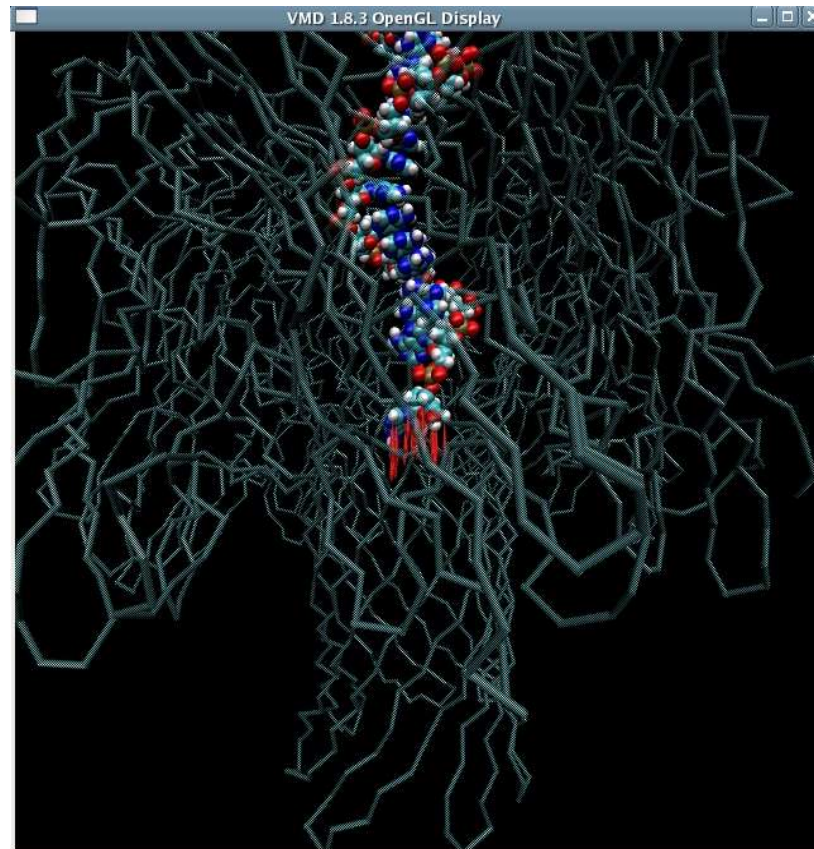
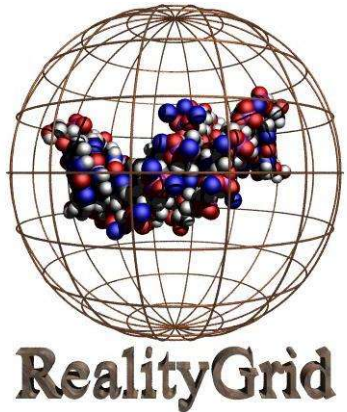


Simulated Pore Interactive Computing Environment: Using grid computing to understand DNA translocation across protein nanopores

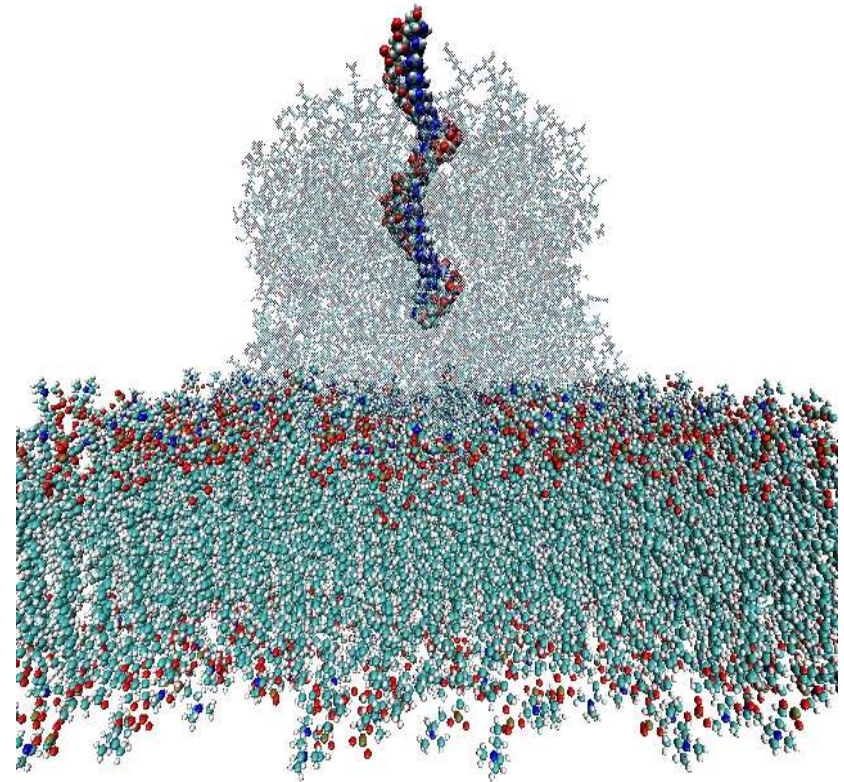


Jha, Harvey, Coveney, Pickles, Pinning, Pezzi & Clarke

Simulated Pore Interactive Computing Environment

- Transport of biomolecules through protein pores not well understood. Semi-flexible polymer in confined geom.
- Fully atomistic simulations crucial to capture pore-protein interaction. Long timescale ($\sim 10^8$ microseconds).
- Size, complexity & timescale make simulations computationally intensive.

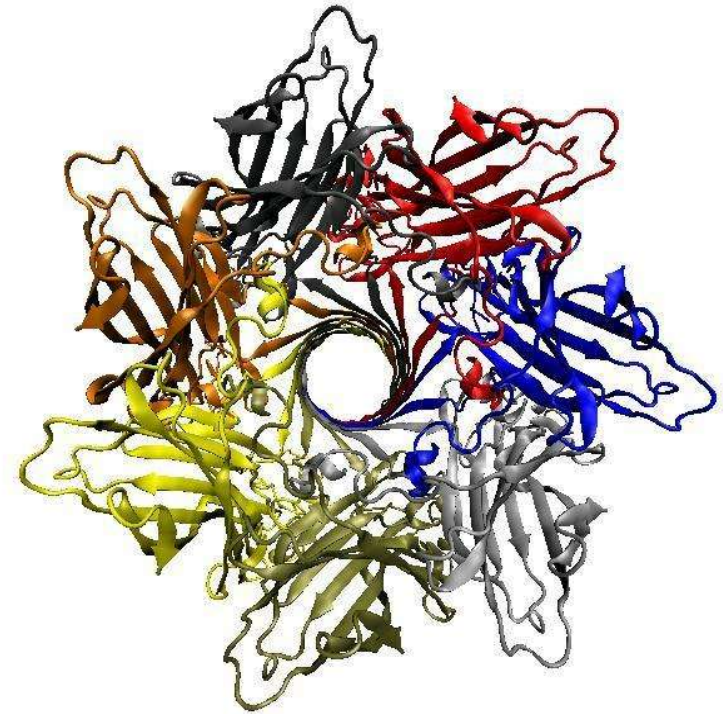
3×10^7 CPU (*tightly-coupled*) hours using “simple” MD. Need to do better...



DNA translocation through an alpha-hemolysin protein pore embedded in a lipid layer. $\sim 275k$ atoms. Water not shown

SPICE: Grid Computing Using Novel Algorithms (1)

- **Novel Algorithm:** Steered Molecular Dynamics (SMD) to “pull DNA through the pore”. Jarzynski's Equation (JE) to compute equilibrium free energy profile from the non-equilibrium pulling.
- Reduce computational cost by 50-100!
- Trivial – in theory, not in practise; Introduces two variable parameters. Determine “optimal” choice of parameters.
- Replace one long sim with multiple (~100) short(er) sims



A view into the pore from the top end. Note the seven fold symmetry of the system.

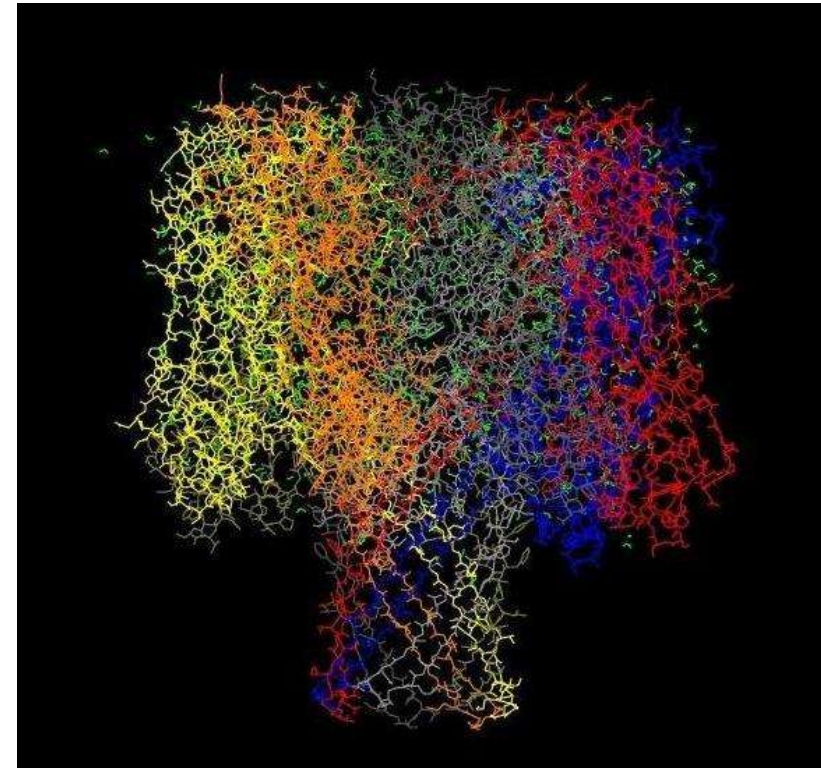
SPICE: Grid Computing Using Novel Algorithms (2)

- Distribute multiple large-scale sims
Coupling delocalized sim and viz resources

“Live coupling”: Interactive simulations
-- use viz to steer sim.

Not just parameters...

- Grid facilitates greater resource utilization, novel analysis & uniform interface making ~100 simulations more manageable



Transform comp intractable problem using SMD+JE
Not just exploits grid infrastructure, but requires it...

SPICE: Computing the Free Energy Profile (FEP)

Step I: Understand structural features using static visualization

Step II: Interactive simulations for dynamic and energetic features

- Steered simulations: bidirectional communication.

Qualitative + Quantitative (SMD+JE)

- Haptic interaction: Use haptic to feel feedback forces

Step III: Simulations to compute “optimal” parameters values

75 simulations on 128/256 processors each.

Step IV: Use computed “optimal” values to calculate full FEP along the cylindrical axis of the pore.

Requires ~250,000 CPU hours (100 simulations of 2500 CPU hours)!

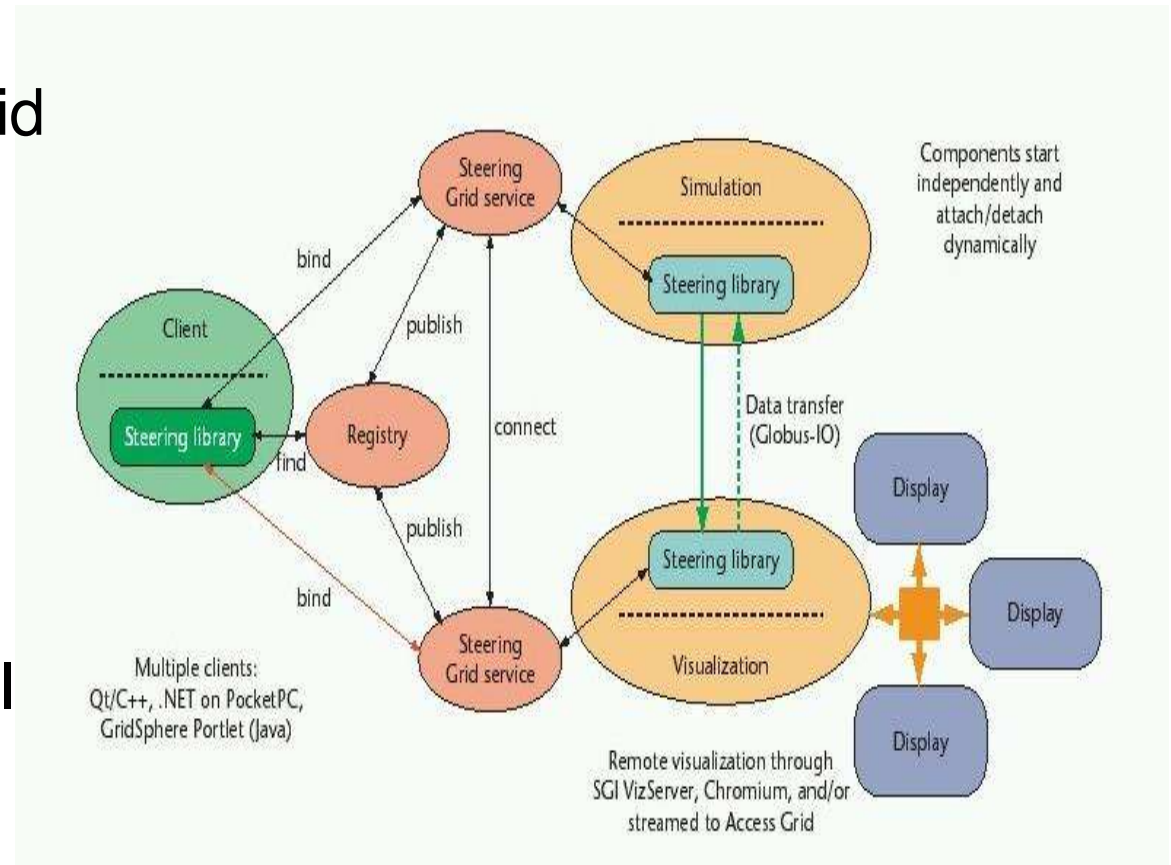
SPICE: Grid Infrastructure (1)

RealityGrid Steering Infrastructure + NAMD (parallel MD engine)

App interfaces grid infrastructure through the ReG steering library

ReG Steering API:

- launcher, steerer use server side API
- App uses client side API



(WSRF::Lite based infrastructure for launching, steering, comm and notification soon)

SPICE: Grid Infrastructure (2)

Simulation: (II, III, IV)

NGS + TeraGrid

Visualization: (I,II)

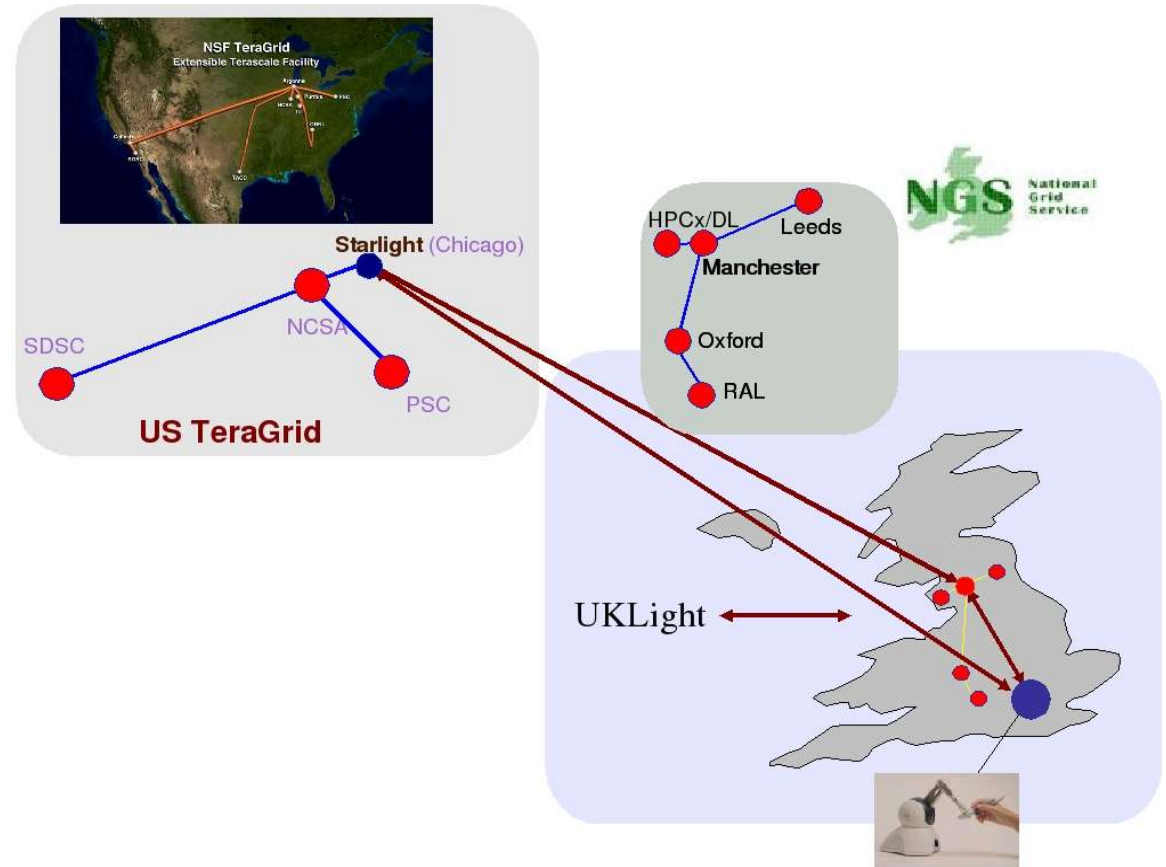
Prism (UCL)

Sim-Viz connection:

UKLight/GLIF

Batch simulations post optimal parameter. *Not batch sim to explore phase space*

Resources more *R-U-M* since TeraGrid...
Middleware better? Or our trouble-shooting?



SPICE -- UKLight

+ Interactive simulations

Qualitative (general) + Quantitative (specific)

Require 128/256px of HPC to compute fast enough for interactivity

Steady-state data stream (up & down) -- few MB/sec

Simple? “Unreliable” sim-vis commn simulation slowdown.?

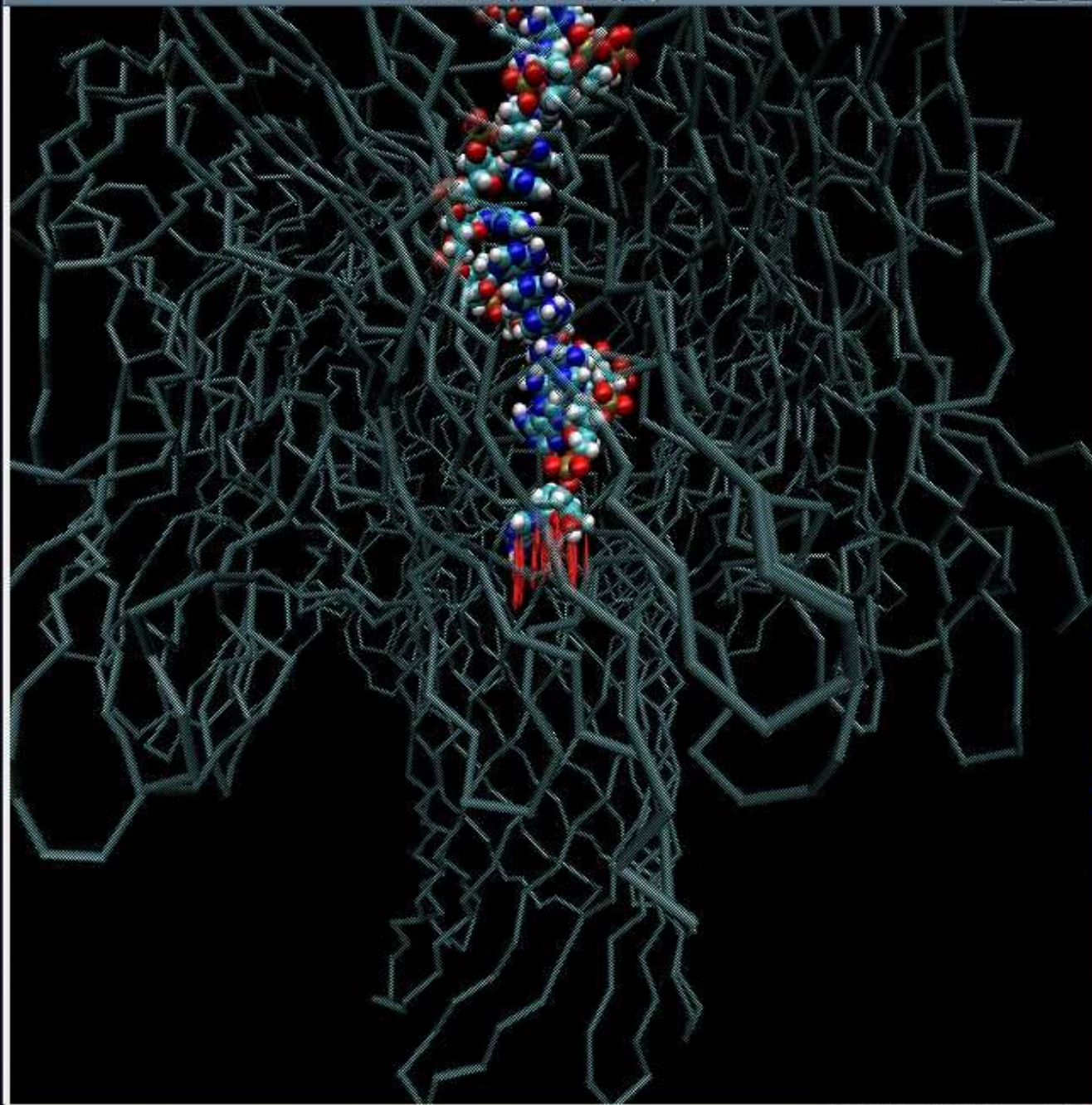
Interactive simulations perform better when using UKLight for communication between simulation and visualization!

Advanced networks provide high QoS in terms of *packet loss, jitter and latency*.

e.g ~20 vs 5 intermediate routers en route to NCSA from UCL-Prism

+ Total data generated in TeraBytes; replicated

VMD 1.8.3 OpenGL Display



IMD Connection

Hostname

Port

Connect

Detach Sim

Stop Sim

Timestep transfer rate

Timestep keep rate

timesteps: 639

temp: 146.202011

energy: -3265436.000000

bond: 4399.485352

angle: 21248.544922

dihedral: 13827.855469

improper: 185.625961

vdw: 0.000000

elec: -3380552.250000

Graphical Representations

Selected Molecule

dna20_hmlysin2.psf

Create Rep

Delete Rep

Style

Color

Selection

PK Name segname DNA

Trace Name protein

Selected Atoms

protein

Draw style

Selections

Trajectory

Periodic

Coloring Method

Material

Name

Transparent

Drawing Method

Trace

Default

[Termi...

vmd c...

VMD ...

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VMD ...

IMD C...

http://...

[The G...

Layers...

Graphi...

Thoughts...

- Getting infrastructure to work needs to be made easier (e.g. dual homing of systems -- administrative nightmare)
- Develop better theoretical underpinnings:
Experiments to understand effect of network (latency, jitter) & RTT with simulation configuration (px's, IMD frequency)
- Testing protocols for low latency?
- User interaction with CPS? (e.g. dynamic app driven reservation of lightpaths)
Co-scheduling with other resources? Via ReG API?
GLIF - Global Plane & Grid Integration Middleware WG

SPICE @ AHM05

- Tue 13:00 - 14:00 UCL
- Wed 09:00 - 13:00 EPSRC
- Wed 14:30 - 15:00 ESNW
- Thu 12:00 - 15:00 EPSRC

SPICE a finalist at the SC05 HPC Analytics Challenge
(also at SC Global and numerous booths at SC05)

<http://www.realitygrid.org/SPICE>