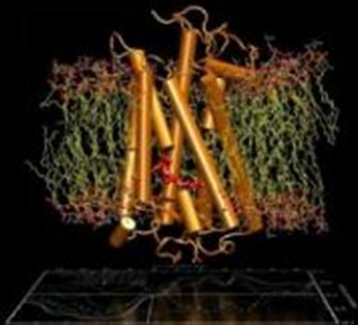


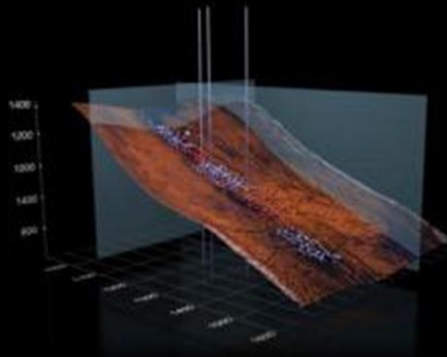
# Introduction to GPU Computing



# Computing is Integral to Science



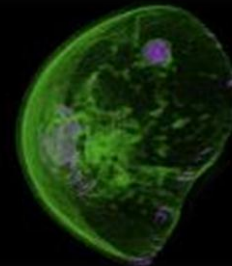
**Drug Design**  
Molecular Dynamics



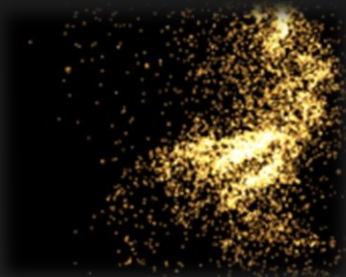
**Seismic Imaging**  
Reverse Time Migration



**Automotive Design**  
Computational Fluid Dynamics



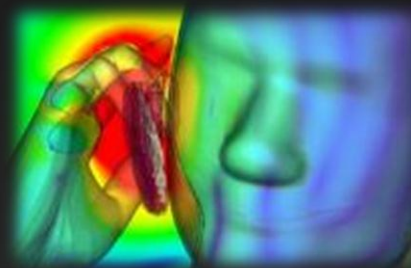
**Medical Imaging**  
Computed Tomography



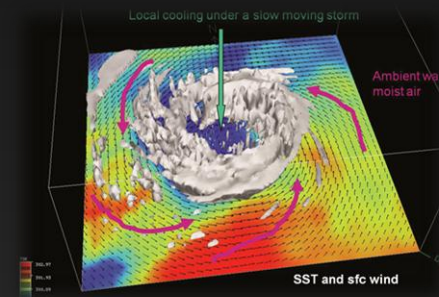
**Astrophysics**  
n-body



**Options Pricing**  
Monte Carlo



**Product Development**  
Finite Difference Time Domain



**Weather Forecasting**  
Atmospheric Physics



# GPUs Accelerate Computing

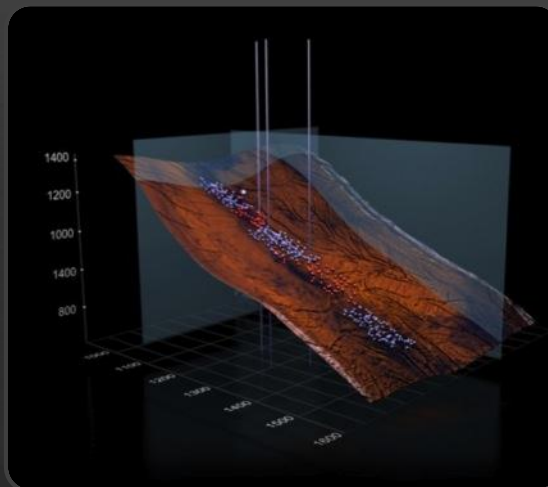
## Understand Risk Faster than Competition

Calculate risk in minutes instead of overnight



## Discovering Oil with More Accuracy

From one to four jobs per month for deeper insight



## Understand Effects of Global Warming

From three months to one year of simulation per computing day





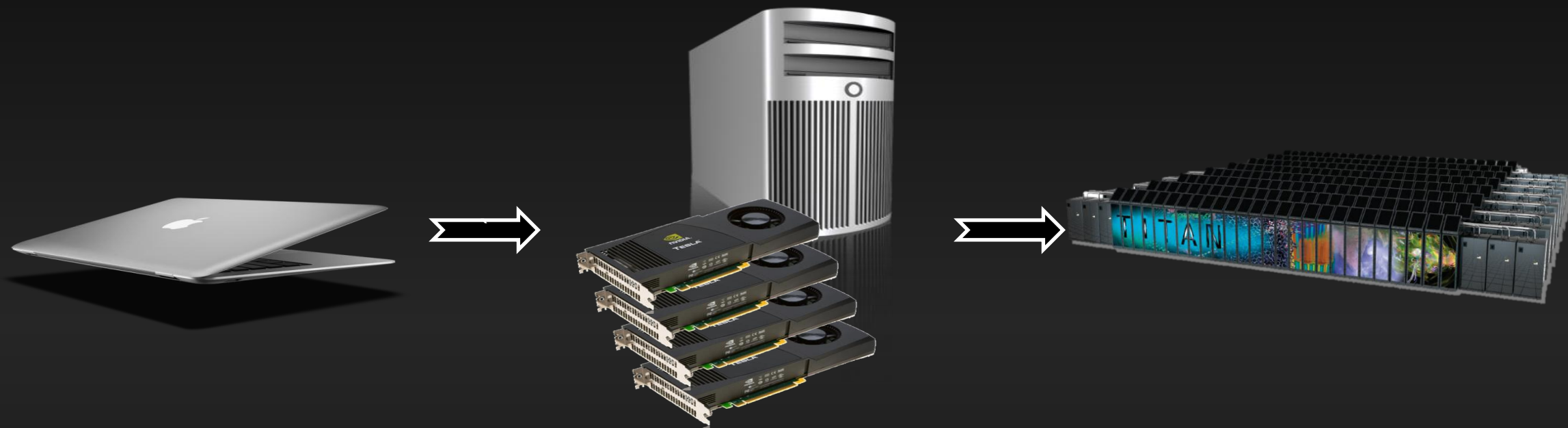
If Computing is Integral to Science  
... And GPUs accelerate Computing.  
... **Then GPUs accelerate Science!**

But GPUs are niche! **WRONG!**

# GPUs are Everywhere!



- Over 375,000,000 CUDA-capable GPUs have been shipped in products from laptops, to workstations, to supercomputers.



# GPU-Computing is Taught Everywhere!



# Explosive Growth of GPU Computing



**150K**  
CUDA Downloads



**1**  
Supercomputer



**60**  
University  
Courses



**4,000**  
Academic Papers



**1.5M**  
CUDA Downloads



**50**  
Supercomputers



**630**  
University  
Courses



**22,500**  
Academic Papers

**2008**

**2012**





# GPUs are Mainstream

Oil & Gas



**Schlumberger**

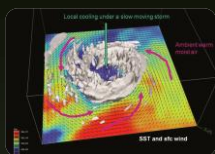


**PETROBRAS**



**Paradigm**

Edu/Research



Chinese  
Academy of  
Sciences

**Georgia  
Tech**



HARVARD  
School of Engineering  
and Applied Sciences



Government



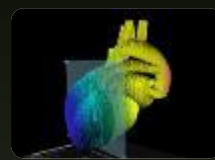
Air Force  
Research  
Laboratory



Naval Research  
Laboratory

**BAE SYSTEMS**

Life Sciences



**Boston  
Scientific**



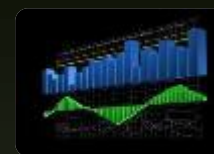
Mass General  
Hospital



Max  
Planck  
Institute



Finance



**Bloomberg**



**J.P.Morgan**

**NumeriX**

Manufacturing



**Agilent**

**ANSYS**

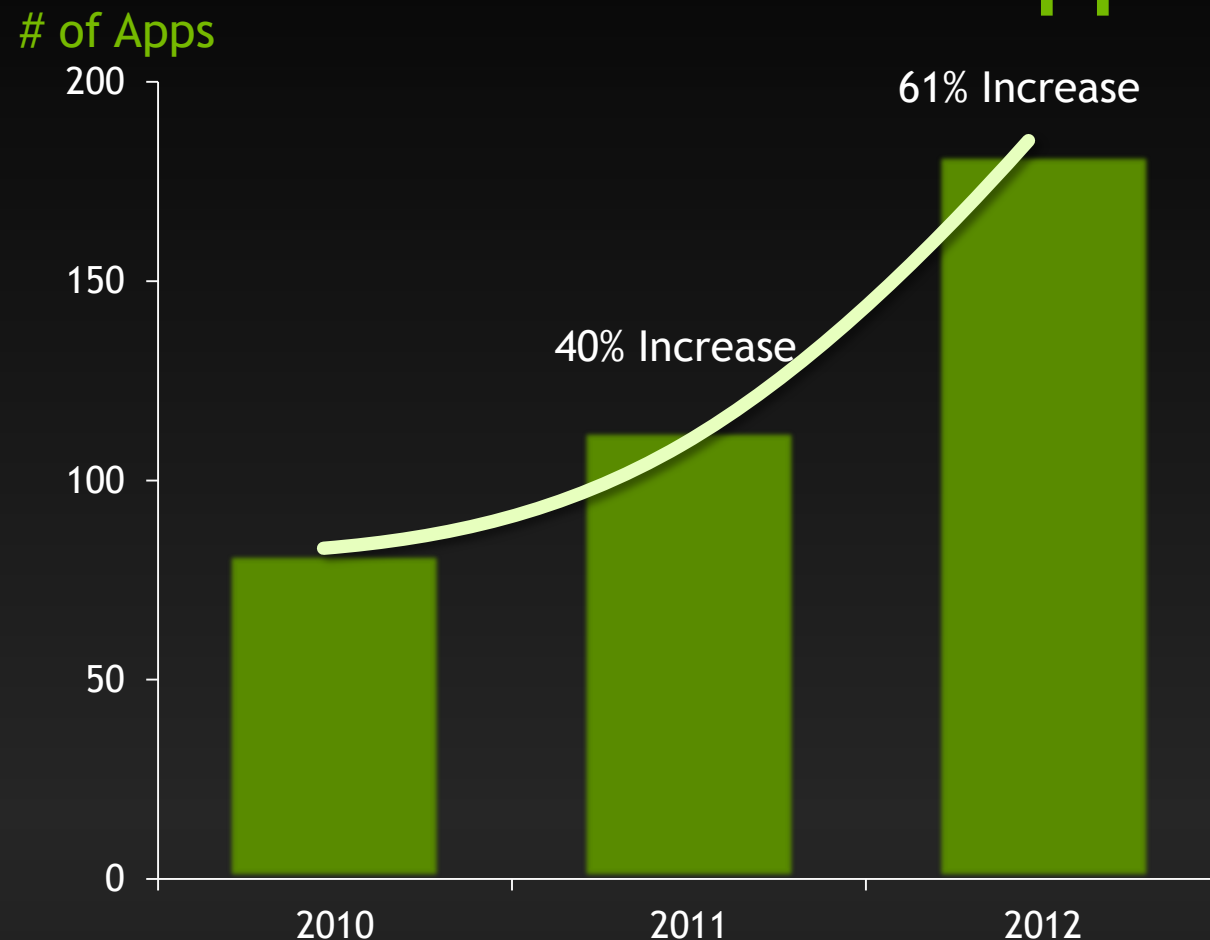
**Autodesk**

**DS  
SIMULIA**

**ACUSIM**  
SOFTWARE



# CUDA Apps Grows 60%, Accelerating Key Apps



## Top Supercomputing Apps

Computational Chemistry	AMBER CHARMM GROMACS	LAMMPS NAMD DL_POLY
Material Science	QMCPACK Quantum Espresso GAMESS	Gaussian NWChem VASP
Climate & Weather	COSMO GEOS-5	CAM-SE NIM WRF
Physics	Chroma Denovo GTC	GTS ENZO MILC
CAE	ANSYS Mechanical MSC Nastran SIMULIA Abaqus	ANSYS Fluent OpenFOAM LS-DYNA

Accelerated, In Development



## POPULAR GPU-ACCELERATED APPLICATIONS

### CONTENTS

- 02 Research: Higher Education and Supercomputing
  - COMPUTATIONAL CHEMISTRY AND BIOLOGY
  - NUMERICAL ANALYTICS
  - PHYSICS
  - WEATHER AND CLIMATE FORECASTING
- 06 Defense and Intelligence
- 07 Computational Finance
- 08 Manufacturing: CAD and CAE
  - COMPUTER AIDED DESIGN
  - COMPUTATIONAL FLUID DYNAMICS
  - COMPUTATIONAL STRUCTURAL MECHANICS
  - ELECTRONIC DESIGN AUTOMATION
- 10 Media and Entertainment
  - ANIMATION, MODELING AND RENDERING
  - COLOR CORRECTION AND GRAIN MANAGEMENT
  - COMPOSITING, FINISHING AND EFFECTS
  - EDITING
  - ENCODING AND DIGITAL DISTRIBUTION
  - ON-AIR GRAPHICS
  - ON-SET, REVIEW AND STEREO TOOLS
  - SIMULATION
  - WEATHER GRAPHICS
- 14 Oil and Gas

## Research: Higher Education and Supercomputing

### COMPUTATIONAL CHEMISTRY AND BIOLOGY

#### Bioinformatics

APPLICATION	DESCRIPTION	SUPPORTED HARDWARE	EXPECTED SPEED UP	RECOMMENDED OPTIM	MULTI-GPU SUPPORT	RELEASE STATUS
BarraCUDA	Sequence mapping software	Alignment of short sequencing reads	8-10x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 0.6.2
CUDASW++	Open source software for Smith-Waterman protein database searches on GPUs	Parallel search of Smith-Waterman database	10-50x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 2.0.8
CUSHAW	Parallelized short read aligner	Parallel, accurate long read aligner - gapped alignments to large genomes	10x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 1.0.40
GPU-BLAST	Local search with fast k-tuple heuristic	Protein alignment according to blastp, multi cpu threads	3-4x	T 2075, 2090, K10, K20, K20X	Single only	Available now Version 2.2.26
GPU-HMMER	Parallelized local and global search with profile Hidden Markov models	Parallel local and global search of Hidden Markov Models	60-100x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 2.3.2
mCUDA-MEME	Ultrafast scalable motif discovery algorithm based on MEME	Scalable motif discovery algorithm based on MEME	4-10x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 3.0.12
SeqFind	A GPU Accelerated Sequence Analysis Toolset	Reference assembly, blast, smith-waterman, hmm, de novo assembly	400x	T 2075, 2090, K10, K20, K20X	Yes	Available now
UGENE	Open-source Smith-Waterman for SSE/CUDA, Suffix array based repeats finder and dotplot	Fast short read alignment	8-8x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 1.11
WideLM	Fits numerous linear models to a fixed design and response	Parallel linear regression on multiple similarly-shaped models	150x	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 0.1-1

#### Molecular Dynamics

APPLICATION	DESCRIPTION	SUPPORTED HARDWARE	EXPECTED SPEED UP	RECOMMENDED OPTIM	MULTI-GPU SUPPORT	RELEASE STATUS
Abalone	Models molecular dynamics of biopolymers for simulations of proteins, DNA and ligands	Simulations (on 1060 GPU)	4-29x	T 2075, 2090, K10, K20, K20X	Single Only	Available now Version 1.8.48
ACEMD	GPU simulation of molecular mechanics force fields, implicit and explicit solvent	Written for use on GPUs	160 ns/day GPU version only	T 2075, 2090, K10, K20, K20X	Yes	Available now
AMBER	Suite of programs to simulate molecular dynamics on biomolecule	PMEMD: explicit and implicit solvent	89.44 ns/day JAC NVE	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 12 + bugfix9
DL-POLY	Simulate macromolecules, polymers, ionic systems, etc on a distributed memory parallel computer	Two-body forces, Link-cell pairs, Ewald SPME forces, Shake W	4x	T 2075, 2090, K10, K20, K20X	Yes	Available now, Version 4.0 Source only
CHARMM	MD package to simulate molecular dynamics on biomolecule	Implicit (Sx), Explicit (2x) Solvent via OpenMM	TBD	T 2075, 2090, K10, K20, K20X	Yes	In Development Q4/12
GROMACS	Simulation of biochemical molecules with complicated bond interactions	Implicit (Sx), Explicit(2x) solvent	165 ns/Day DHFR	T 2075, 2090, K10, K20, K20X	Single only	Available now Version 4.6 in Q4/12
HOOMD-Blue	Particle dynamics package written grounds up for GPUs	Written for GPUs	2x	T 2075, 2090, K10, K20, K20X	Yes	Available now
LAMMPS	Classical molecular dynamics package	Lennard-Jones, Morse, Buckingham, CHARMM, Tabulated, Course grain SDK, Anisotropic Gay-Bern, RE-squared, "hybrid" combinations	3-18x	T 2075, 2090, K10, K20, K20X	Yes	Available now
AMD	Designed for high-performance simulation of large molecular systems	100M atom capable	6-44 ns/days STMV SRS 2050s	T 2075, 2090, K10, K20, K20X	Yes	Available now, Version 2.9
OpenMM	Library and application for molecular dynamics for HPC with GPUs	Implicit and explicit solvent, custom forces	Implicit: 127-213 ns/day, Explicit: 18-35 ns/day DHFR	T 2075, 2090, K10, K20, K20X	Yes	Available now Version 4.1.1

POPULAR GPU-ACCELERATED APPLICATIONS CATEGORY 1 | 2012

# 207 GPU-Accelerated Applications

[www.nvidia.com/appscatalog](http://www.nvidia.com/appscatalog)

# It's Not Just About CUDA



Applications

Libraries

OpenACC  
Directives

Programming  
Languages

“Drop-in”  
Acceleration

Easily Accelerate  
Applications

Maximum  
Performance

# GPU Accelerated Libraries

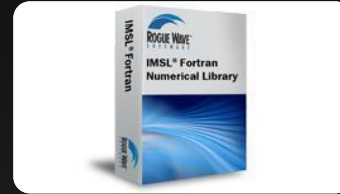
## “Drop-in” Acceleration for your Applications



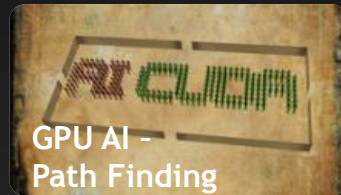
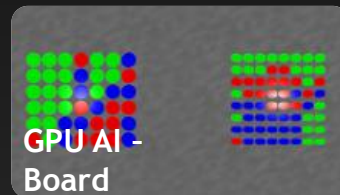
Linear Algebra  
FFT, BLAS,  
SPARSE, Matrix



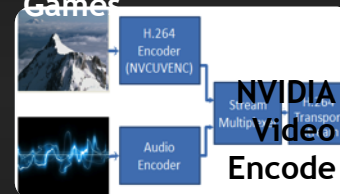
Numerical & Math  
RAND, Statistics



Data Struct. & AI  
Sort, Scan, Zero Sum



Visual Processing  
Image & Video





# OpenACC

## Open Programming Standard for Parallel Computing



“OpenACC will enable programmers to easily develop portable applications that maximize the performance and power efficiency benefits of the hybrid CPU/GPU architecture of Titan.”

*--Buddy Bland, Titan Project Director, Oak Ridge National Lab*



“OpenACC is a technically impressive initiative brought together by members of the OpenMP Working Group on Accelerators, as well as many others. We look forward to releasing a version of this proposal in the next release of OpenMP.”

*--Michael Wong, CEO OpenMP Directives Board*



## OpenACC Standard



## OIL & GAS



Schlumberger



## EDU/RESEARCH



Chinese Academy Of Sciences



## GOVERNMENT



Air Force Research Laboratory



## MANUFACTURING



ANSYS



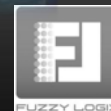
# GPUs

Central To Computing

## DATA ANALYTICS



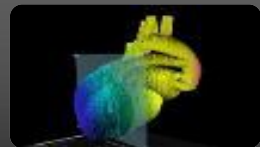
synerscope



## MEDIA & ENTMT.

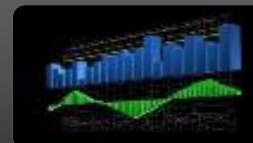


## LIFE SCIENCES



life technologies™

## FINANCE



Bloomberg





# Get Computing!

[developer.nvidia.com](http://developer.nvidia.com)

