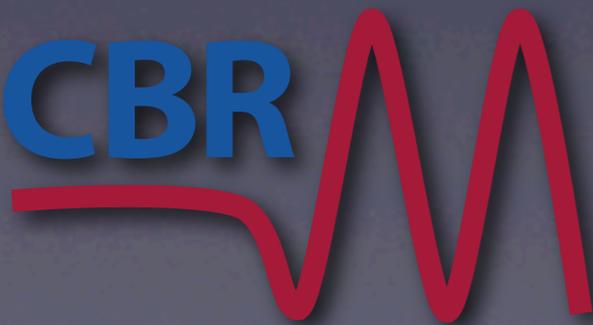


Divide-and-Conquer Molecular Simulation: GROMACS, OpenMM & CUDA

ISC 2010-05-31

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CBR



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**Center for Biomembrane Research
Stockholm University**





These will soon be small computers

~2024: 1B 'cores'

2022: ~300M cores

2020: ~100M cores

2018: ~30M cores

2016: ~10M cores

2014: ~3M cores

2012: ~1M cores

2010: ~300,000 cores

How will YOU use a billion cores?

We're all doing Embarrassing Parallelism

But not the way you think.

We're investing huge efforts in parallelizing algorithms that only reach 50-75% scaling efficiency on large problems

Not a chance they will scale to 1B cores

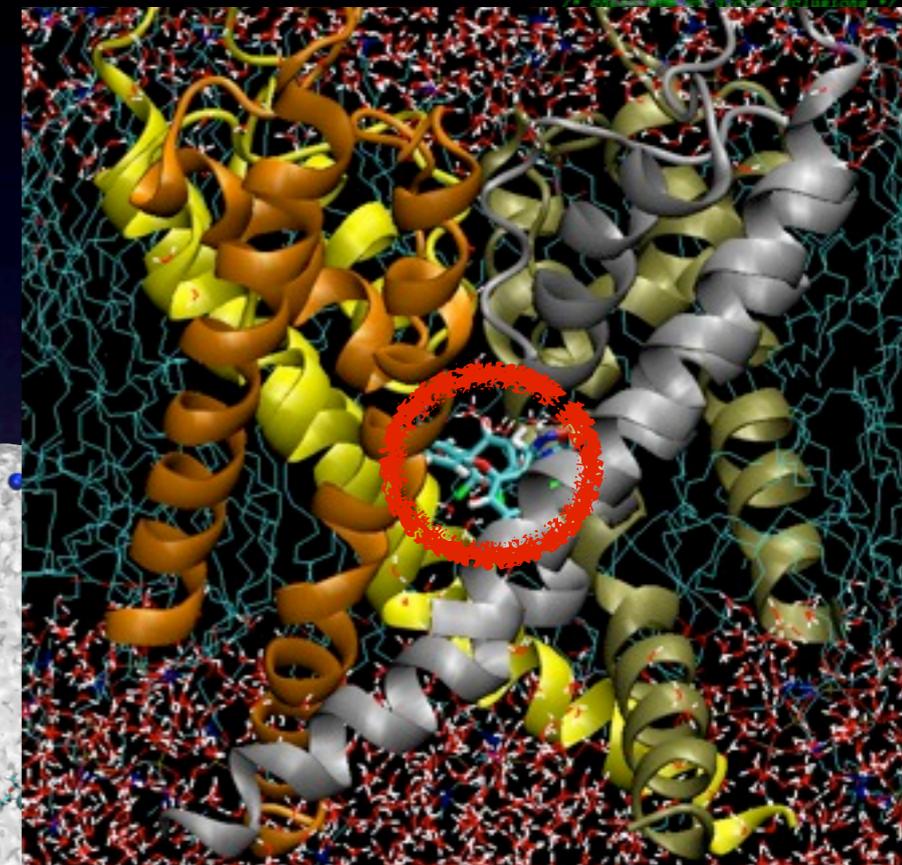
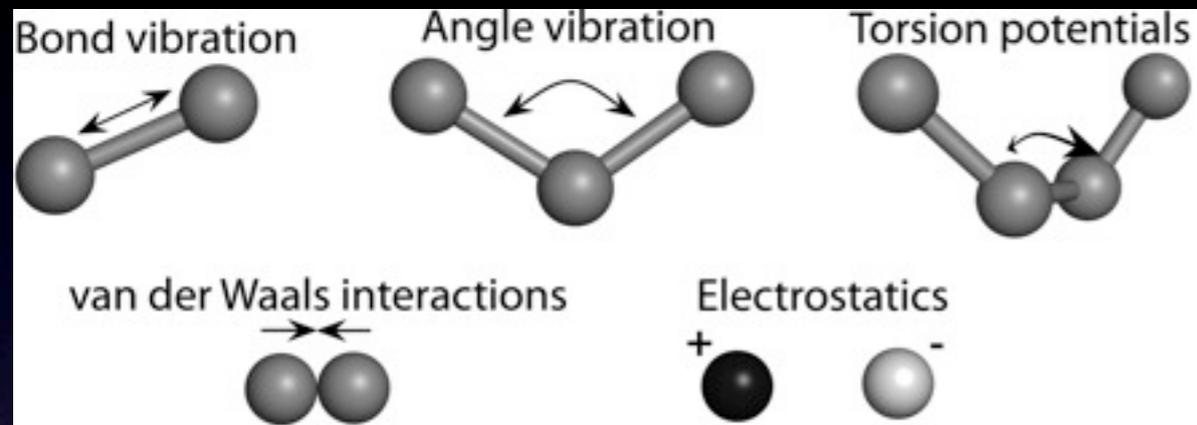
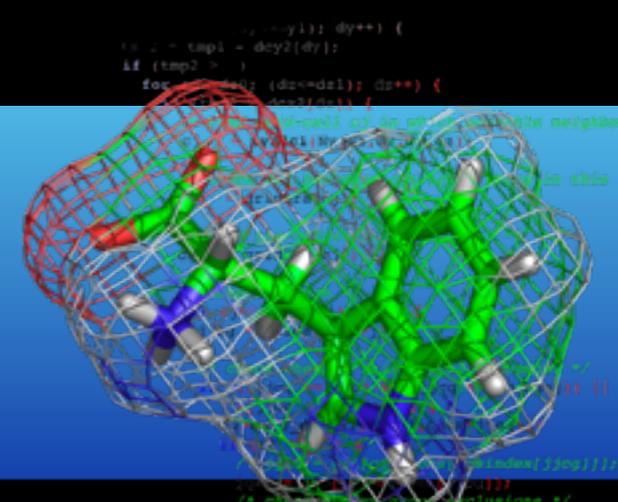
Close-to-useless for smaller problems of commercial interest

100% focus on programs, forget the problem we're solving

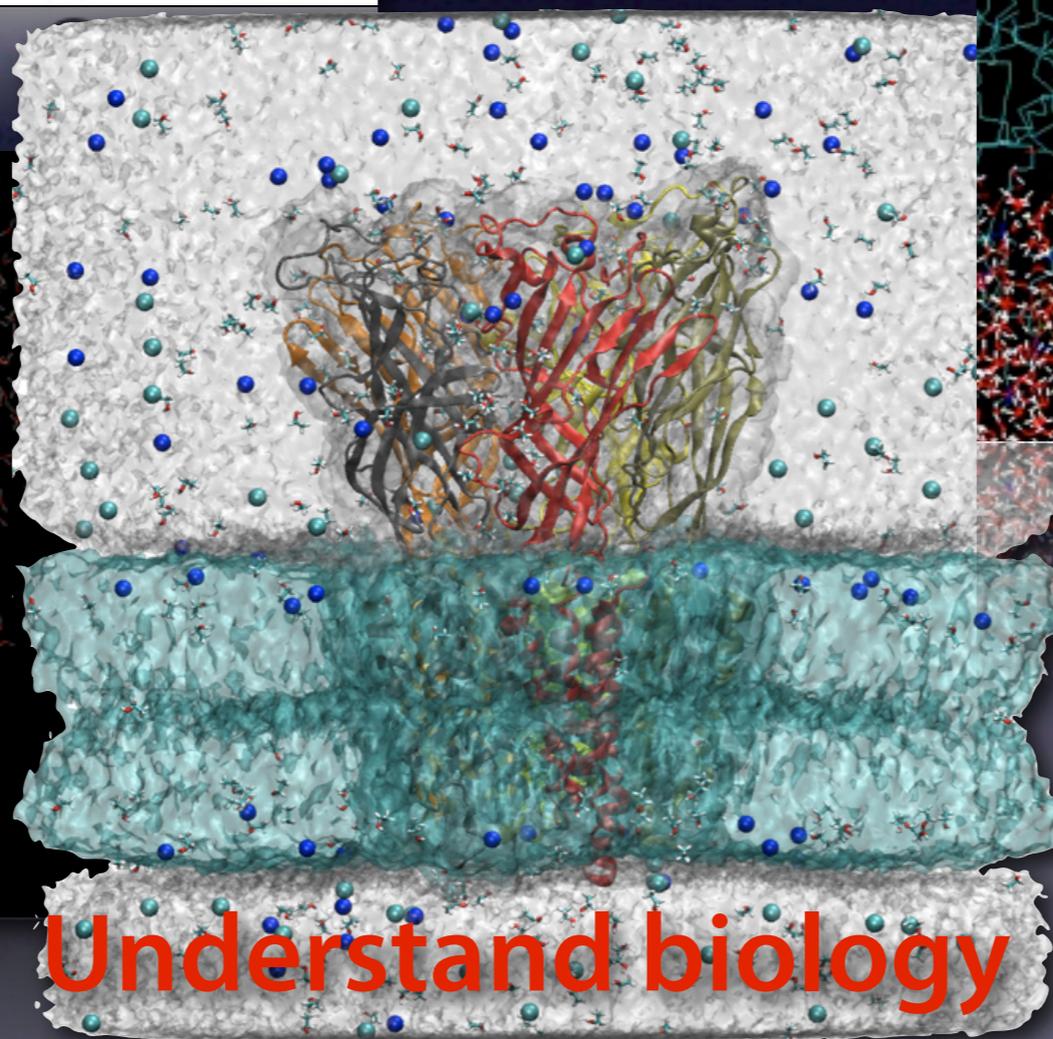
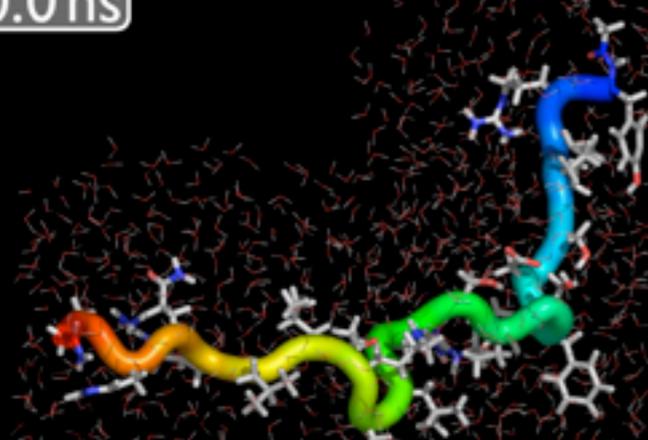
Ask taxpayers to foot the bill

Pretty much the definition of 'embarrassing'?

Molecular Dynamics



0.0 ns



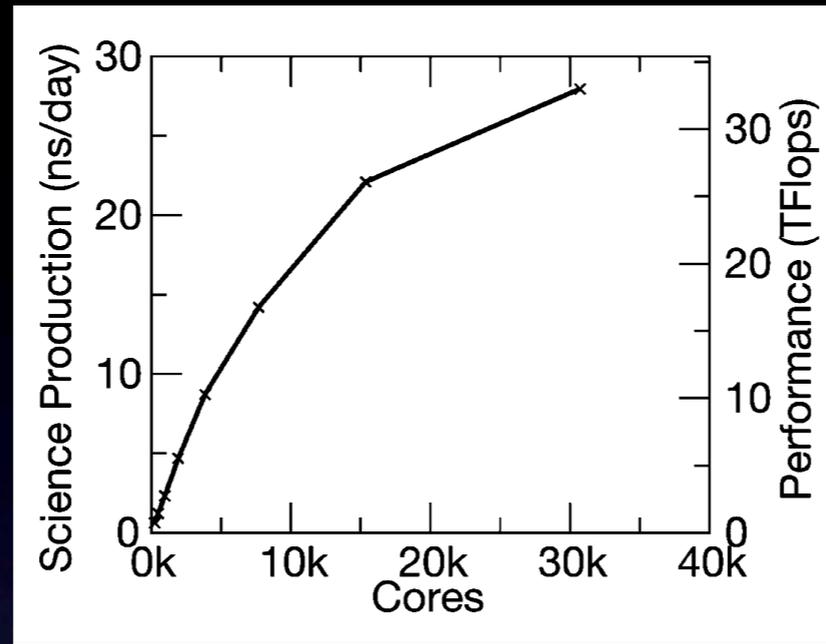
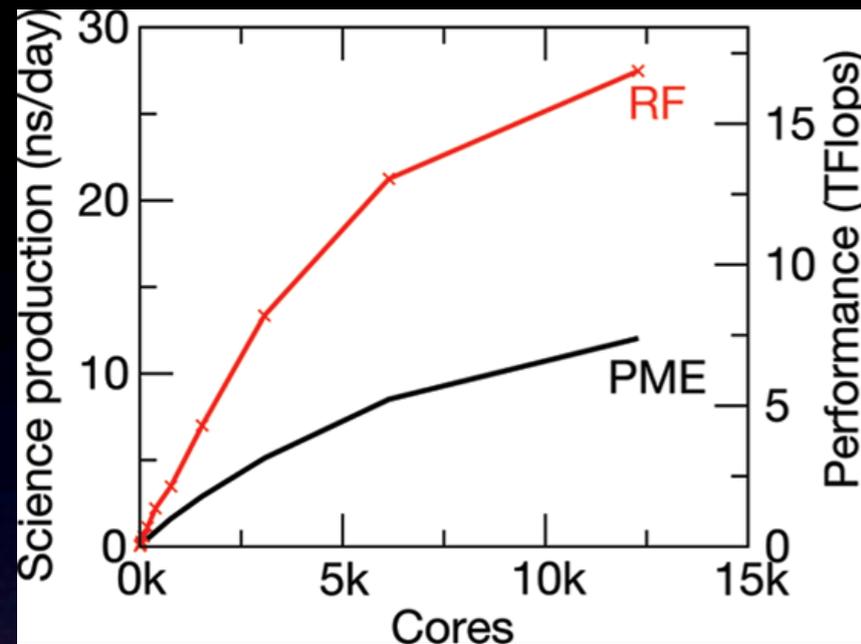
Free Energy &
Drug Design

Protein Folding

Understand biology

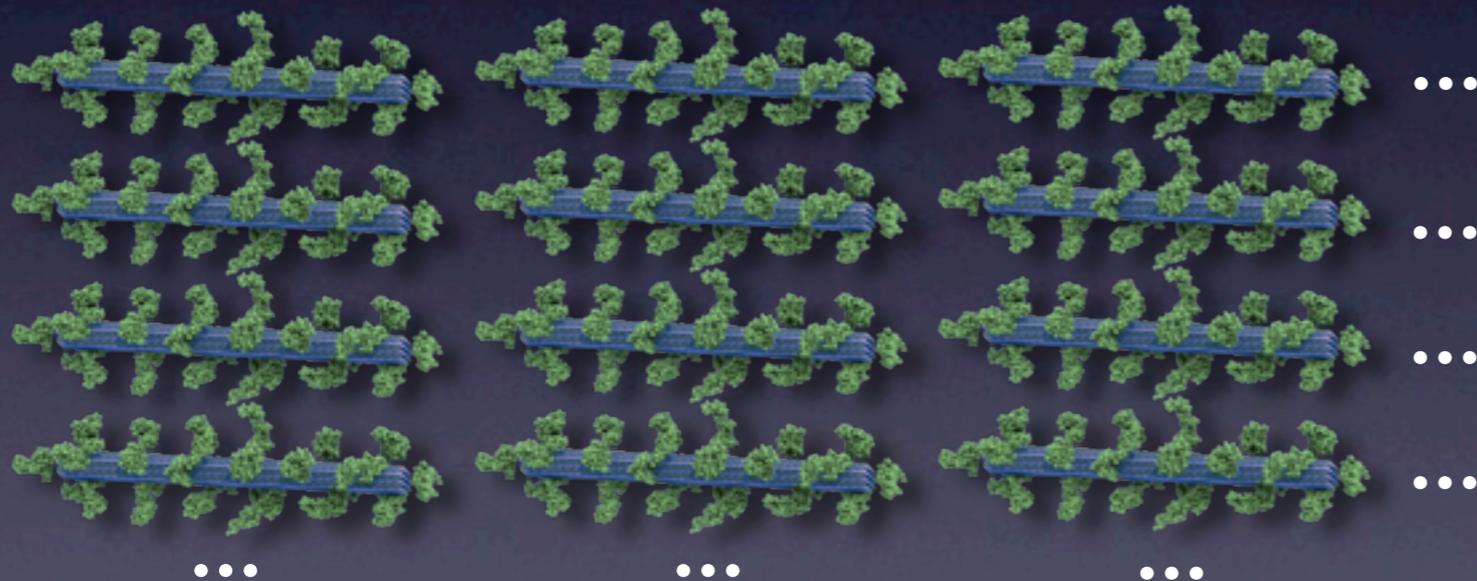
GROMACS
www.gromacs.org

Scaling as an Obsession?

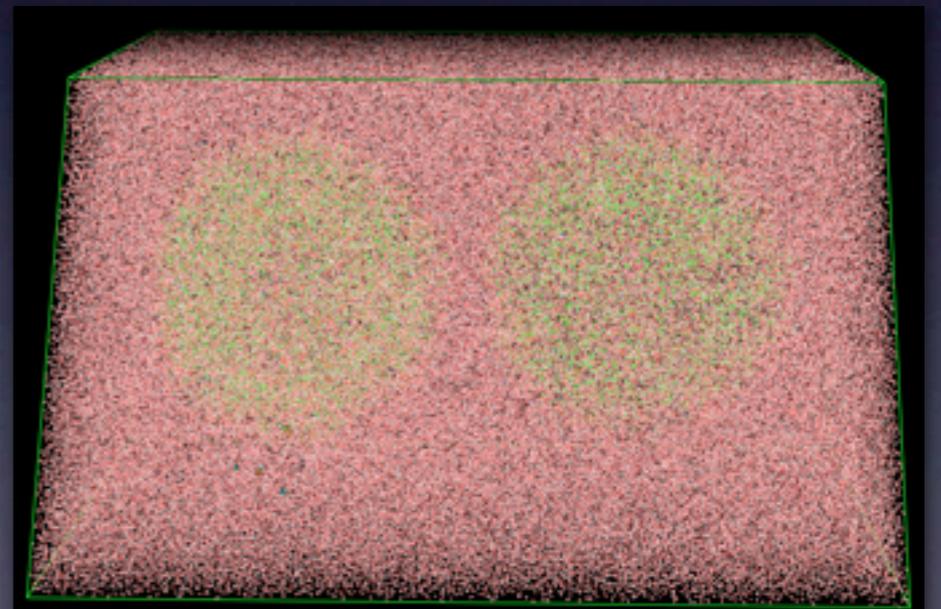


Gromacs has scaled to 150k cores on Jaguar @ ORNL

Only gigantic systems scale - limited number of applications



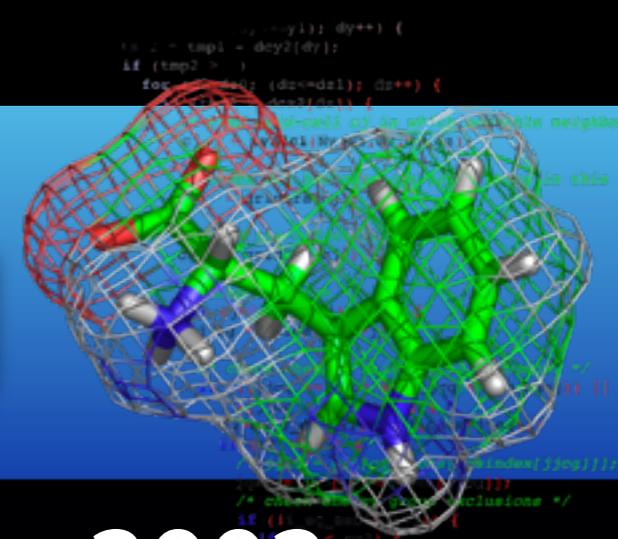
1M-100M atoms



But: Small systems won't scale to large numbers of cores!

How shall we break this impasse?

Stream computing

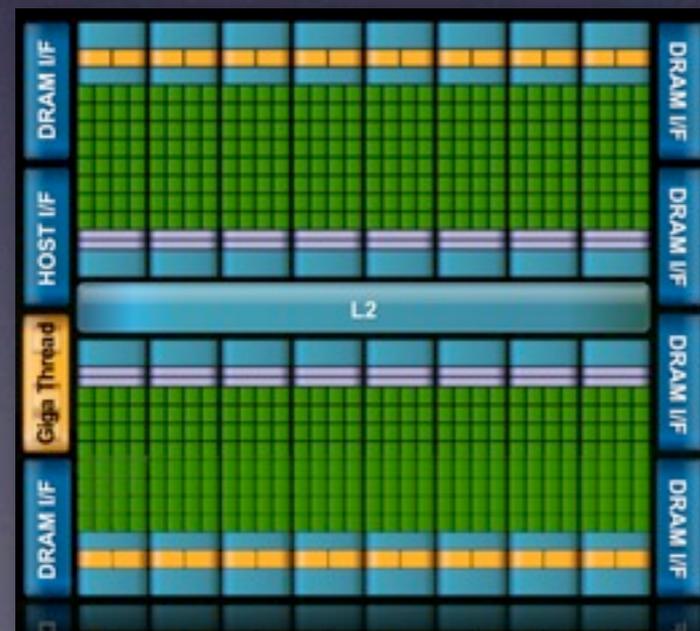


First Gromacs GPU project in 2002
with Ian Buck & Pat Hanrahan, Stanford

*Promise of theoretical high FP
performance on GeForce4*

Severe limitations in practice...

More general than mere hardware acceleration!



Fermi: 448 cores
TFLOP-desktops!

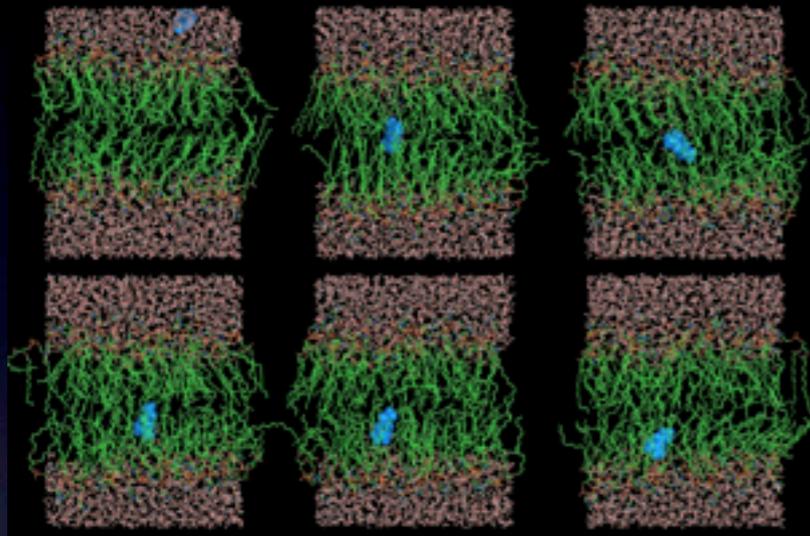
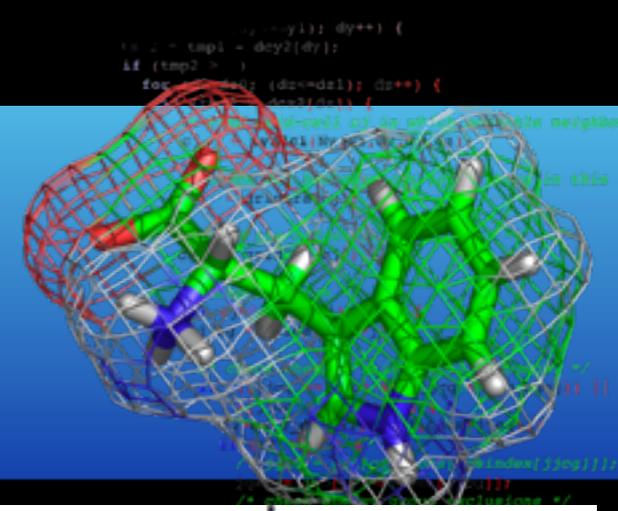
**Think in
Parallel
Problems!**



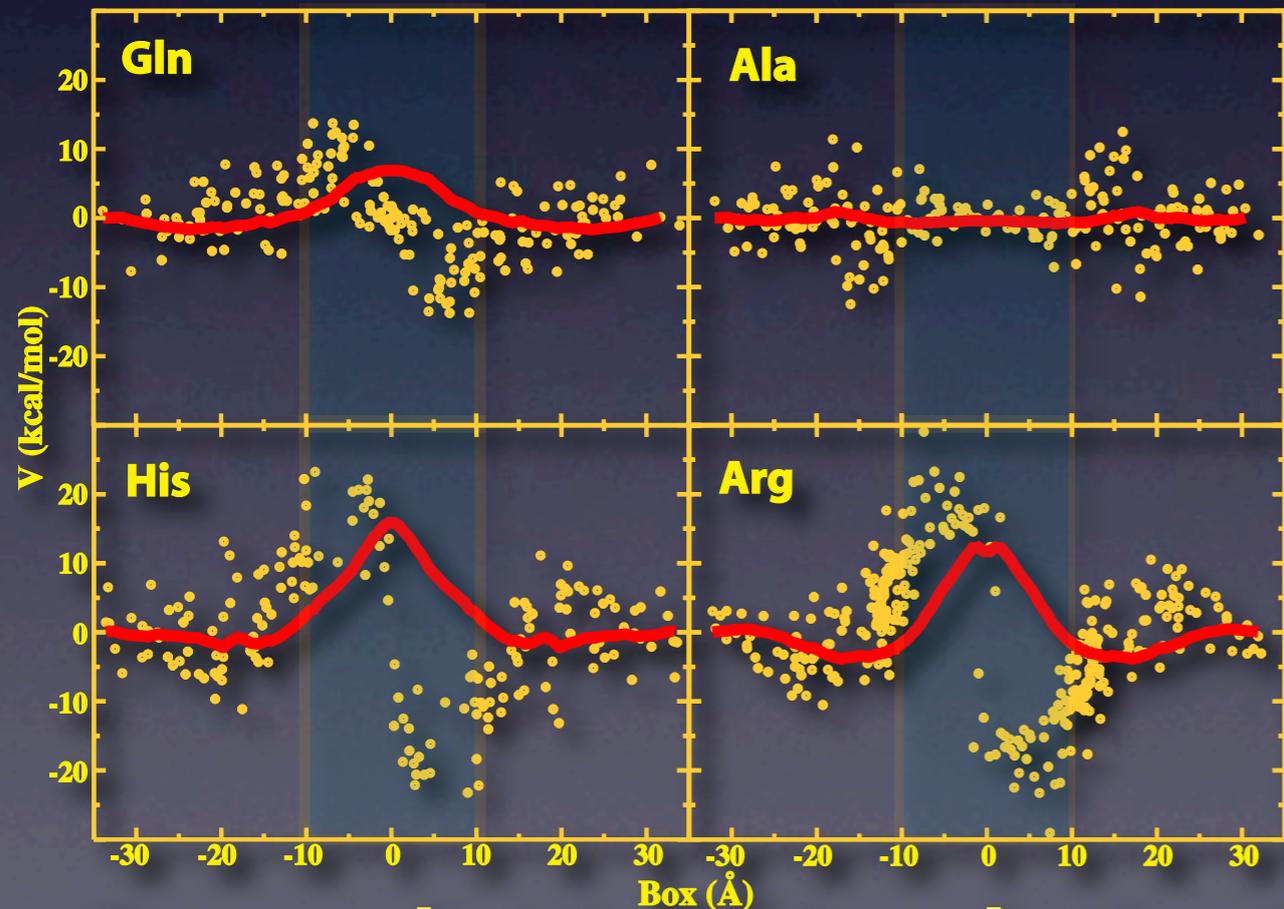
ScalaLife

Life Science on next-gen hardware

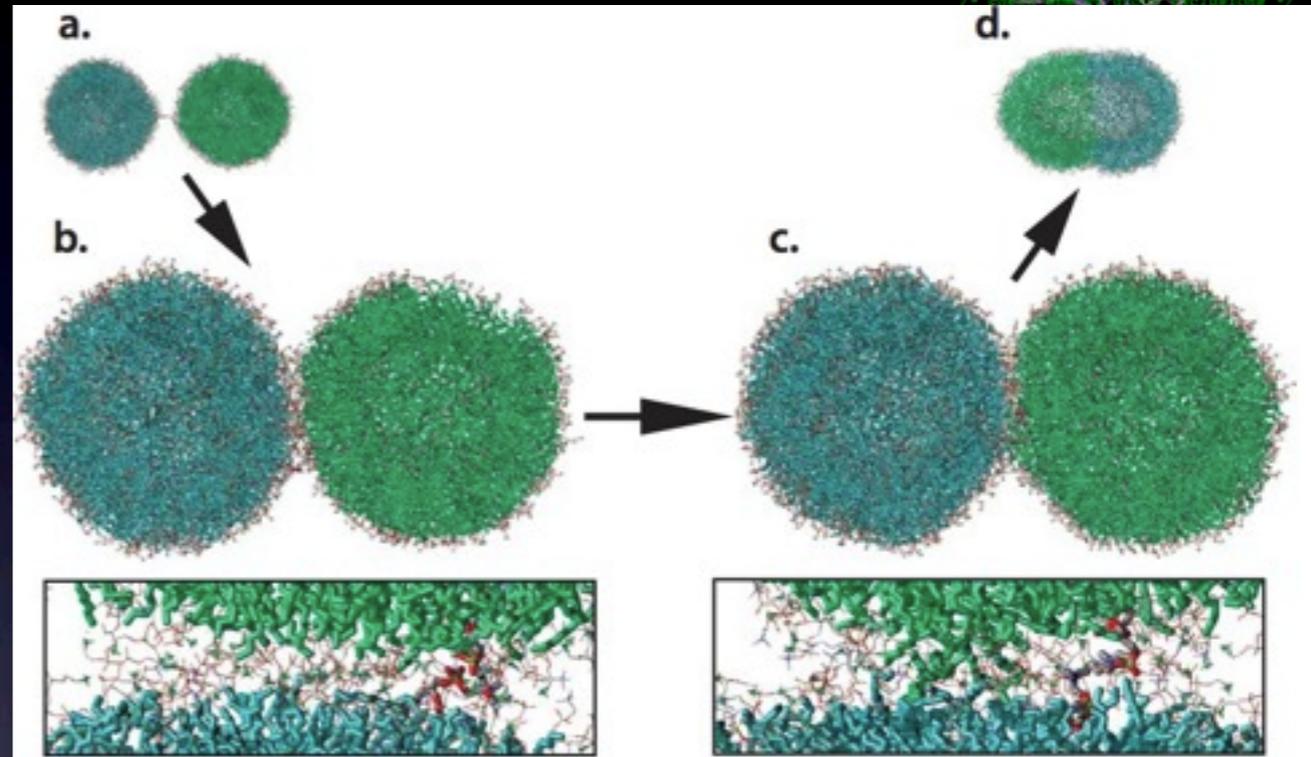
Ensemble Simulation



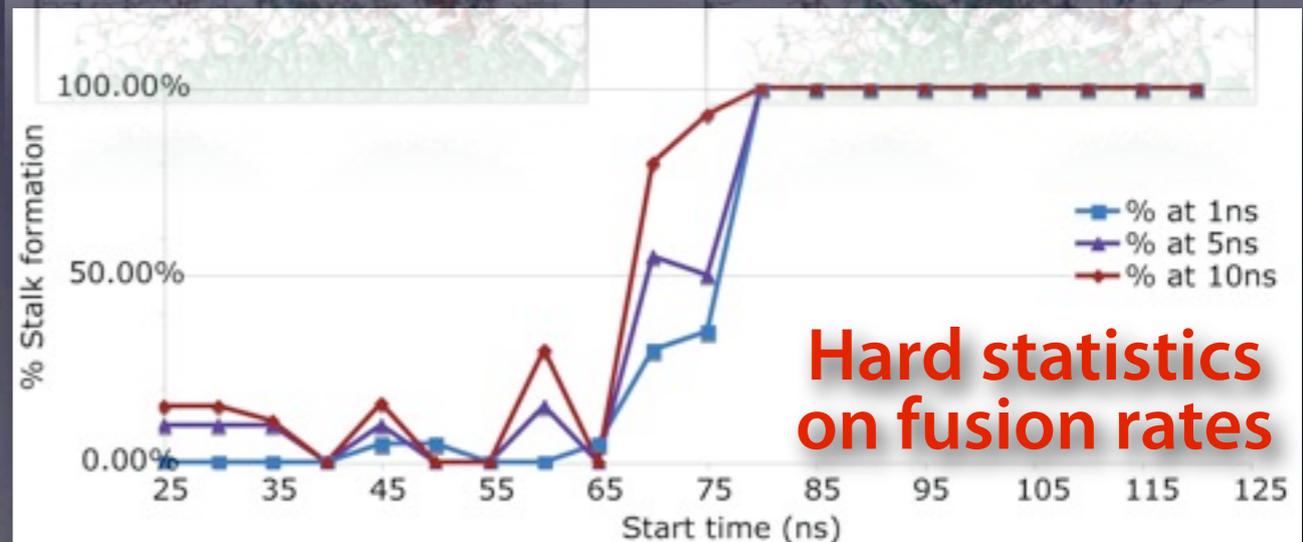
Membrane
Protein
Insertion
Free Energy



Every dot is a simulation!



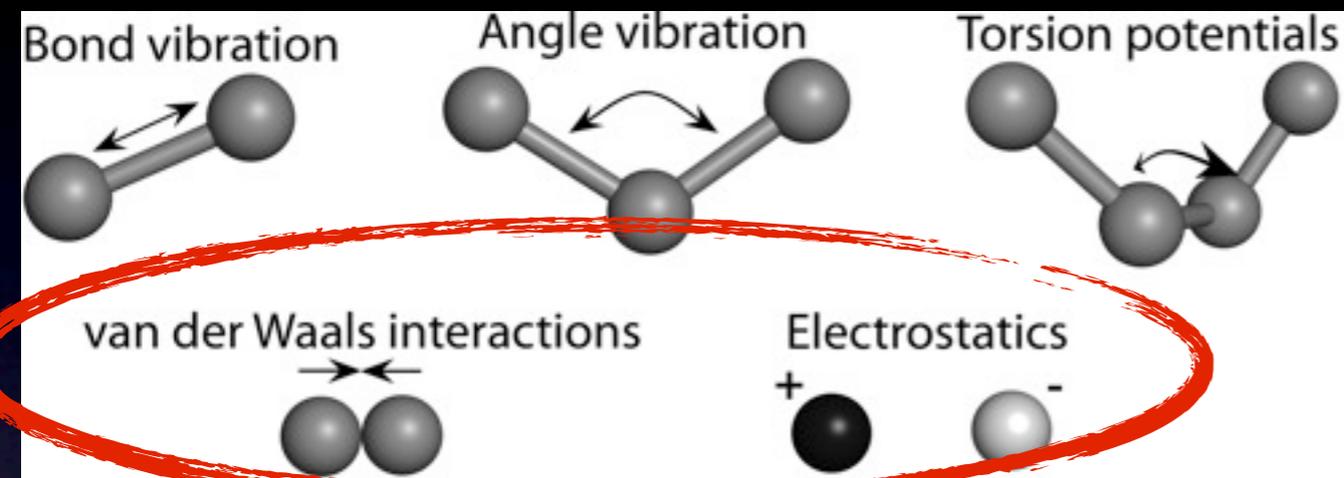
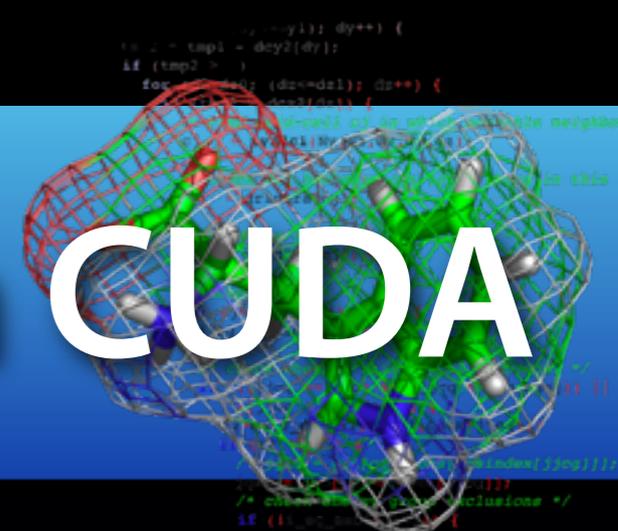
4,000 20-ns simulations



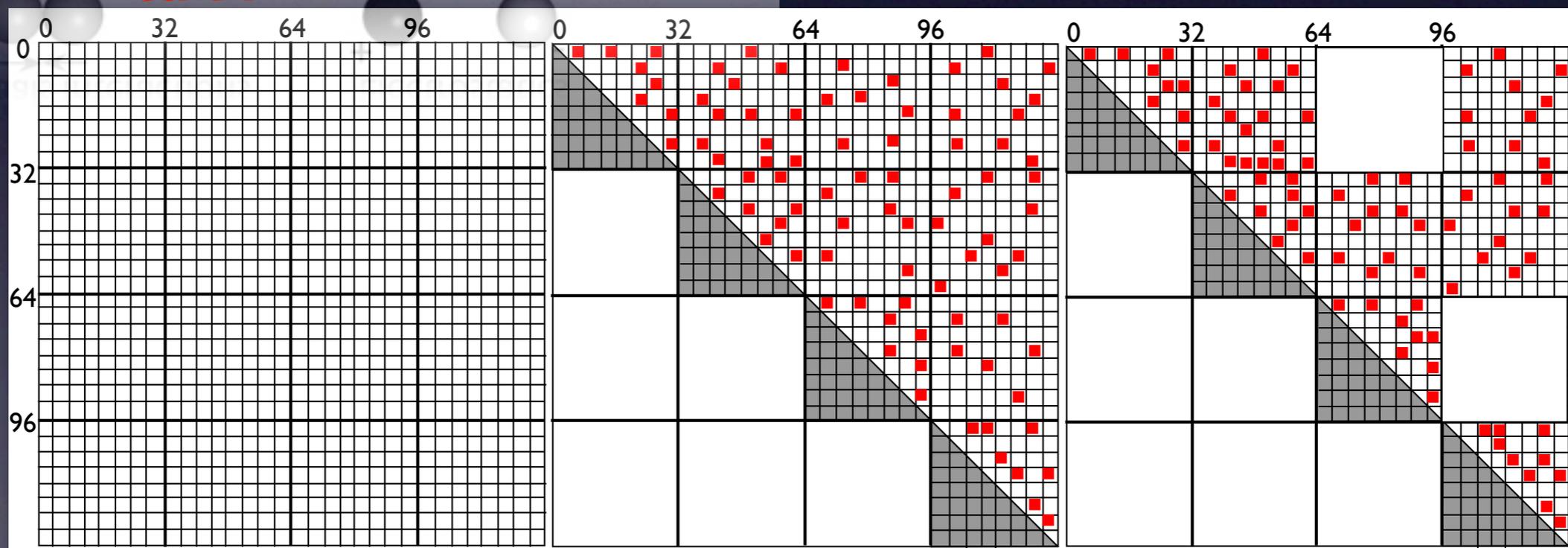
Hard statistics
on fusion rates

Anna Johansson, Peter Kasson

Molecular Dynamics with CUDA



*Absolute performance critical,
not speedup relative to a
reference implementation!*



All-vs-all (CUDA book)

$$N^2$$

Newton's 3rd law

$$(N^2)/2$$

Sort atoms in tiles

$$N \log N$$

MD Performance in CUDA

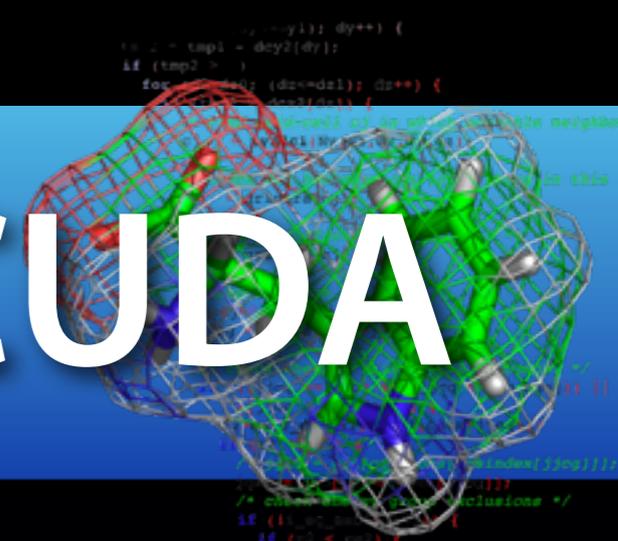
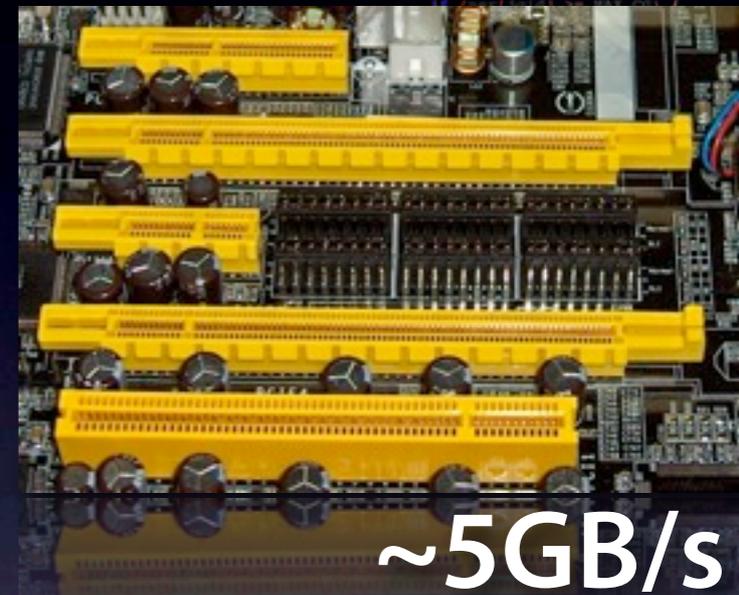
Not sufficient to accelerate nonbonded interactions - need to send to/from GPU

Prefer to do entire simulation on GPU

Don't rewrite 2M lines-of-code in a separate CUDA-Gromacs...

OpenMM: Core MD functionality in separate library
Stanford, Stockholm, Nvidia & AMD

Fully public API, hardware-agnostic, use anywhere



Gromacs & OpenMM in practice

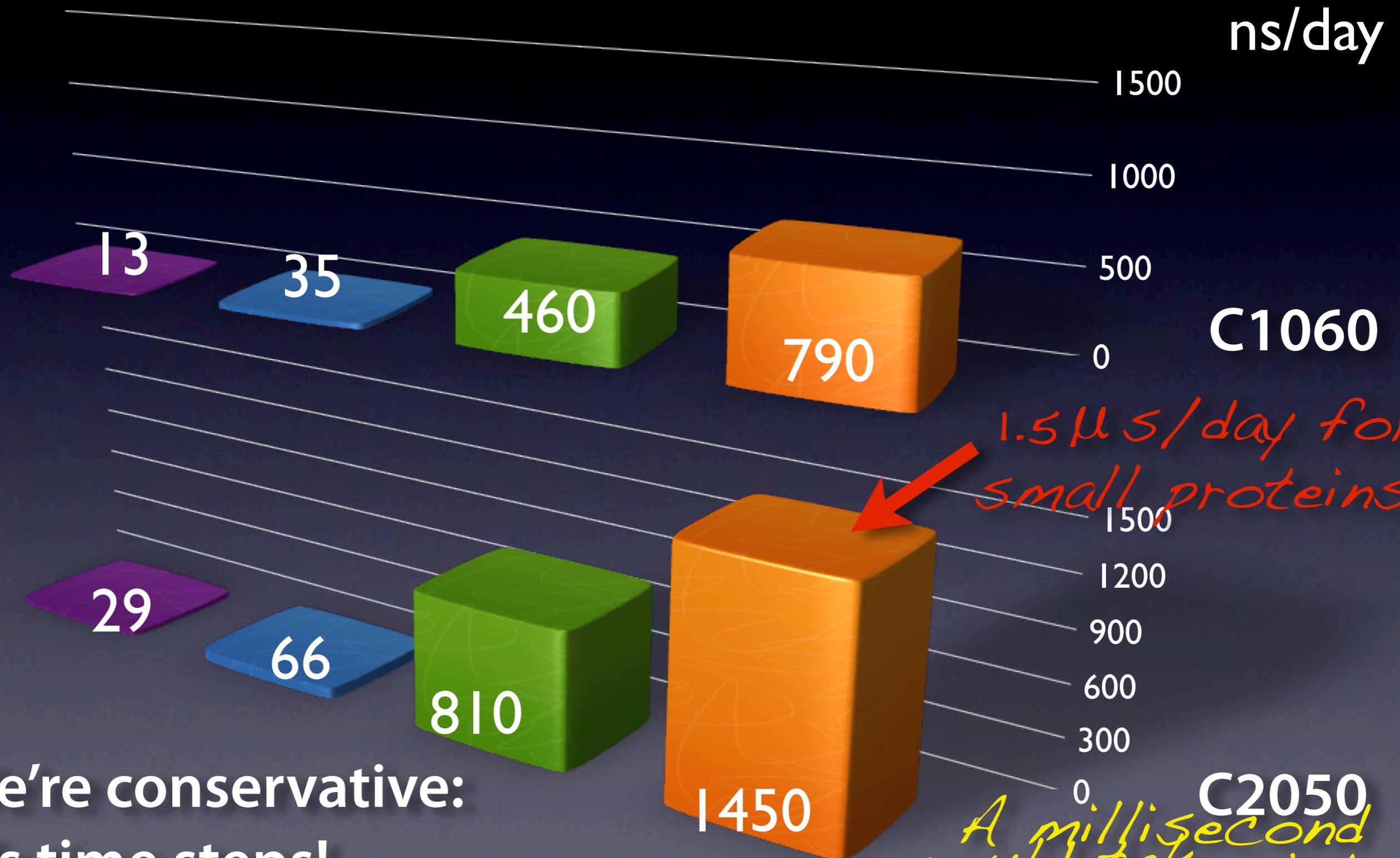


- GPUs supported in Gromacs 4.5
mdrun ... **-device "OpenMM:CuDa"**
- Same input files, same output files: "It just works"
- Subset of features work on GPUs for now (checked)
- No shortcuts taken on the GPU:
 - At least same accuracy as on the CPU ($<1e-6$)
 - Potential energies calculated, free energy works
- Prerelease availability: **NOW!** www.gromacs.org/gpu

Fermi (C20) performance over C10

BPTI (~21k atoms)

Villin (600 atoms, implicit)



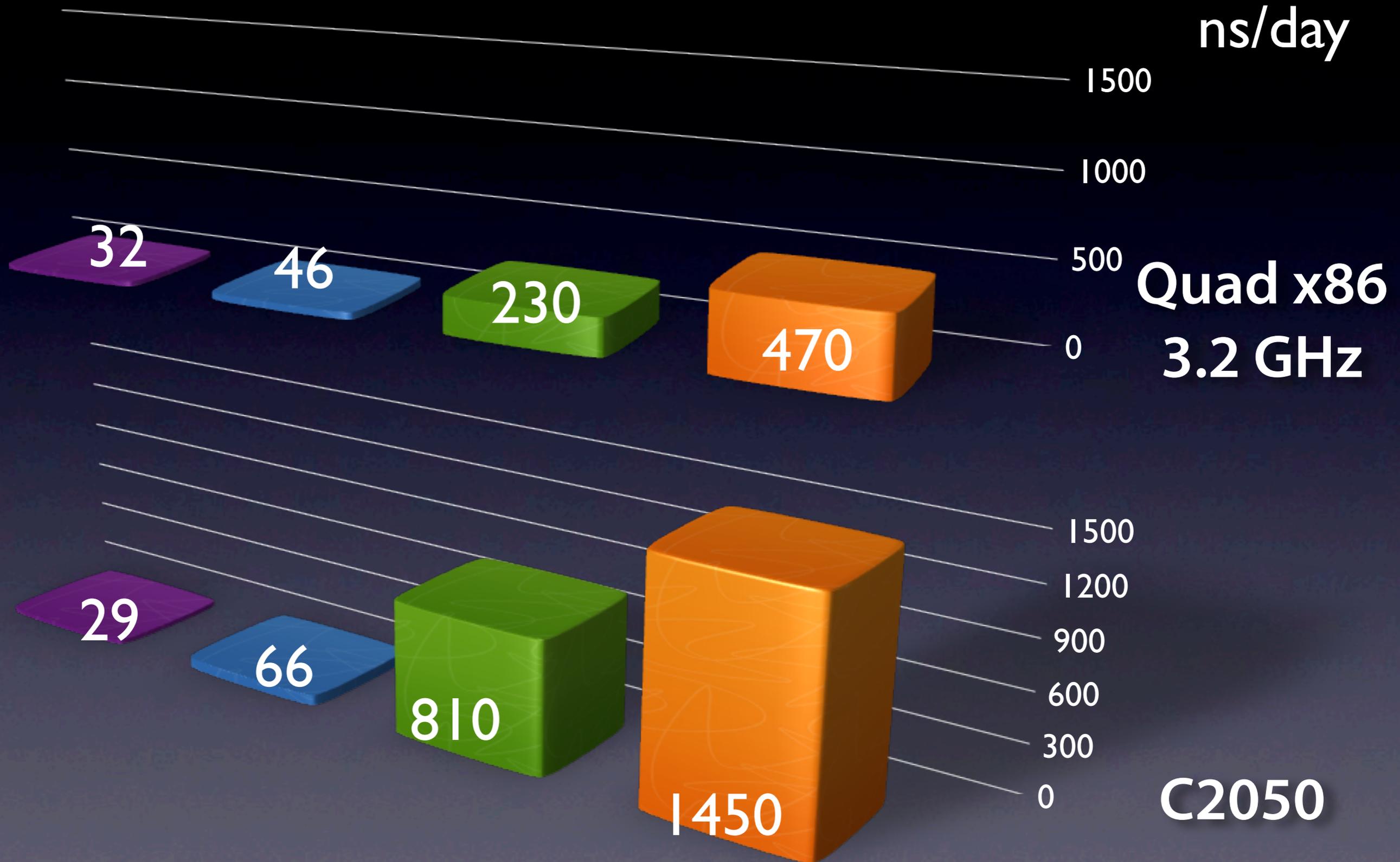
1.5 μs/day for small proteins!

A millisecond would take ~1 year

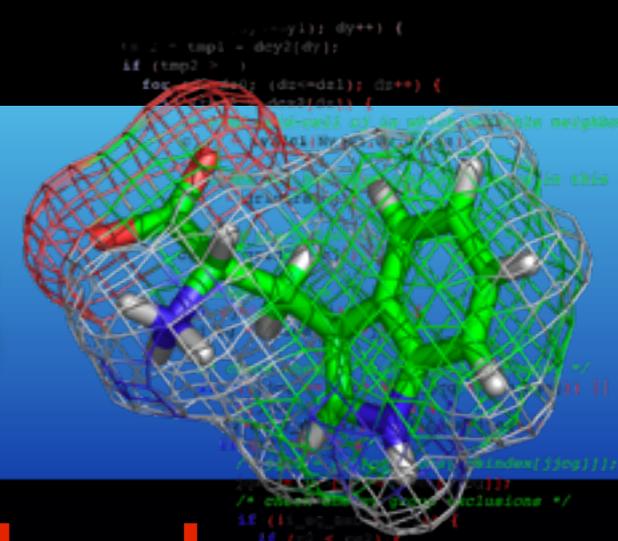
**We're conservative:
2fs time steps!**

GPU performance over x86 CPU

- PME
- Reaction-field
- Implicit
- All-vs-all



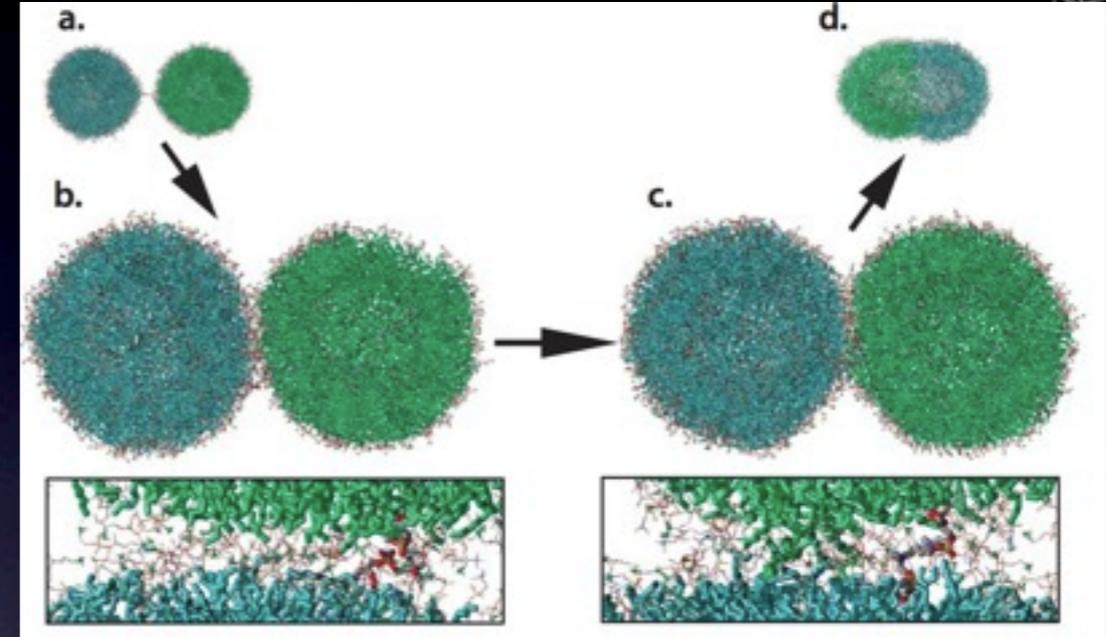
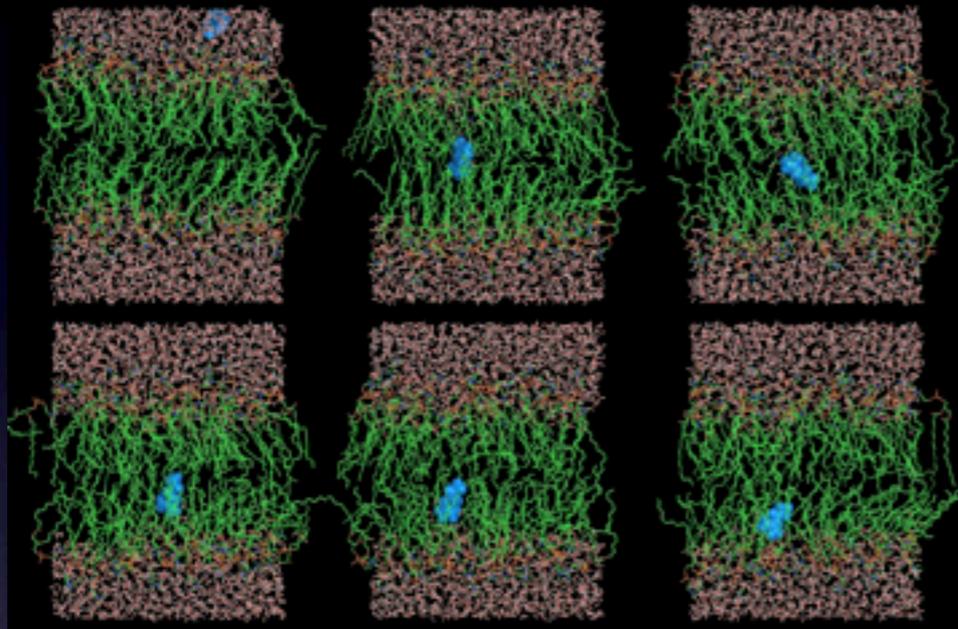
Caveats/Limitations



- **Beware of Memory Errors: happens on all hardware**
- Gromacs runs tests to check for GPU memory errors
 - Low-end consumer cards can sometimes be bad
 - Even fine cards can exhibit random errors
 - For production scientific work we strongly recommend Fermi Tesla C20 cards
 - Why? ECC memory! (C2050/C2070)

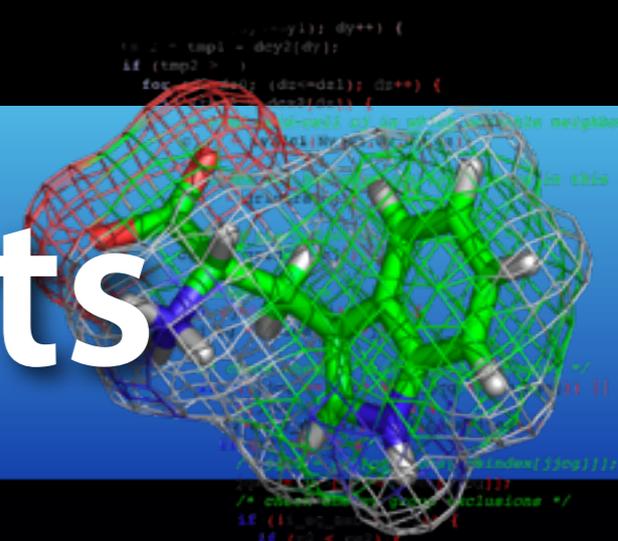


Think Massively Parallel - Scale the Problem, not Runs



- Stream Computing is the future
- Everything is *statistical* mechanics!
- No algorithm will parallelize 5000 degrees of freedom over 1 billion processors
- Parallelize in the problem domain instead
- CUDA provides amazing performance on each node

Acknowledgments



- **GROMACS:** Berk Hess, David van der Spoel, Per Larsson
- **OpenMM:** Rossen Apostolov, Szilard Pall, Peter Eastman, Vijay Pande
- **Nvidia:** Scott LeGrand, Duncan Poole, Andrew Walsh, Chris Butler
- **Ensemble Simulations:** Peter Kasson



NVIDIA

AMD

