

NSCI Framework: Software: SCALE-MS – Scalable **Adaptive Large Ensembles of Molecular Simulations**

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Scaleable: <u>Weakly</u> coupled algorithms can make it possible to get near-linear scaling in time-tosolution with 10⁴ to 10⁶ instances of simulation ensembles, even with large (minutes) latency



Adaptive: A framework for simulations to communicate both synchronously and asynchronously, and with this information, make decisions altering and shaping the simulation ensemble



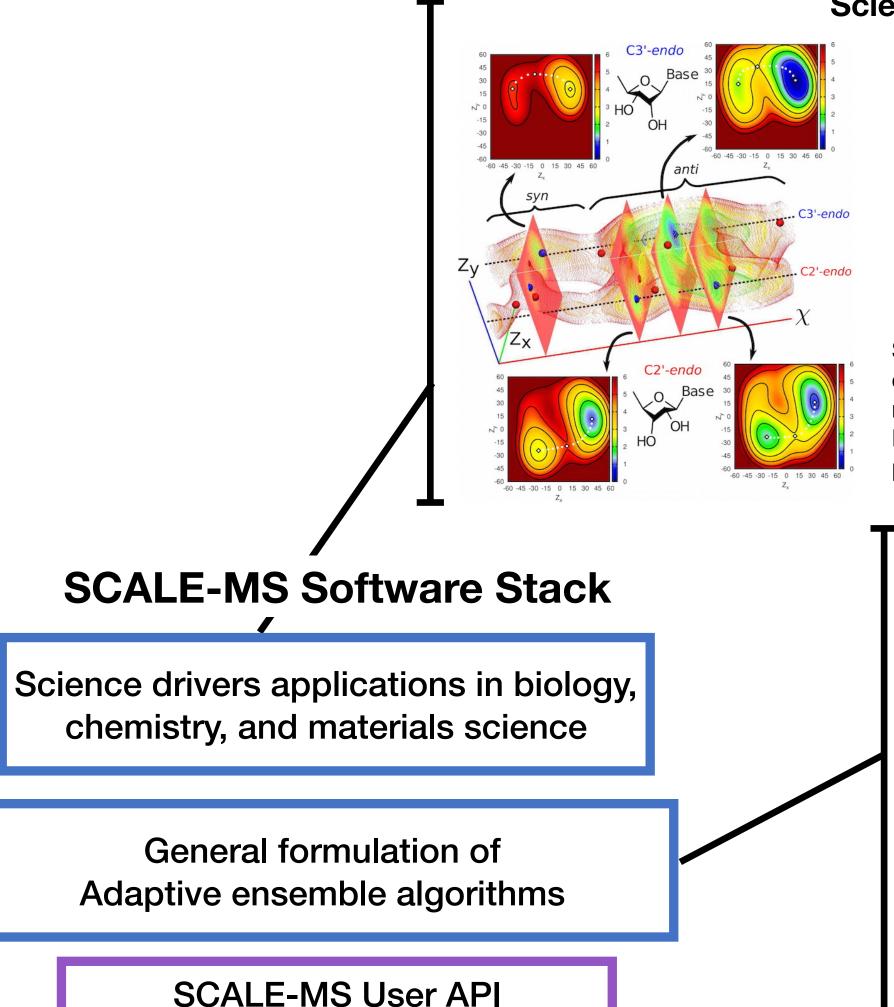
Large: With linear-scaling, weakly-coupled algorithms, it is possible to effectively use leadership computing and cloud computing for molecular problems in chemistry, biology, and materials science

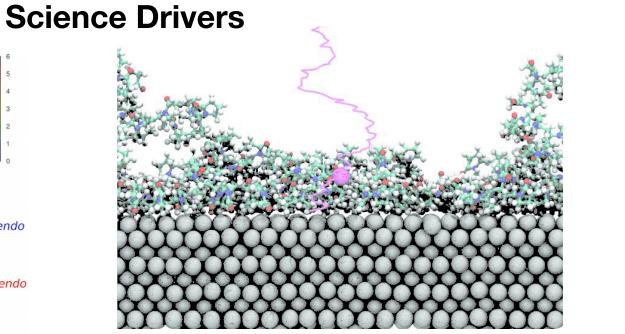


Ensembles: Many accelerated simulation methods can be parallelized by running infrequently communicating copies that only exchange partial information



Molecular Simulations: Approach designed for molecular simulation problems that have widely separated timescales, but should be adaptable to multiple-time scale algorithms in other areas





Science is driven by need to sample rare events in complex configuration spaces, such as determining multidimensional free energy surfaces (left, PMF of RNA) and understanding multiple timescale phenomena (top, diffusion onto coated surface

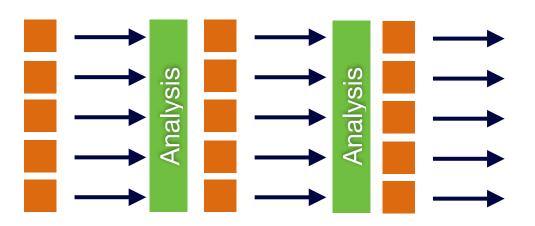
Software kernels: • GROMACS

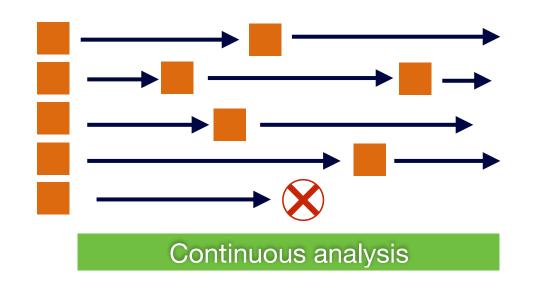
- LAMMPS
- OpenMM
- NAMD
- Extensible to others

Types of ensemble members:

- 'Vanilla' molecular dynamics
- Metadynamics instances
- Replica exchange sets
- Umbrella sampling
- Nonequilibrium dynamics

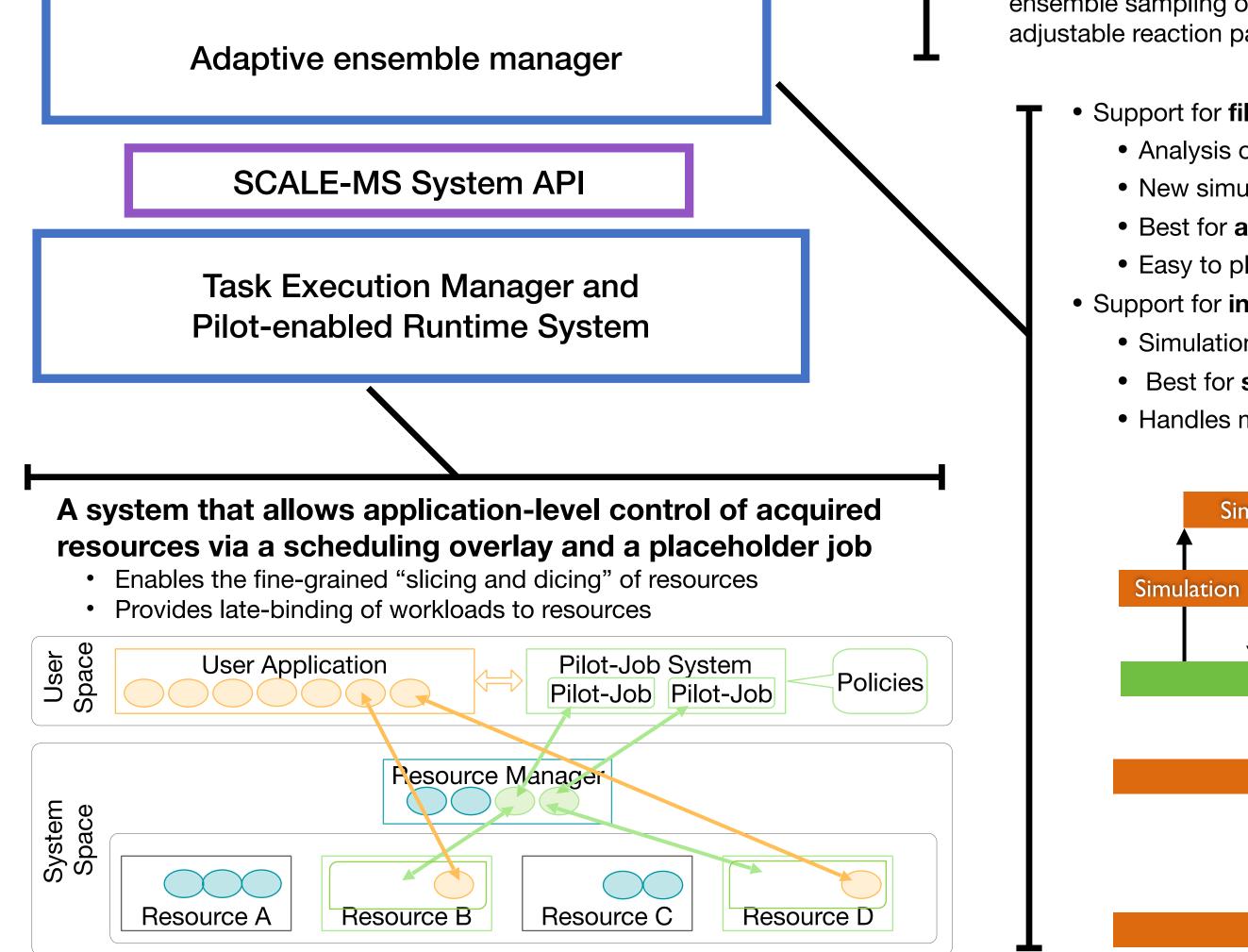
Typical ensemble patterns





Example ensemble algorithms

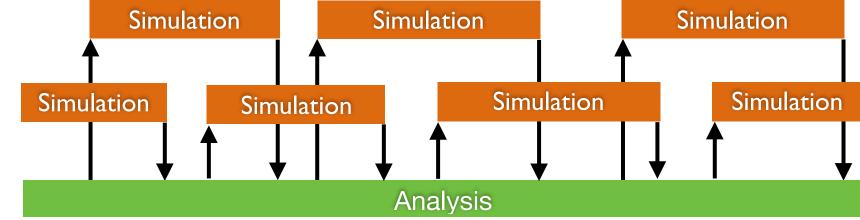
- Umbrella sampling simulations adaptively adjusting biasing potentials
- Communicating sets of replica exchange simulations
- Metadynamics simulations simultaneously exploring large numbers of biasing potentials
- Adaptive Markov State modeling
- Adaptive placement of umbrella biasing potentials
- Forward flux sampling, milestoning, and weighted



ensemble sampling over adjustable reaction paths.

- Support for **file-based** communication between ensemble members
 - Analysis occurs on file outputs
 - New simulations relaunched with adaptive created inputs
 - Best for asynchronous algorithms where data doesn't get 'stale'
 - Easy to plug in new software, adapters require no application changes
 - Support for **in-flight** communication between ensemble members
 - Simulations exchange **limited** data, less need for high performance comms
 - Best for **synchronous** algorithms that need only most recent data
 - Handles more rapid communication, but requires application changes

Asynchronous communication



Synchronous communication

