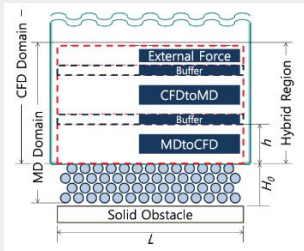
RADICAL-Pilot is being used by Chemistry researchers to support large-scale and multidimensional replica exchange simulations on supercomputers.



Nektar++ is a finite element package which uses SAGA in the backend to submit jobs to a variety of clusters. It tackles problems such as modeling air flow around automobiles.



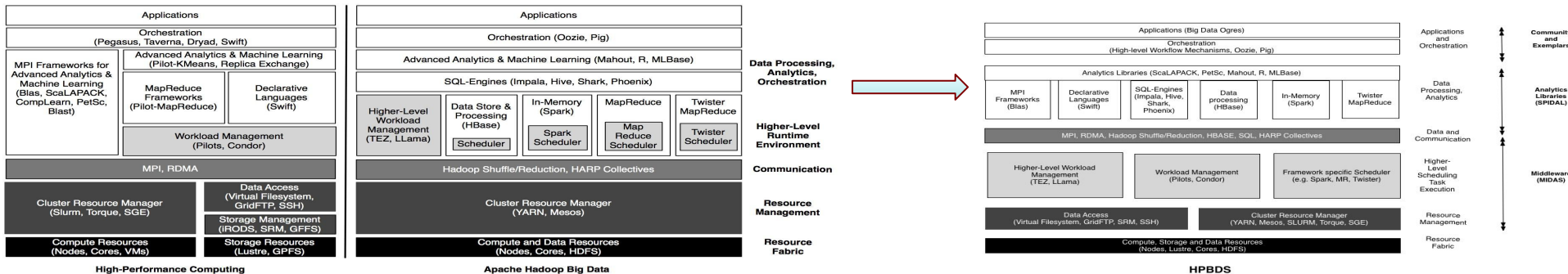
Researchers at UCL London are using RADICAL-Pilot to advance understanding of HIV drug resistance and make personalized treatment possible.



RADICAL-Pilot supports multi-physics and coupled simulations, such as hybrid CFD-MD simulations to understand Couette Flow, as well as PBM-DEM simulations for Cybermanufacturing.

# Convergence of HPC and “Data Intensive” Computing:

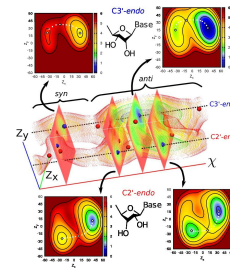
- Supercomputers were (historically) net producers of data, not consumers
- Convergence at multiple levels, including Software Environment
  - HP-ABDS: Integration of High Performance with Advanced Functionality
  - SPIDAL and MIDAS (<http://spidal.org>)



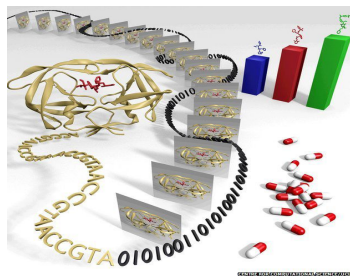
A Tale of Two Data-Intensive Paradigms:  
Data Intensive Applications, Abstractions and Architectures

Jha, Qiu, Fox

<http://arxiv.org/abs/1403.1528>



# Case Study: Biomolecular Sciences



## NCI-DOE Collaboration Paving Way for Large-Scale Computational Cancer Science

Subscribe

February 17, 2016 by Warren Kibbe, Ph.D.

Imagine the concentrated power of more than one million laptops working to screen a tumor sample from a patient against thousands of drugs and millions of drug combinations. At the end of this screening process, this mega-computer would help to identify a specific treatment with the greatest potential to combat that patient's cancer.

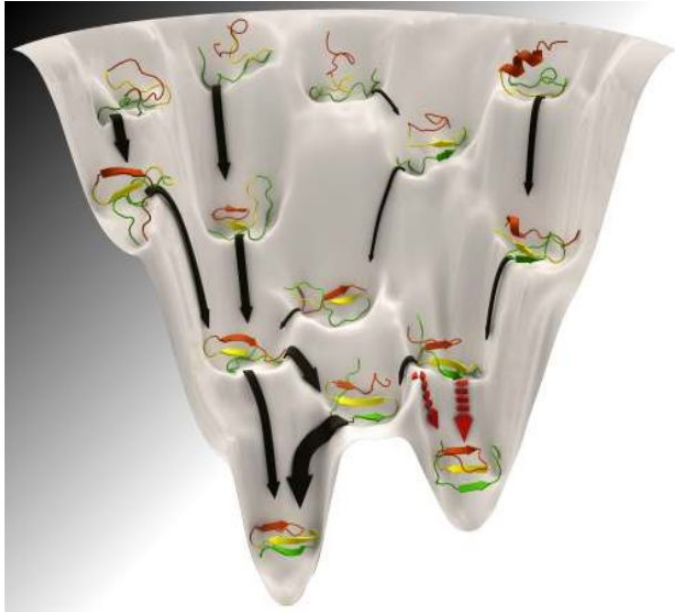
NCI scientists, in collaboration with colleagues with the Department of Energy (DOE) [Exascale Computing Initiative](#) (ECI) and the [National Strategic Computing Initiative](#) (NSCI), have been hard at work for the past 14 months developing a plan to use this type of large-scale computing to influence cancer science and,



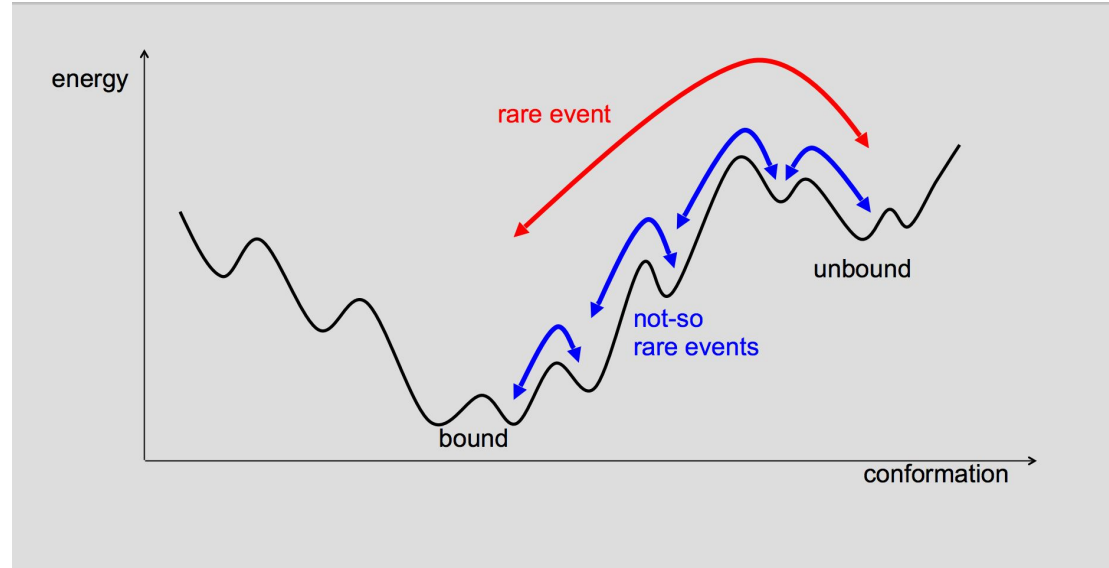
The Titan supercomputer at the U.S. Oak Ridge National Laboratory in Tennessee will be one of several supercomputers used in the NCI-DOE National Strategic Computing Initiative.  
Credit: Oak Ridge National Laboratory, U.S. Department of Energy



# Protein folding mechanisms



Noé et al, **PNAS** (2009)



# A Schism in Biomolecular Simulations?

- Given a finite amount of computing which is better:
  - Many simulations or Longer simulations?

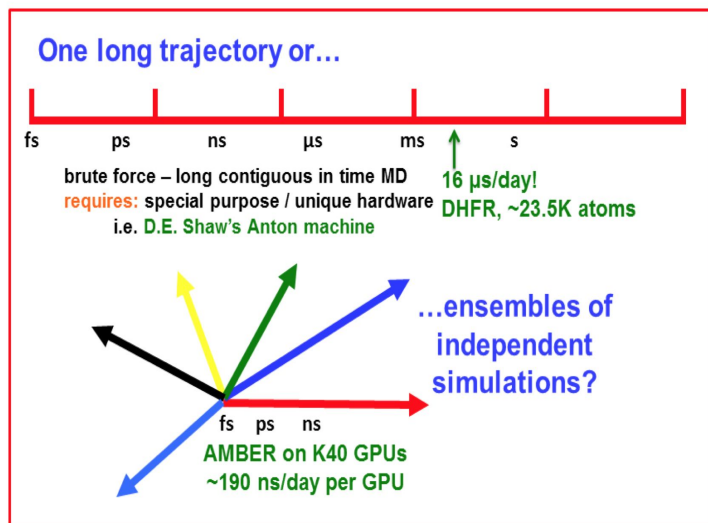
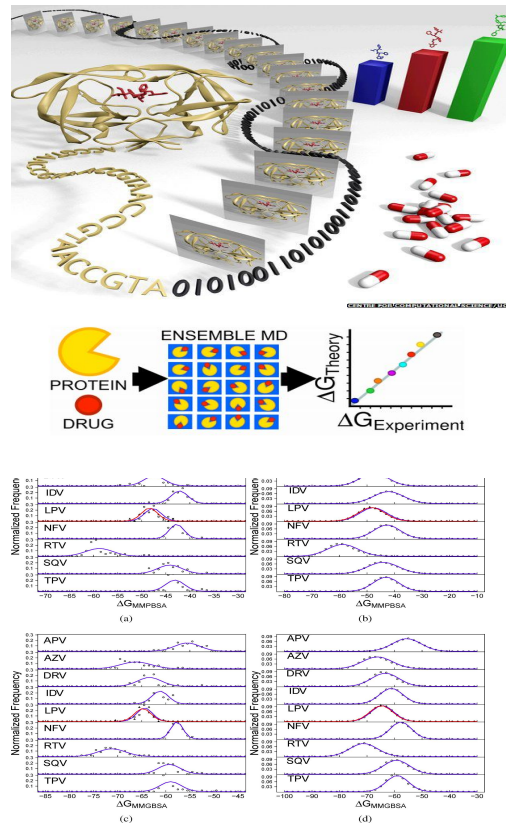
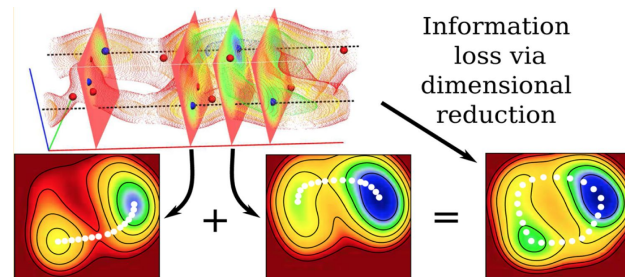


Figure 2: Schematic of the MD simulation time scale comparing long MD simulation on a special purpose machine like Anton to multiple independent MD runs on accelerators.



# Landscape of Biomolecular Simulations

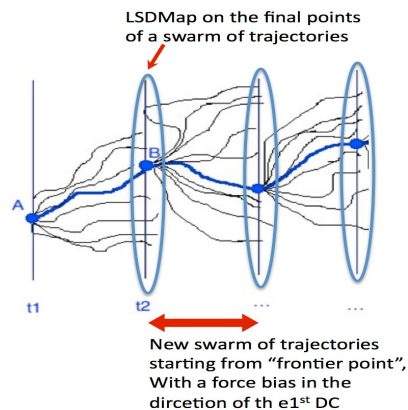
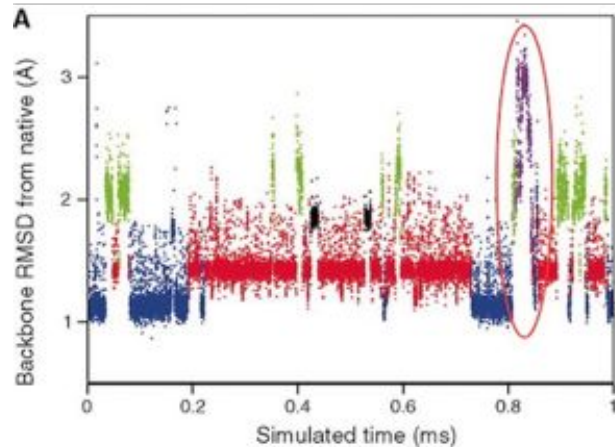
- Larger biological systems
  - Weak scaling
  - Status Quo: Size of systems: > 10M atoms
- Long time scale problem
  - Strong scaling
  - Status Quo: Duration of systems: > 10 ms
- Scaling challenges > than either single-partition strong and weak scaling.
  - Accurate estimation of complex physical processes, e.g., M-REMD
- **Gap between weak scaling and strong scaling** capabilities will grow.



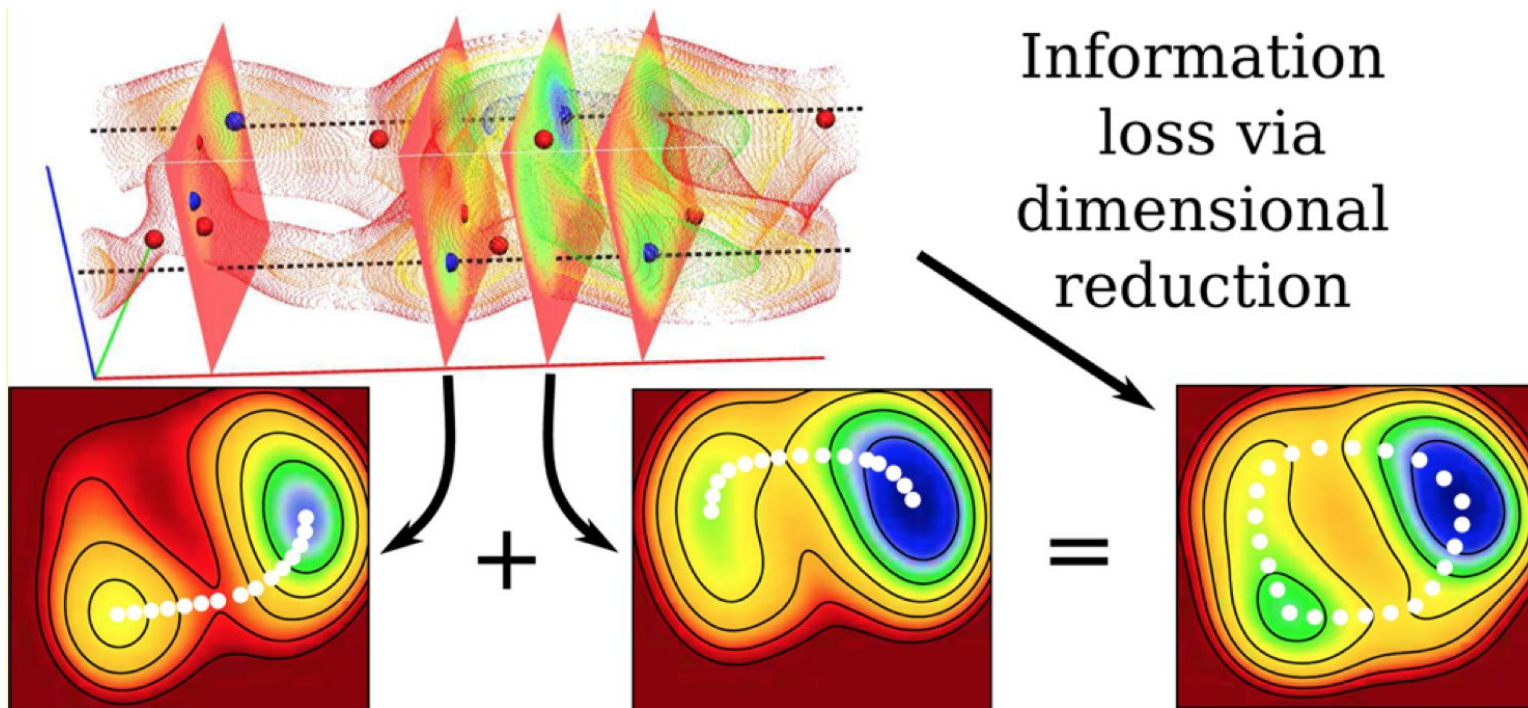
Multidimensional replica exchange umbrella sampling (REUS) simulations of a single uracil ribonucleoside.

# Brief Introduction to Sampling

- Sampling: BPTI, 1ms MD ~3 months on Anton (Shaw *et al*, Science 2010).
  - *More* sampling
  - *Better* sampling
  - *Faster* sampling
- **More sampling:** Hundreds or thousands of concurrent MD jobs
- **Better Sampling:** Drive systems towards unexplored regions, don't waste time sampling behaviour already observed
  - E.g. DM-d-MD, AMBER-COCO



# Multi-dimensional Replica-Exchange

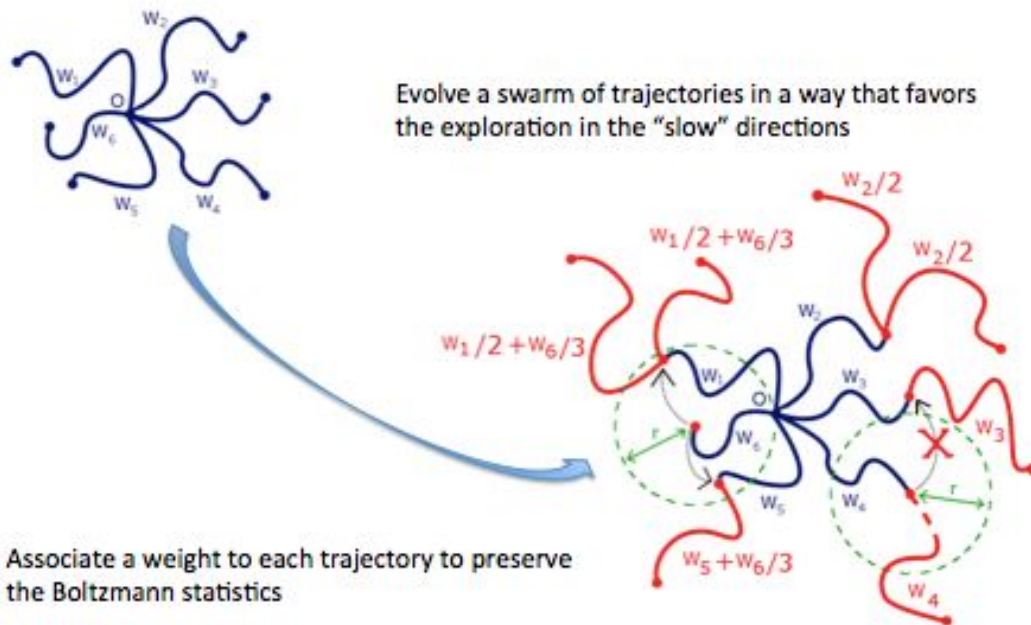


When the number of replicas cannot  $>$  number of nodes/cores, 1D replica exchange is the “default” (only!) option

# DM-D-MD: Diffusion Map Driven Molecular Dynamics

(Courtesy: Cecilia Clementi, Rice)

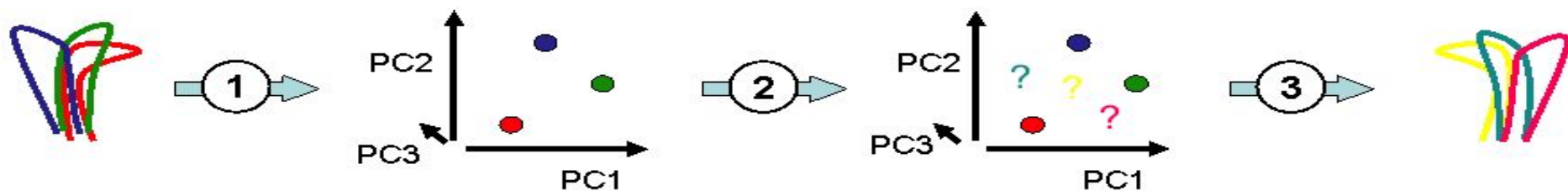
Speeding up the sampling of a protein landscape





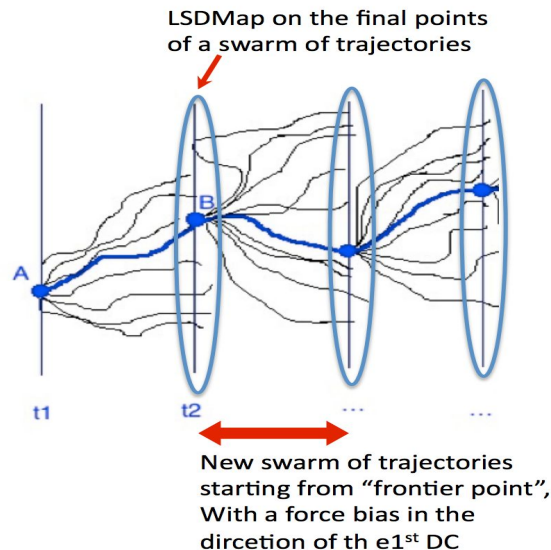
## COCO: A simple tool to enrich the representation of conformational variability in NMR structures

Charles A. Laughton,<sup>1\*</sup> Modesto Orozco,<sup>2,3,4</sup> and Wim Vranken<sup>5</sup>



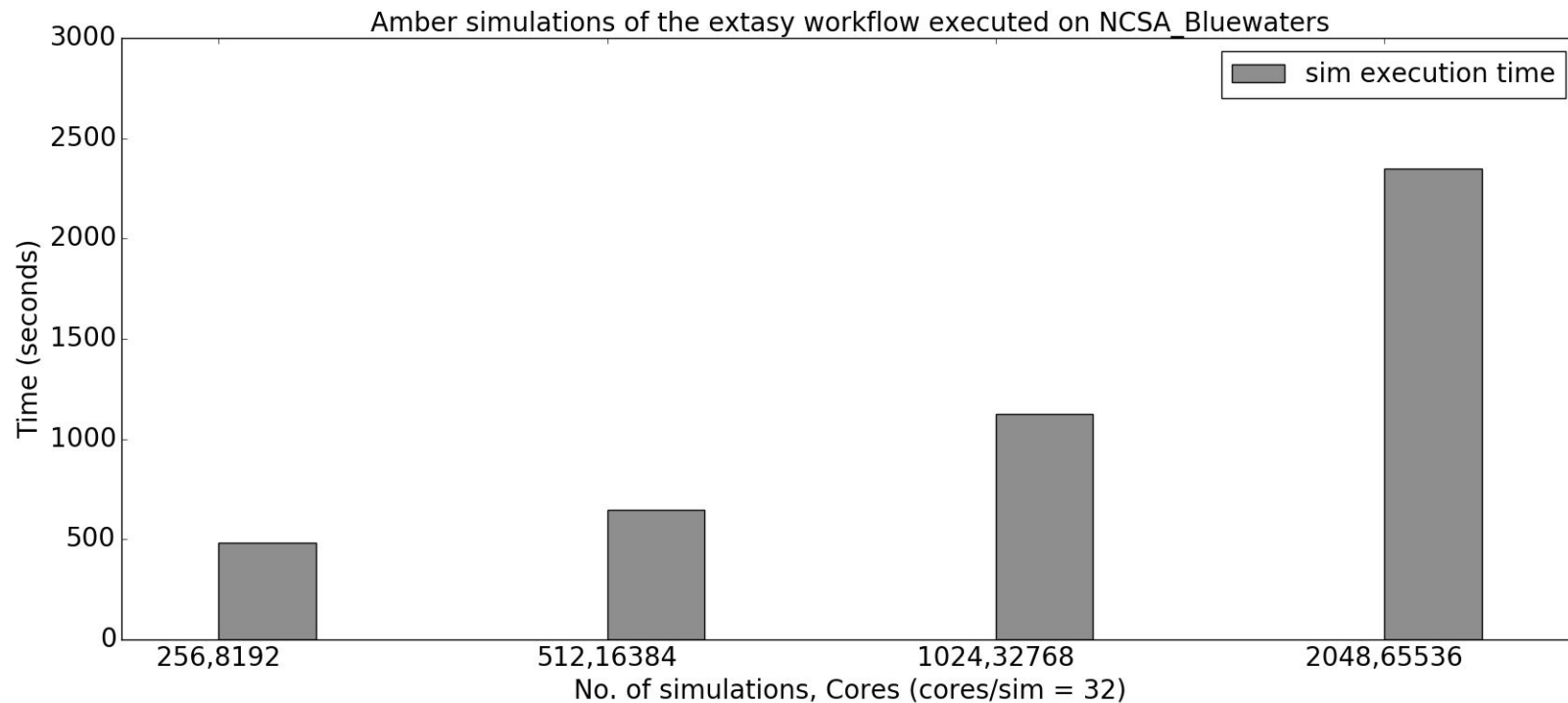
# Advanced Sampling

- **Better Sampling:** Drive systems towards unexplored regions, don't waste time sampling behaviour already observed
- Iteratively run “analysis” and “sampling” phase
  - **Sampling phase:** multitude of trajectories are run in parallel
  - **Analysis phase:** Information gathered by the trajectories is analyzed and used to restart new trajectories to explore new regions of the configurational space.

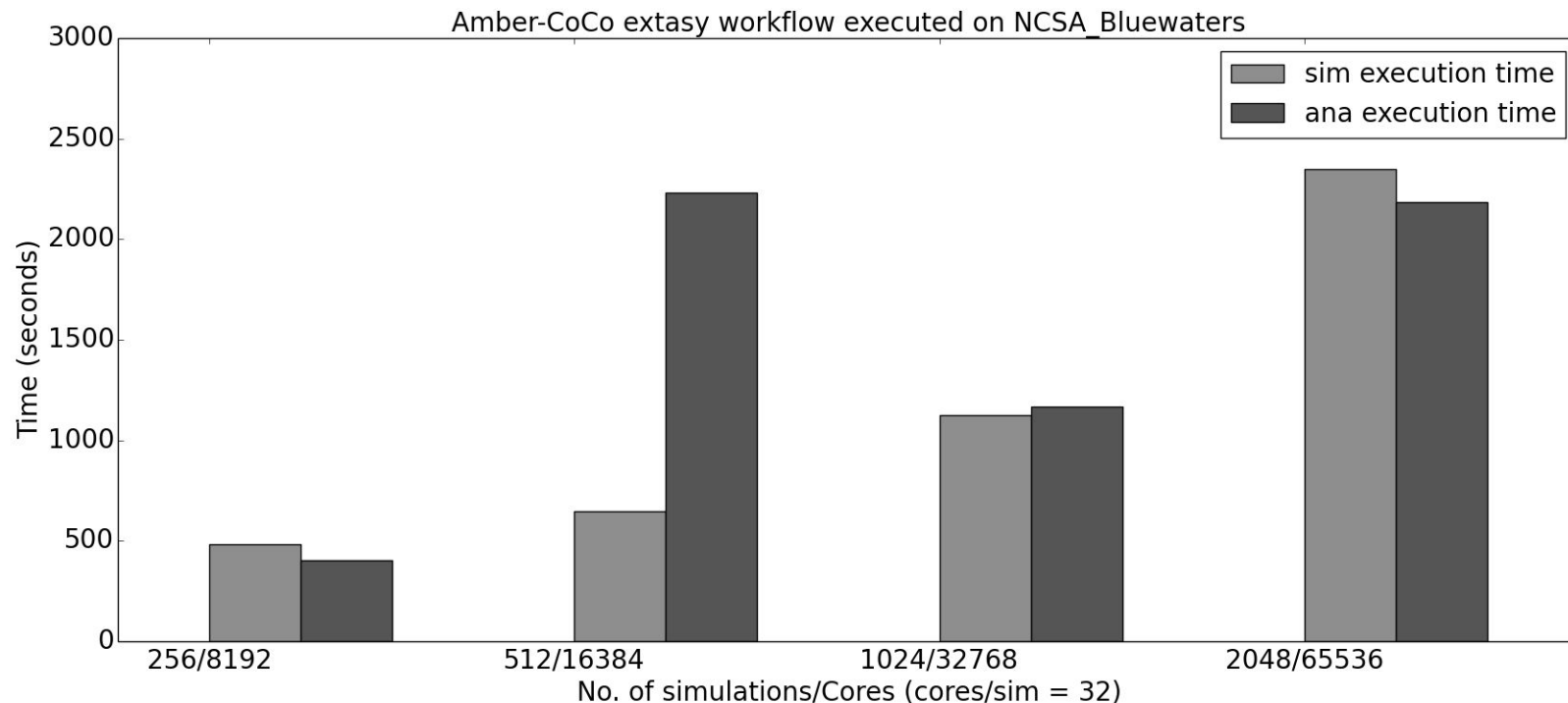


Diffusion Map driven Molecular Dynamics (DM-d-MD), uses dimensionality reduction method of “Diffusion map” to extract a good reaction coordinate and use it to redistribute a large set of trajectories in the sampling of a complex configurational space.

# Weak Scaling

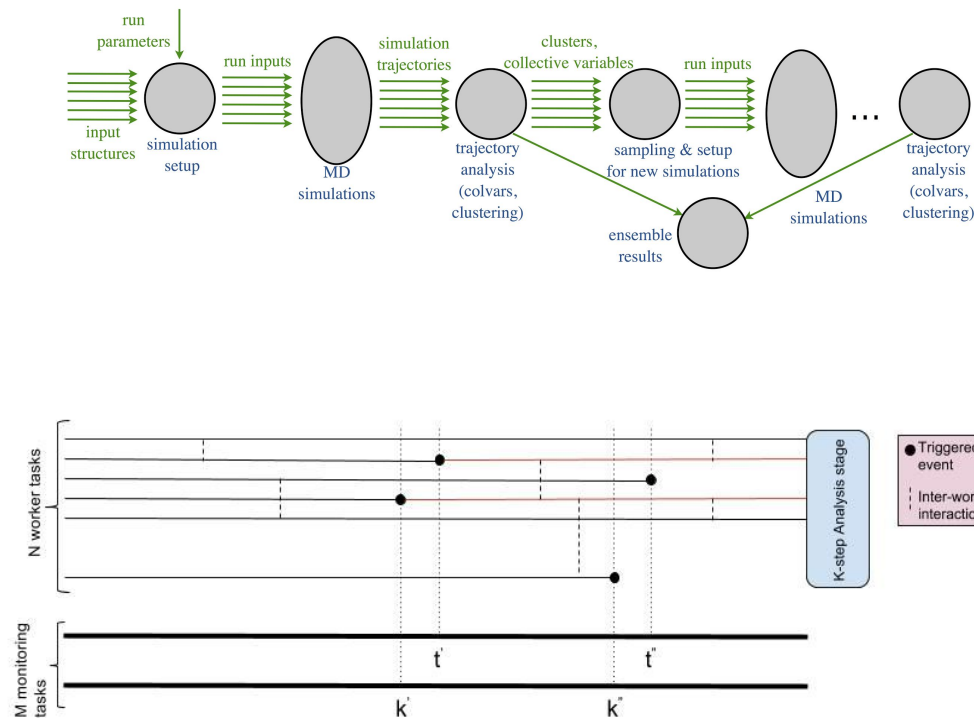


# Weak Scaling: Simulation and Analysis



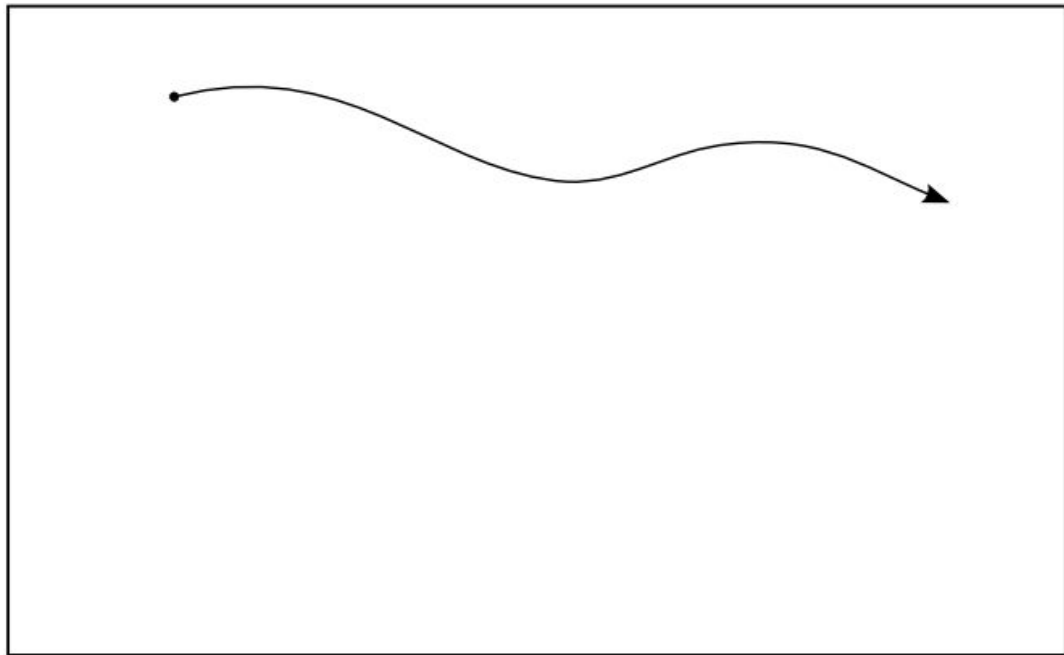
# Adaptive and Steered Patterns

- However many applications involve adaptive execution and steering.
- Examples of **simulation algorithms**:
  - Commingle replica exchange simulation with a coarse-grained potential
  - Steer ensemble simulations based on intermediate analyses
  - Add more ensemble members...
- A framework that expresses different **simulation algorithms** as “adaptive execution patterns”. **How ?**
  - Generalise static patterns EnTK
  - Opens many research questions



# MSM: ML-driven Sampling

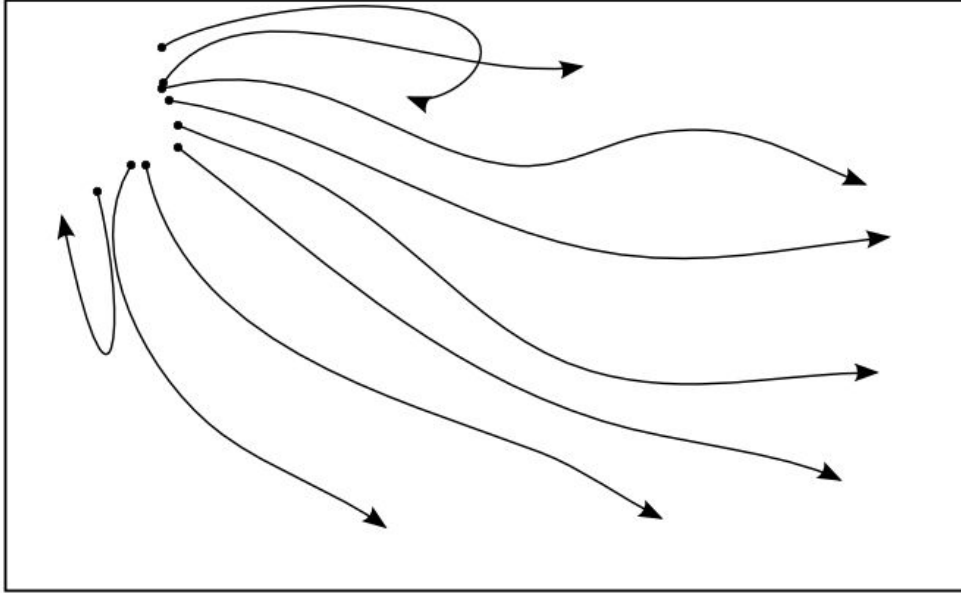
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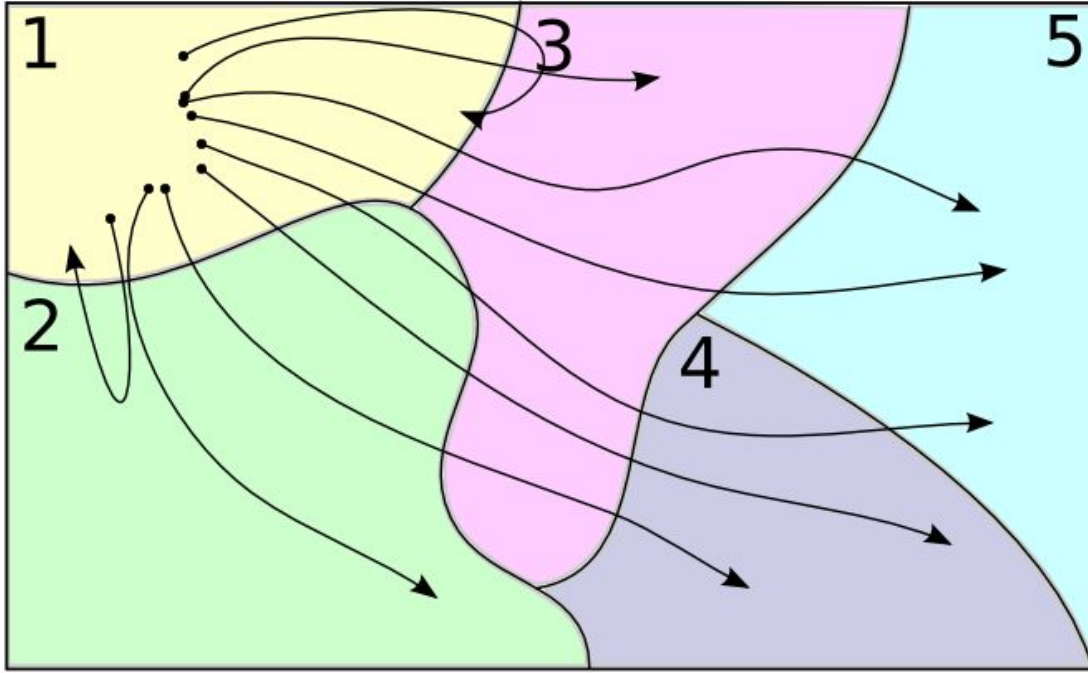
# MSM: ML-driven Sampling

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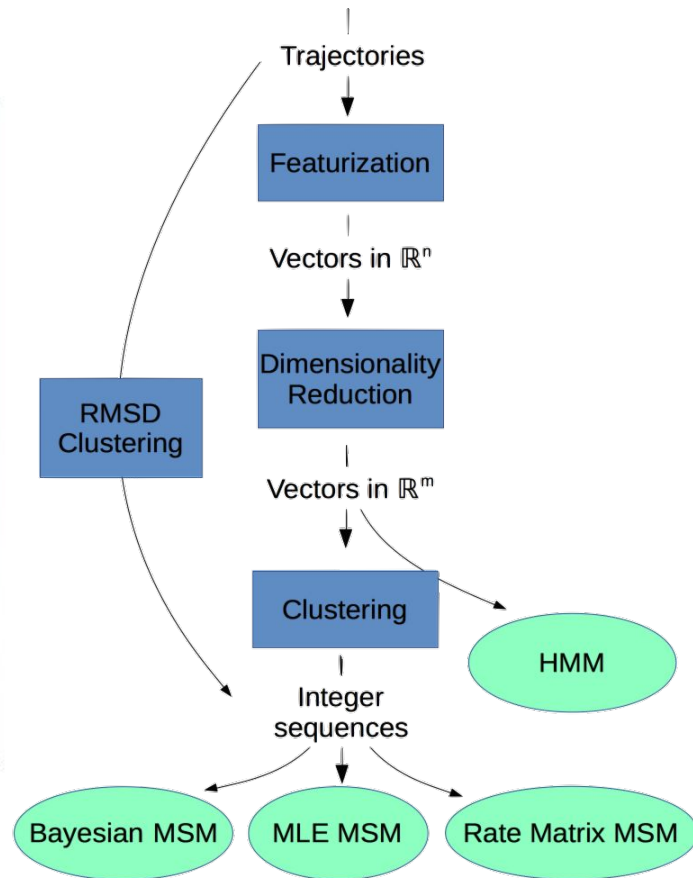
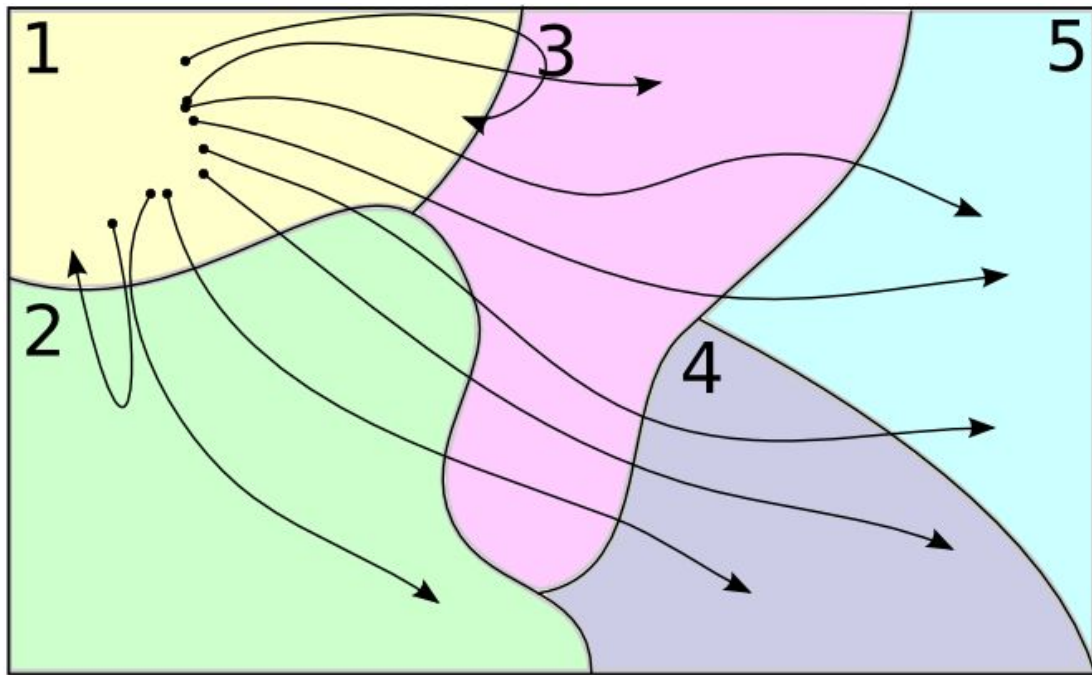
# MSM: ML-driven Sampling

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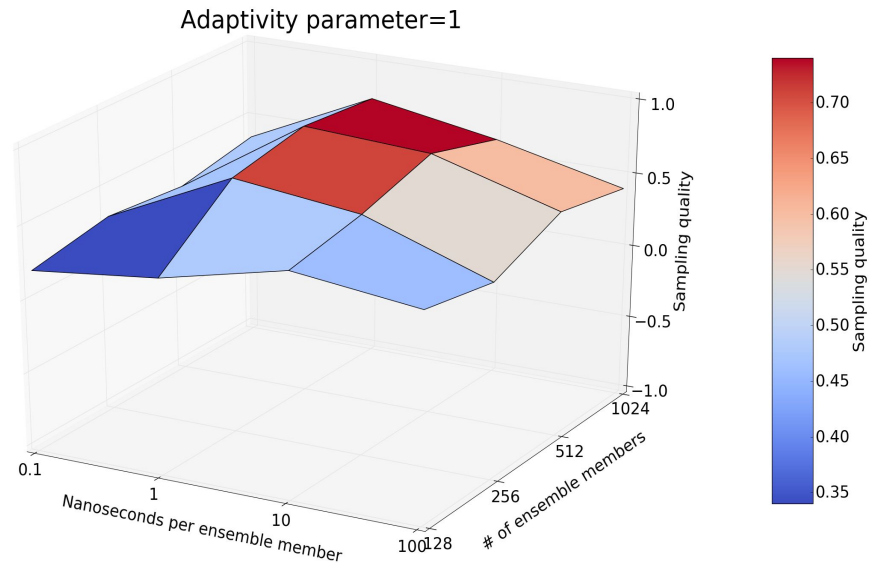
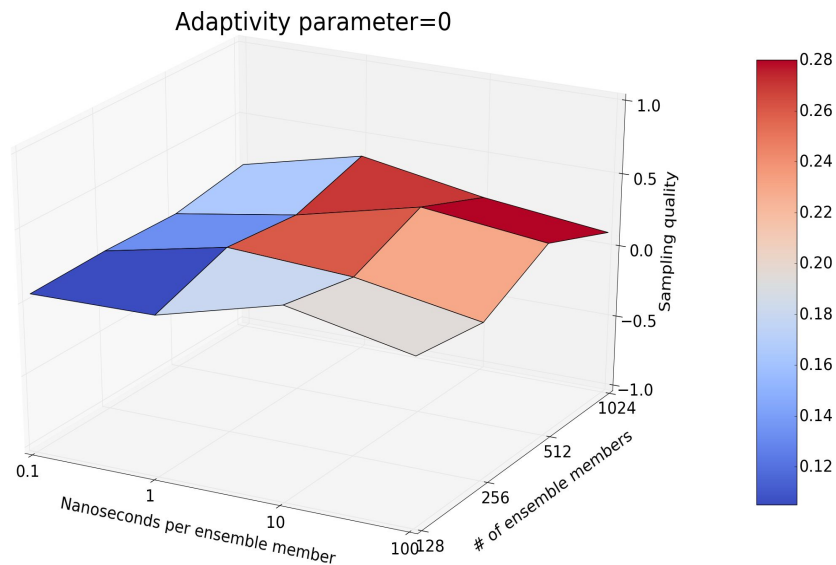


Credit: Kyle Beauchamp

# MSM: ML-driven Sampling



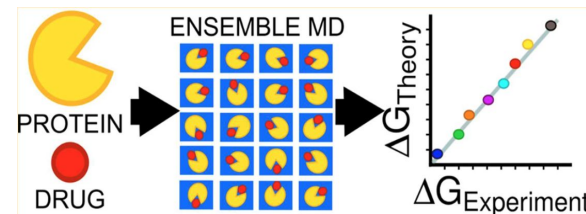
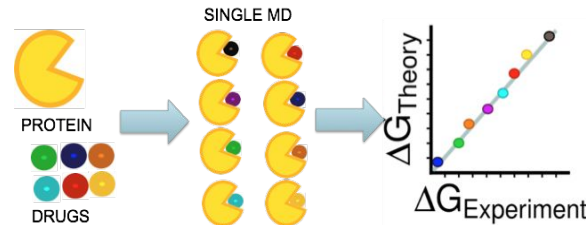
# Better Sampling -- Requires Learning “on the fly”



Finding the optimal resource configuration.

# The Power of Many: RADICAL-Ensemble Toolkit

- Support for **heterogeneous** tasks
  - Multi-node and sub-node, application kernels, MPI/non-MPI
- Adaptive: Workload and resource: tasks and/or relations between tasks unknown *a priori*
- Range of concurrency and coupling of tasks
  - Multiple-levels and degree
- Multiple dimensions of scalability:
  - Concurrency: O(100K)-O(1,000K) tasks
  - Task size: O(1) - O(1,000) cores
  - Launch: O(100+) tasks per second
  - Task duration: O(1) - O(10,000) seconds
  - ....

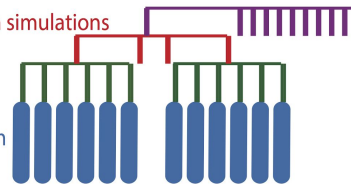


Ensemble coupling

Tight coupling between simulations

Multi-node parallelism  
within simulation

Within-node parallelism  
(SIMD/SIMT)



Parallelism:      Communication  
Sensitivity:

10,000's

100's

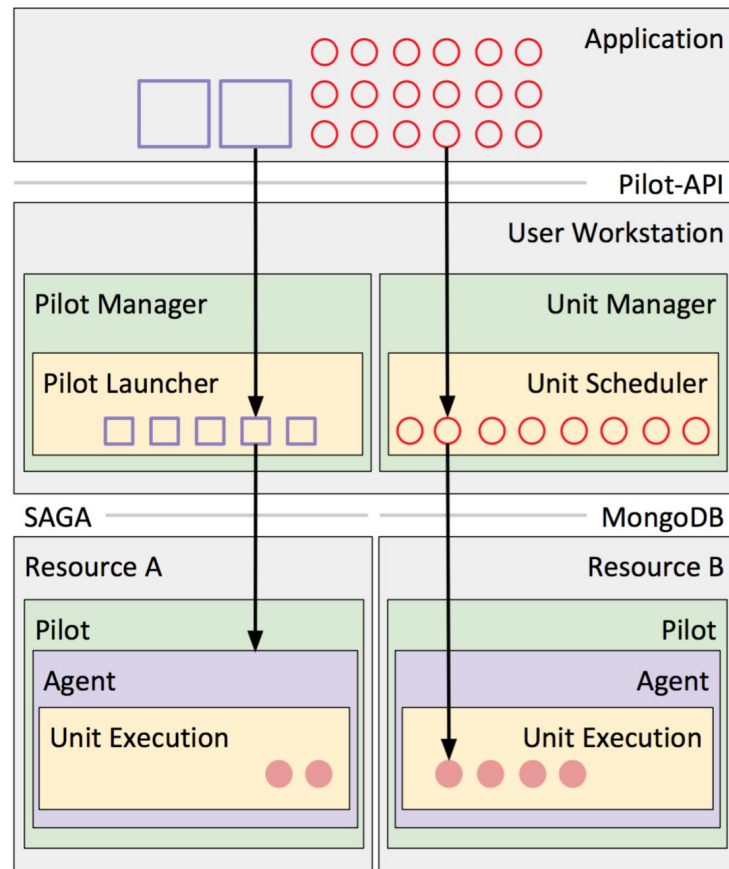
100's

10's



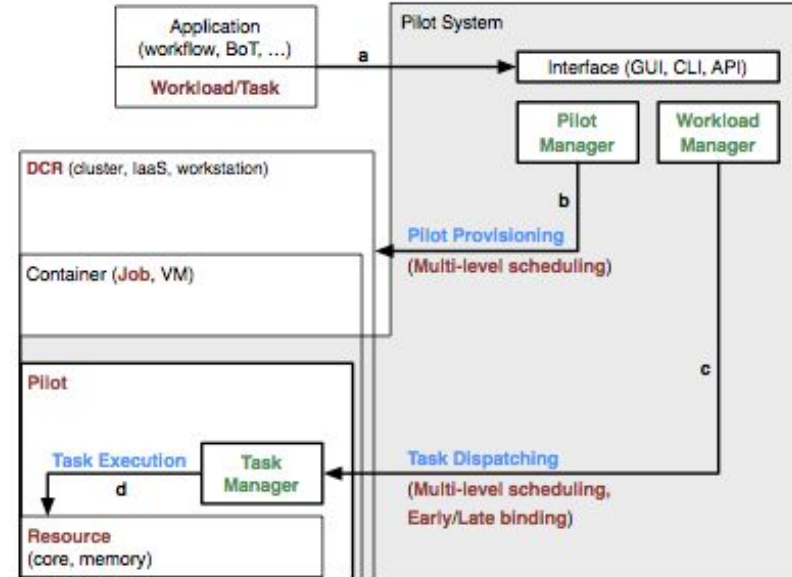
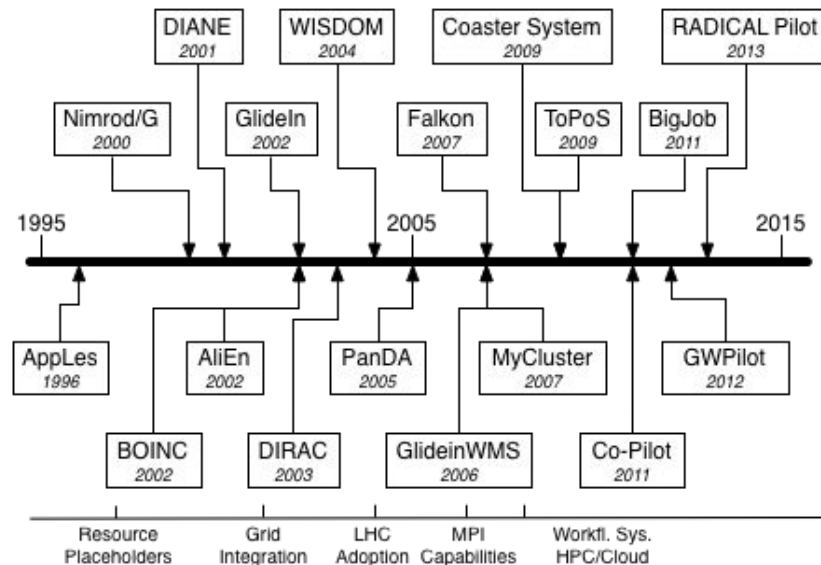
# RADICAL-Pilot Overview

- **Programmable interface (arguably unique)**
  - Defined state models for pilots and units.
- **Supports research whilst supporting production scalable science:**
  - Agent, communication, throughput.
  - Pluggable components; introspection.
- **Portability and Interoperability:**
  - SAGA (batch-queue system interface)
  - Modular pilot agent for diff. architectures
  - Works on Crays, XSEDE resources, most clusters, OSG, Amazon EC2...





# Pilot Jobs: Many Variations on a Theme

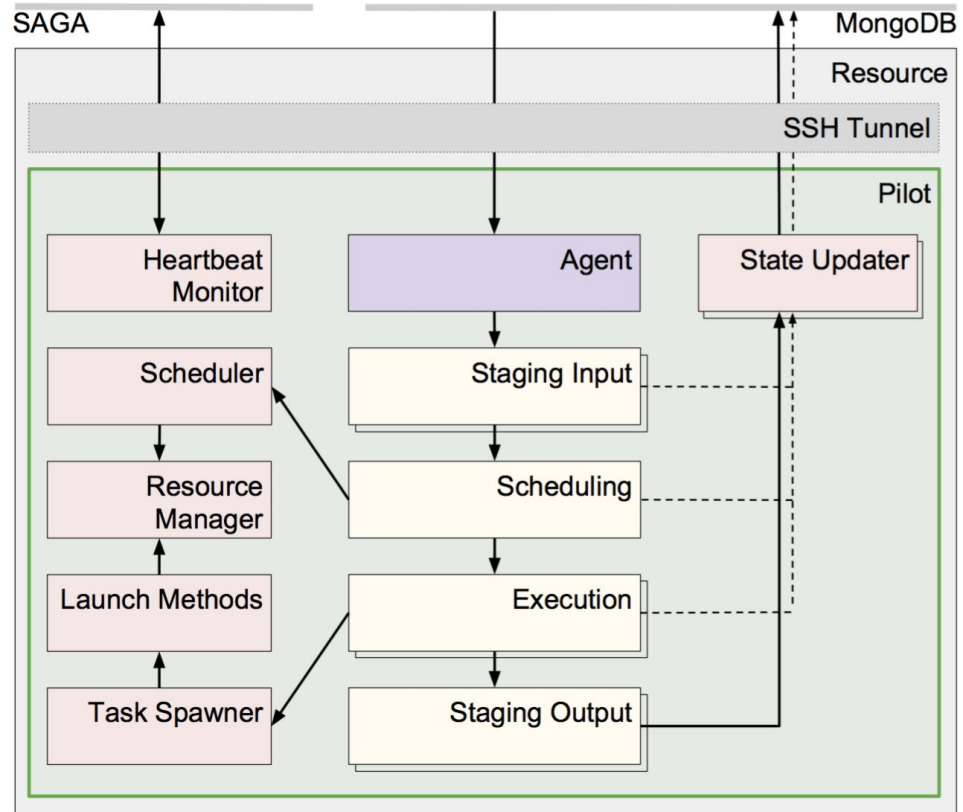


*"Perfection is achieved, not when there is nothing more to add, but when there is nothing left to take away."*  
- Antoine Saint-Exupéry

- "P\*: A Model of Pilot-Abstractions", 8th IEEE International Conference on e-Science (2012)
- A Comprehensive Perspective on Pilot-Jobs <http://arxiv.org/abs/1508.04180> (2015)

# Agent Architecture

- **Components:** Enact state transitions for Units
- **State Updater:** Communicate with client library and DB
- **Scheduler:** Maps Units onto compute nodes
- **Resource Manager:** Interfaces with batch queuing system, e.g. PBS, SLURM, etc.
- **Launch Methods:** Constructs command line, e.g. APRUN, SSH, ORTE, MPIRUN
- **Task Spawner:** Executes tasks on compute nodes



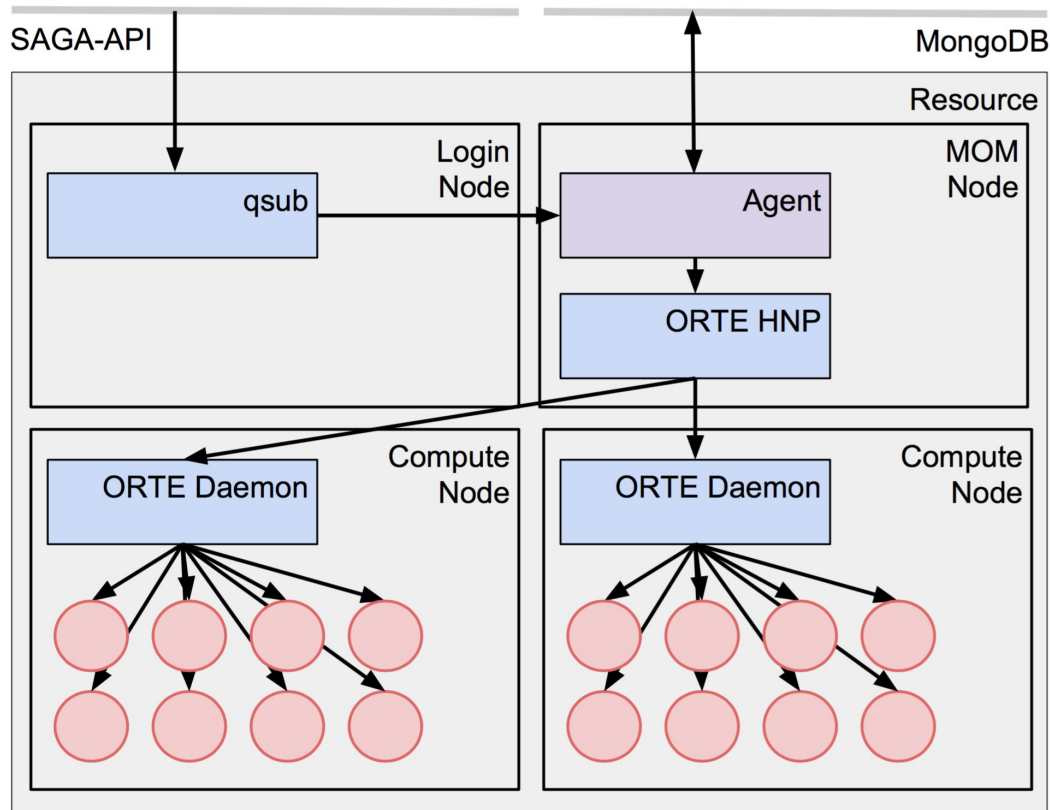
# RADICAL-Pilot: ORTE

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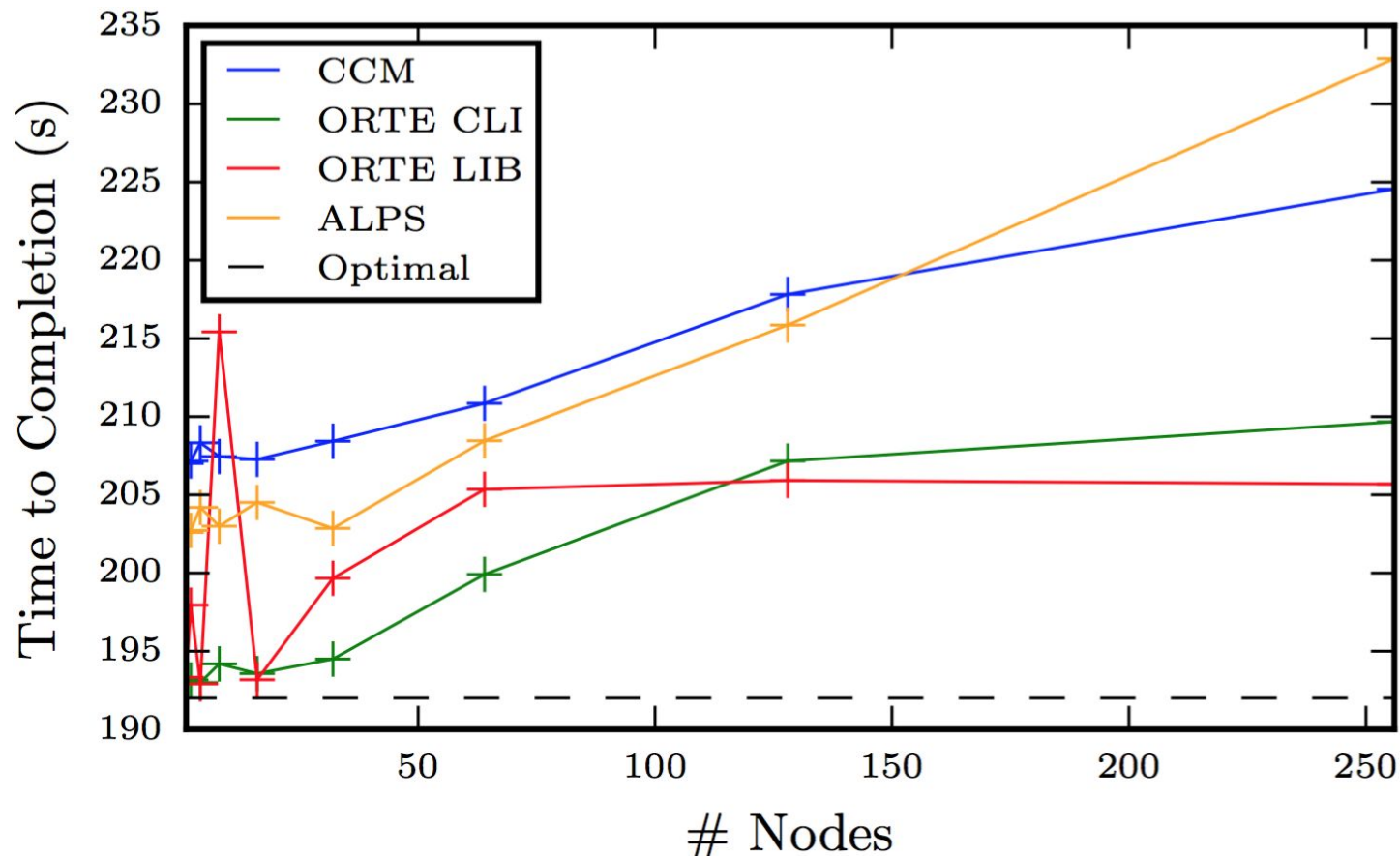
- ORTE: **O**pen **R**un**T**ime **E**nvironment
  - Isolated layer used by Open MPI to coordinate task layout
  - Runs a set of daemons over compute nodes
  - No ALPS concurrency limits
  - Supports multiple tasks per node
- orte-submit is CLI which submits tasks to those daemons
  - 'sub-agent' on compute node that executes these
  - Limited by fork/exec behavior
  - Limited by open sockets/file descriptors
  - Limited by file system interactions

# RADICAL-Pilot + ORTE-LIB

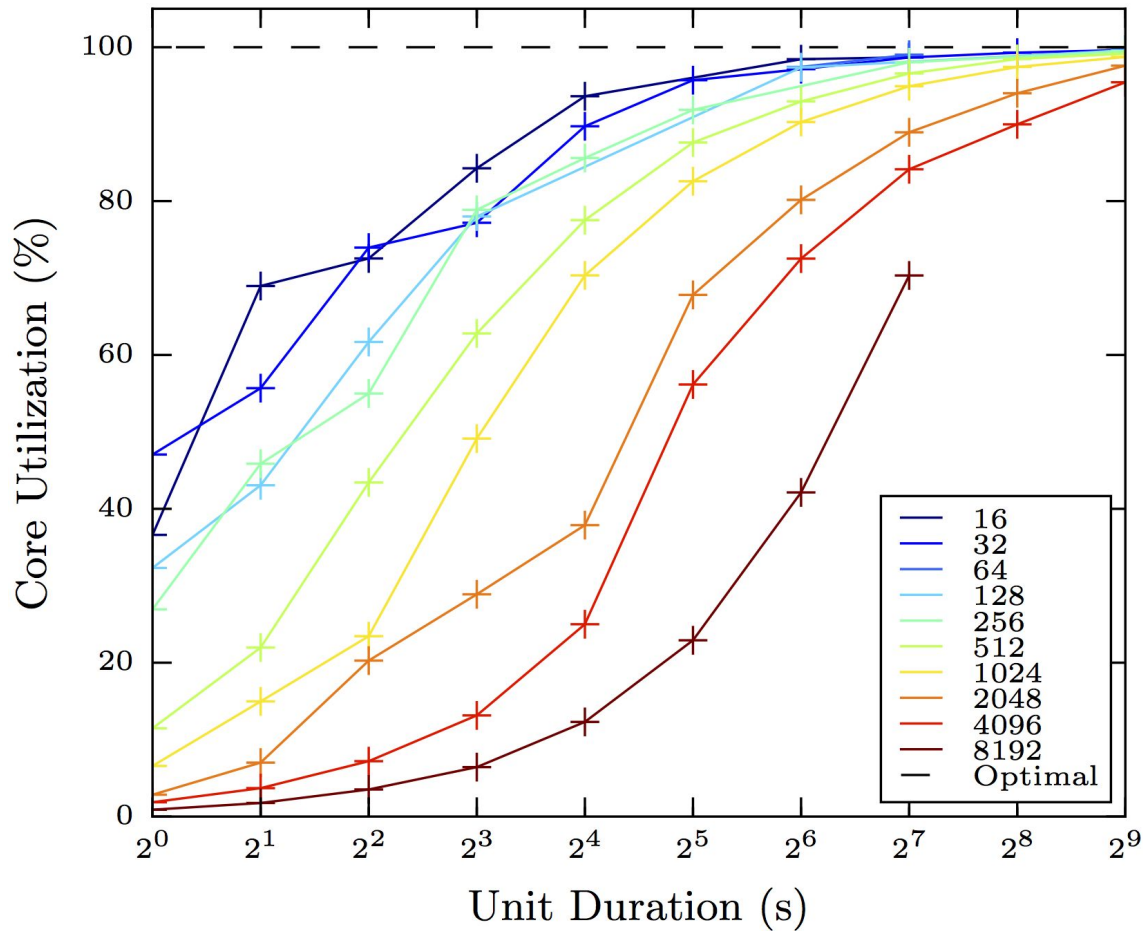
- All the same as ORTE-CLI, but
  - Uses library calls instead of `orterun` processes
  - No central fork/exec limits
  - Shared network socket
  - (Hardly) no central file system interactions



# Agent Performance: Full Node Tasks (3xN, 64s)



# Agent Performance: Resource Utilization





# Challenges of O(100K) Concurrent Tasks

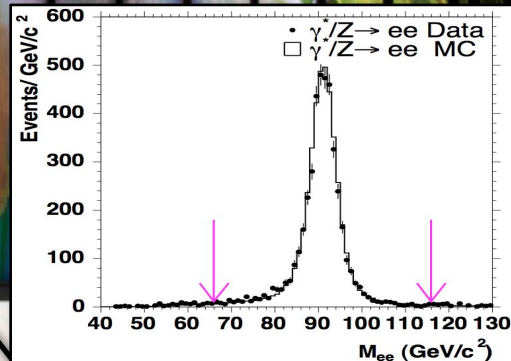
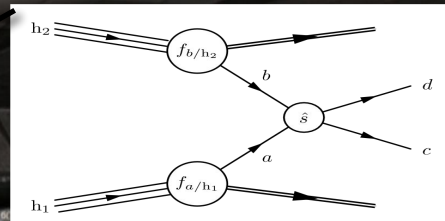
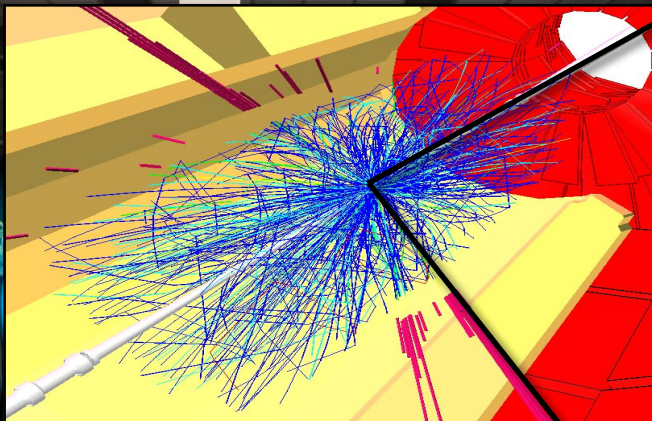
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- Agent communication layer (ZMQ) has limited throughput
  - limit is not yet reached
  - bulk messages (is implemented now)
  - separate message channels
  - code optimization
- Agent scheduler (node placement) does not scale well with number of cores
  - bulk operations (schedule bag of tasks at once)
  - good scheduling algorithms and implementations exist
  - code optimization, C-module (instead of pure Python)
- Collecting complete jobs is just as hard as spawning new ones
  - decouple
- Interaction with DB and client side has limited scalability
  - replace with proper messaging protocol (also ZMQ?)

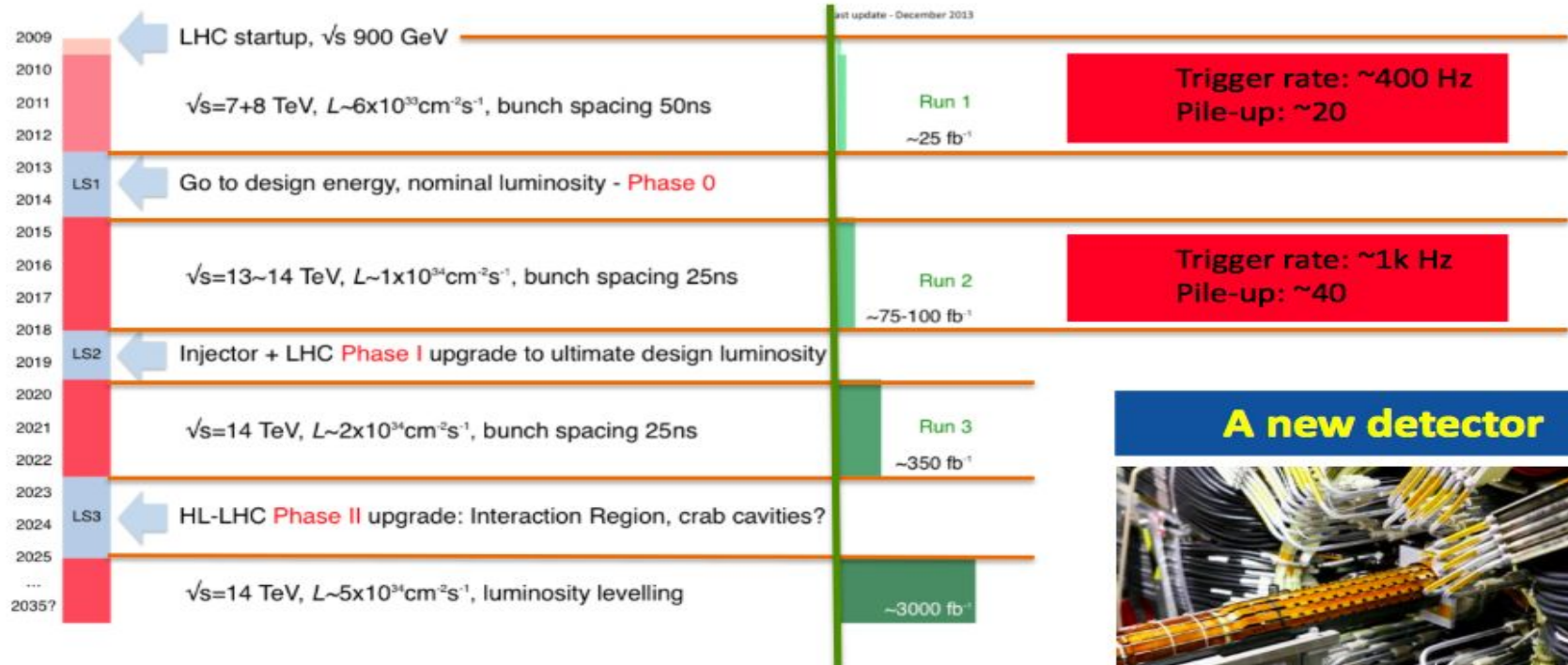
# **Distributed WLMS**

# Next Generation Workflow Management for High Energy Physics

B0



# LHC Upgrade Timeline



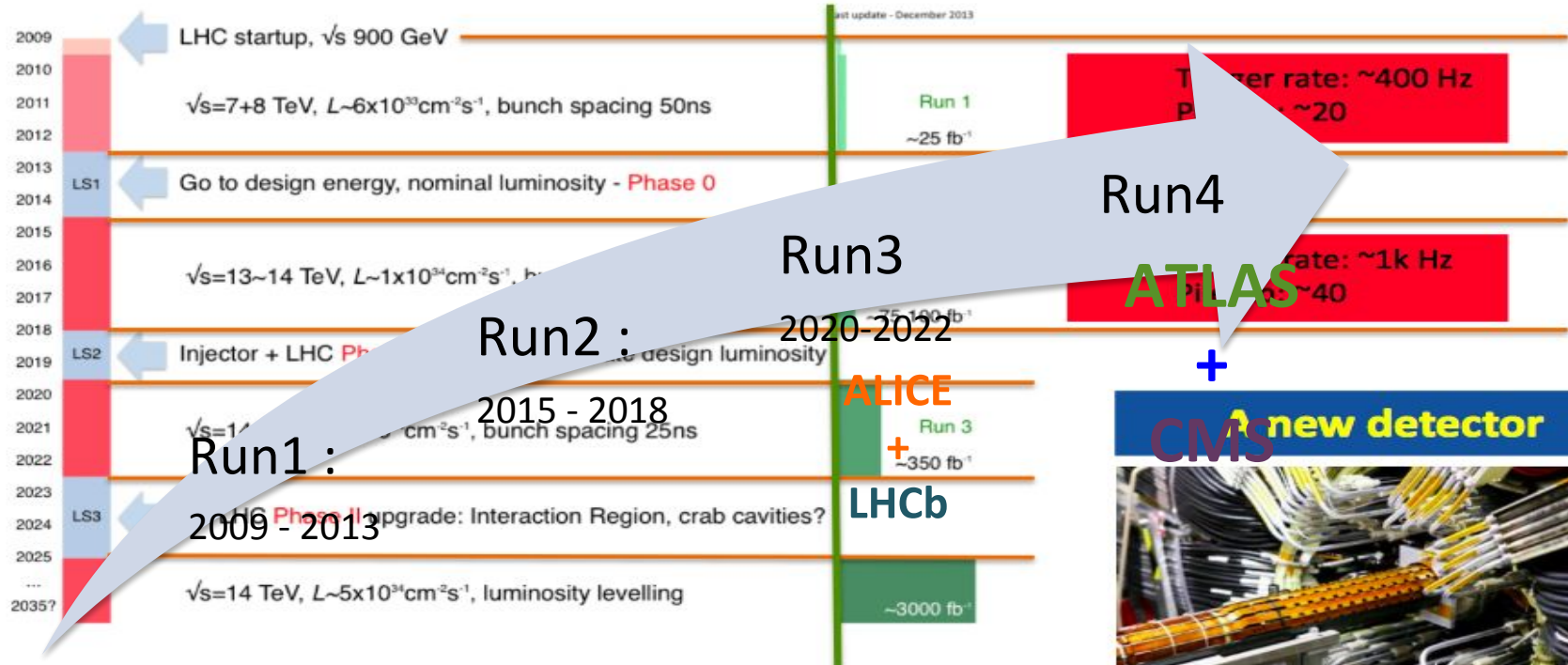
## A new detector



e.g. tracking, calorimeters

In 10 years, increase by factor 10 the LHC luminosity  
→ More complex events  
→ More Computing Capacity

# LHC Upgrade Timeline



In 10 years, increase by factor 10 the LHC luminosity

→ More complex events

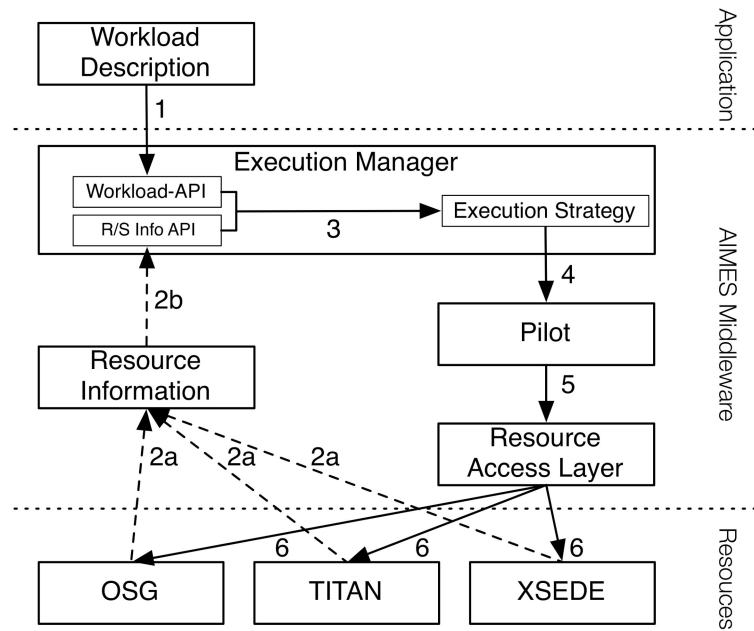
→ More Computing Capacity



e.g. tracking, calorimeters

# AIMES

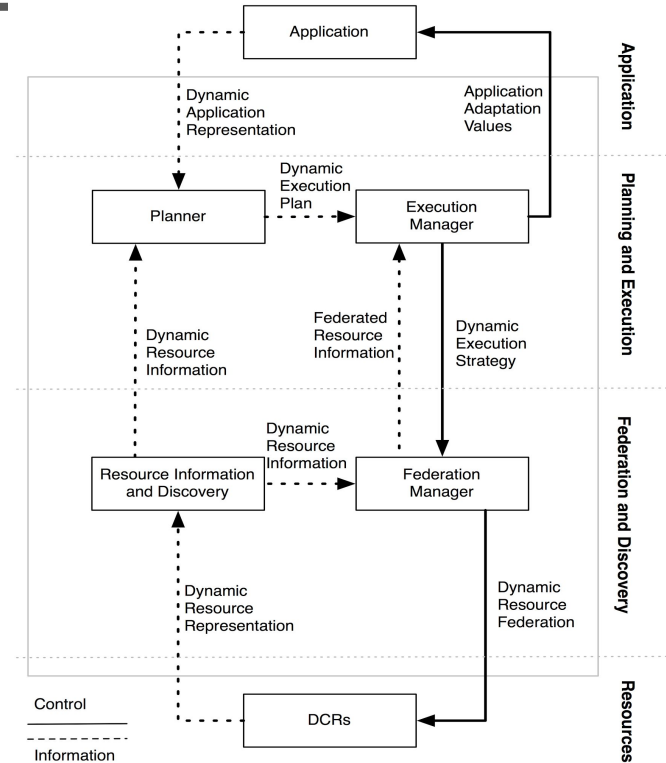
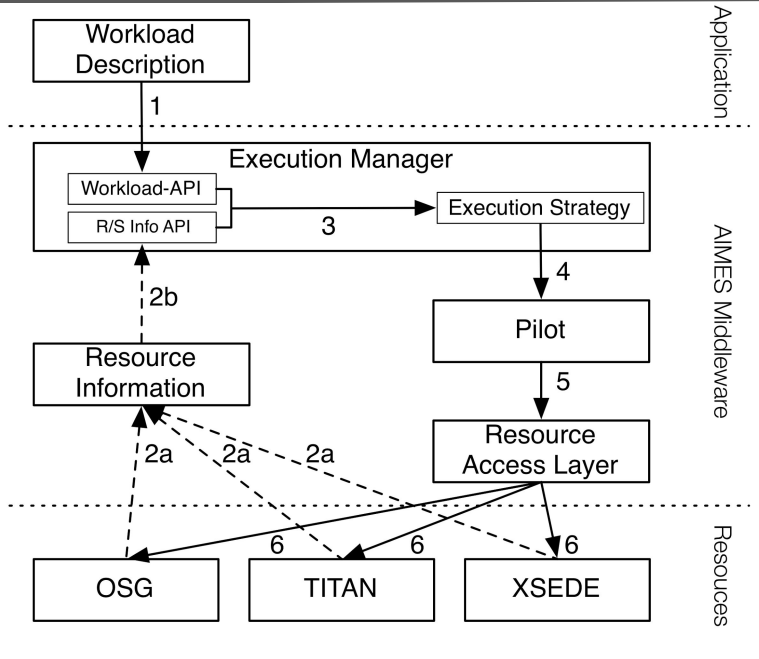
- AIMES: Investigate principles and identify abstractions for distributed execution.
  - *Uniformity in execution* across dynamically federated heterogeneous resources.
  - Conceptual → **implementation** improvements: “*Better*” mapping of workloads to infrastructure and thus also utilization
- AIMES Model of Workload Management:
  - Importance of **dynamic integration** of workload and resource information.
  - Pilot-based **Execution Strategy**: Temporally ordered set of decisions that need to be made when executing a given workload.



*Schematic of **RADICAL-WLMS** approach to workload-resource integration: Evaluate workload requirements & resource capabilities, derive an execution strategy, and enact it, executing the workload on the federated resources.*



# Dynamic Resource Management



- PANDA-SAGA : BigPANDA Project (2012-2016)
- PANDA-Pilot : Ongoing redesign for TITAN
- PANDA-AIMES : Heterogeneous workloads and unified execution

**Lessons for how we build  
workflow systems?**



# “Building Blocks” Approach to Workflow Systems ?

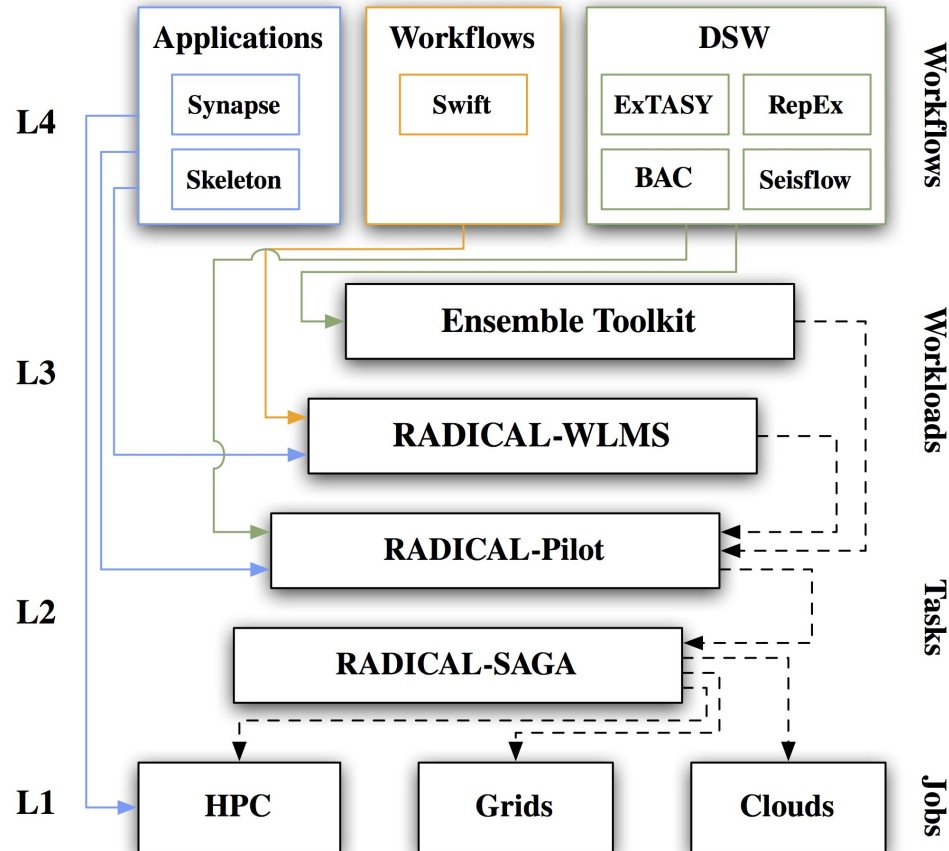
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- Workflows aren't what they used to be!
  - More pervasive, sophisticated but no longer confined to “big science”
  - Diverse requirements, “design points”; unlikely “one size fits all”
- Extend traditional focus from **end-users to workflow system/tool developers!**
  - Building Blocks (BB) permit workflow tools and applications can be built.
- **An illustrative example of a building block common across WFMS**
  - Pilot Job Systems to support scalable execution of multiple tasks

# **RADICAL-Cybertools:**

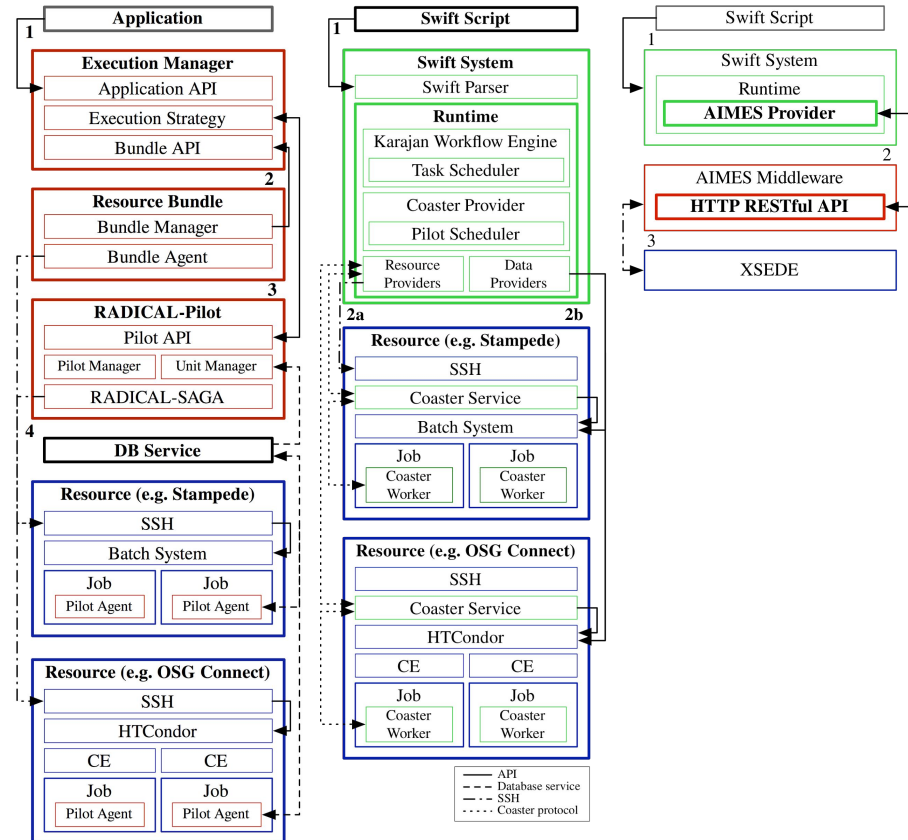
## **Abstractions driven building block CI.**

# RADICAL Cybertools: Abstraction based BB



# SWIFT - RADICAL Cybertools Integration

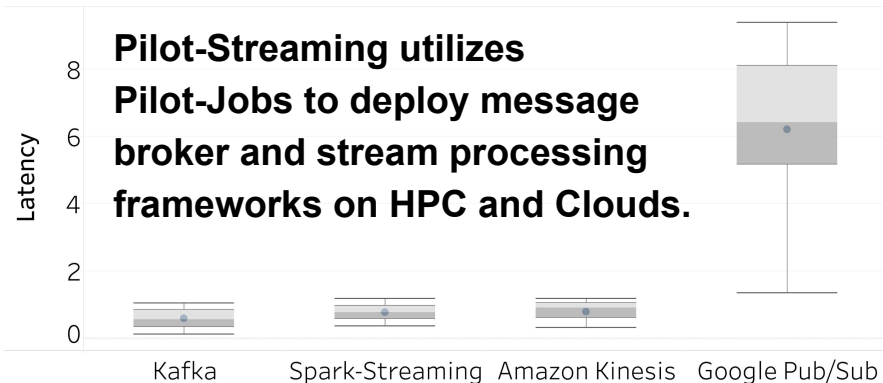
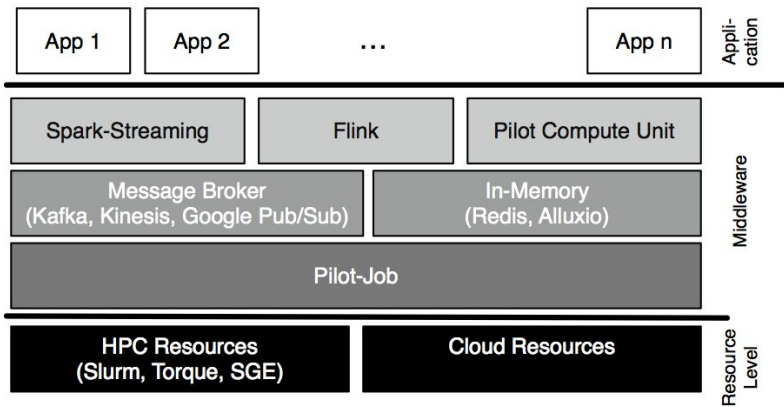
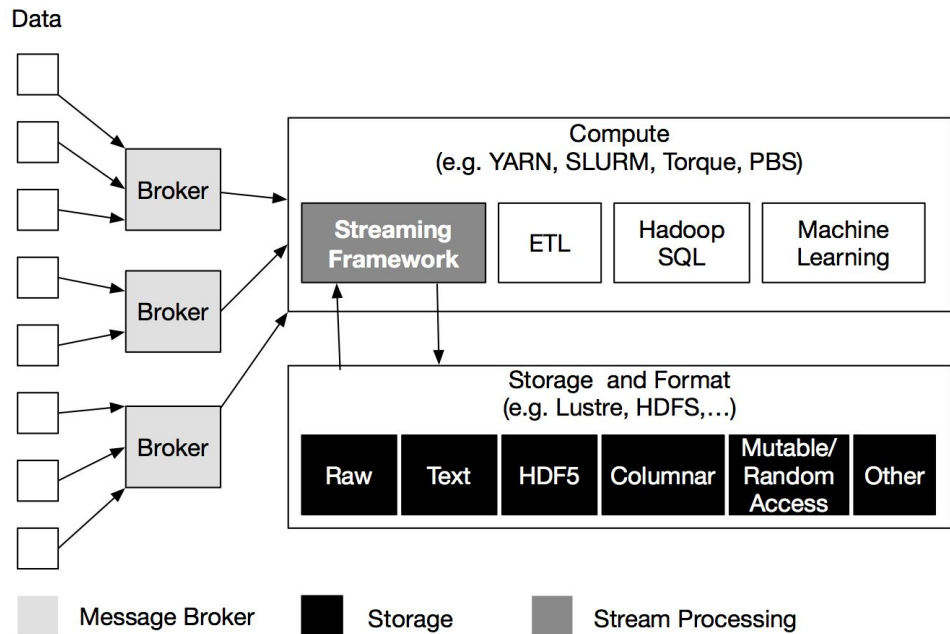
- Many WFMS use pilot systems; greater variance in use of WLMS:
  - Pegasus → Corral/glidein-WMS
  - Condor/glidein → glidein-WMS
  - Swift, Galaxy → No (XSEDE)
- Swift-RCT comparison and integration:
  - Workflow → Workload → Tasks abstractions
  - Uniform execution Model: Binding of tasks and pilots to resources**
  - Efficient scheduling across pilots and resources**



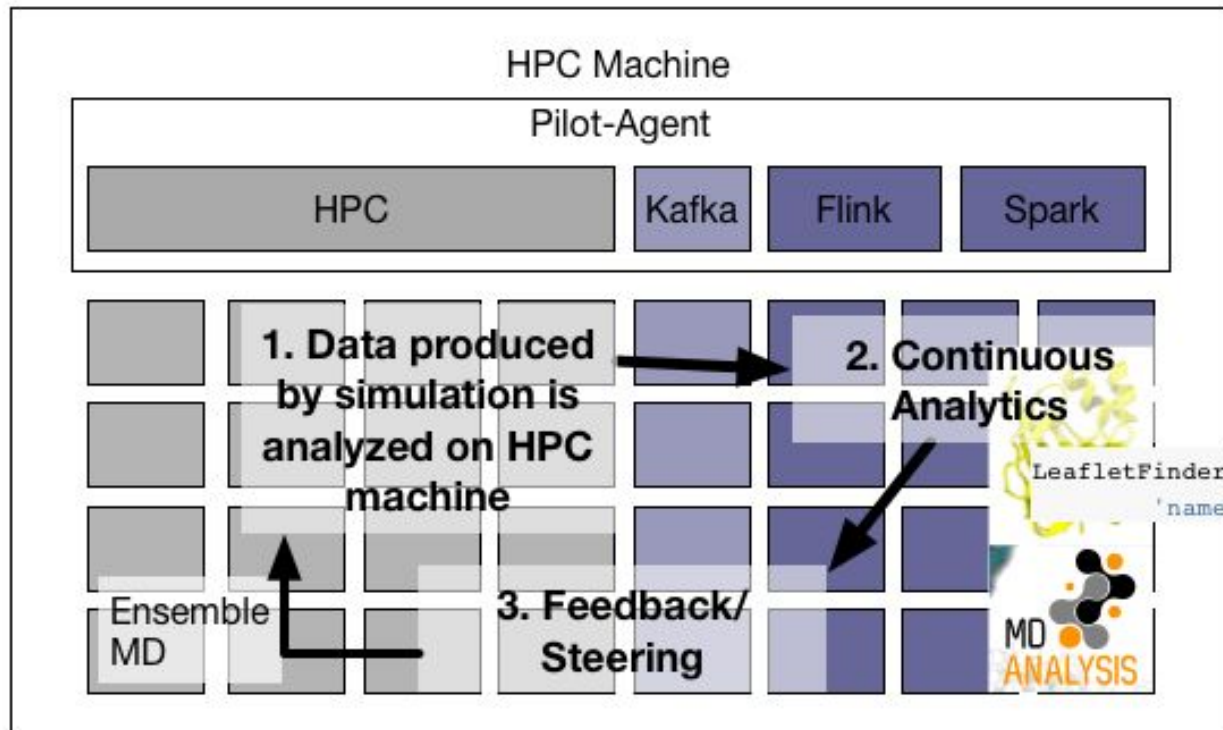
Reference: “Analysis of Distributed Execution of Workloads”,  
<https://arxiv.org/abs/1605.09513>

# Pilot-Streaming

Pilot-Streaming enables the coupling of data production (simulations) and analysis within HPC environment.



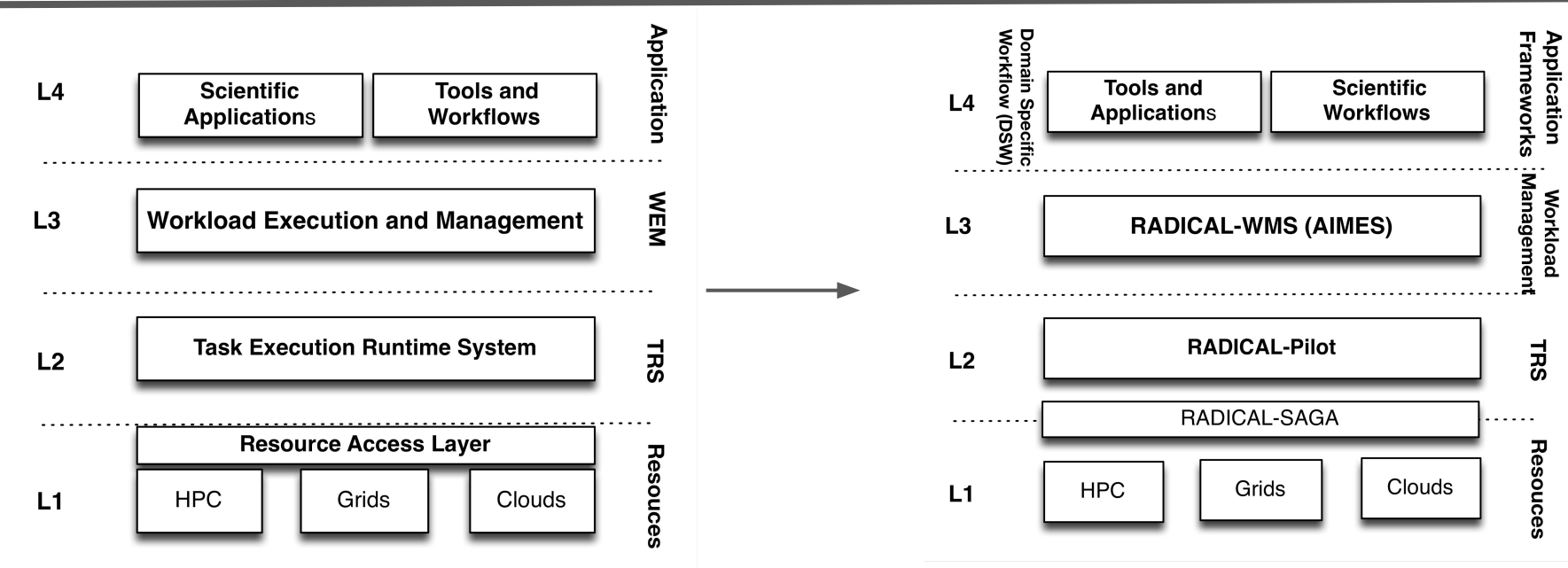
# Pilot Streaming: EnsembleMD and MDAnalysis



Pilot-Streaming is utilized to couple MD simulations and continuous analytics (LeafletFinder). By continuously monitoring developed Leaflets.

Dynamic resource management is critical to balance data production rates and analytics needs.

# PanDA: BIG and RADICAL!



- PANDA-SAGA : BigPANDA Project (2012-2016)
- PANDA-Pilot : Ongoing redesign for HPC Systems/TITAN
- PANDA-AIMES : Heterogeneous workloads and unified execution model.

Thank you!



Thanks to RADICAL Team

Geoffrey Fox, A Klimentov, K De, J Weissman, D Katz (CS/CI)

Cecilia Clementi, Peter Kasson, Frank Noe (BMS)

Thanks to NSF and DOE

**<http://radical.rutgers.edu>**