UMASS MEDICAL SCHOOL
IT INFORMATION TECHNOLOGY

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RESEARCH COMPUTING

Scientific Computing

Research Computing

Scientific Computing

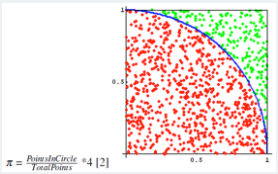
Scientific computing runs the Massachusetts Green High Performance Computing Cluster for all five UMass campuses. Researchers can utilize it to run custom and open software to analyze, distribute, and calculate large data sets, decreasing their calculation run times several fold. Additionally Scientific Computing provides support for researchers employing high performance computing in basic and clinical computational research outside the MGHPCC.

WHAT IS HPC?

- HPC is used to solve problems in:
- Medical Physics
- Protein Structure
- Molecular Dynamics
- Comparative Genomics
- Computational Biology
- Next Gen Sequencing data analysis

EXAMPLE JOBS USING MONTE CARLO SIMULATION:

Simple example of estimating p where we randomly select the number of points in a set A that lies inside box R (1/4 of a circle in our case).



JOB SCHEDULING

- We utilize LSF for the scheduling and the setting of Job priority
- LSF provides a common interface for submit ting, maintaining, and organizing HPC related jobs
- LSF provides management and scheduling for user jobs across the following resources: Processors, Memory, Storage

SOFTWARE AVAILABLE

- Bowtie, Cufflinks, TopHat
- BWA, BLAT, BFast
- DeepSeq related software for Illumina and PacBio
- SamTools, MACS
- RNA tools such as: RNAfold, ViennaRNA
- And many more...

Bringing Technology & Innovative Solutions to Labs

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