

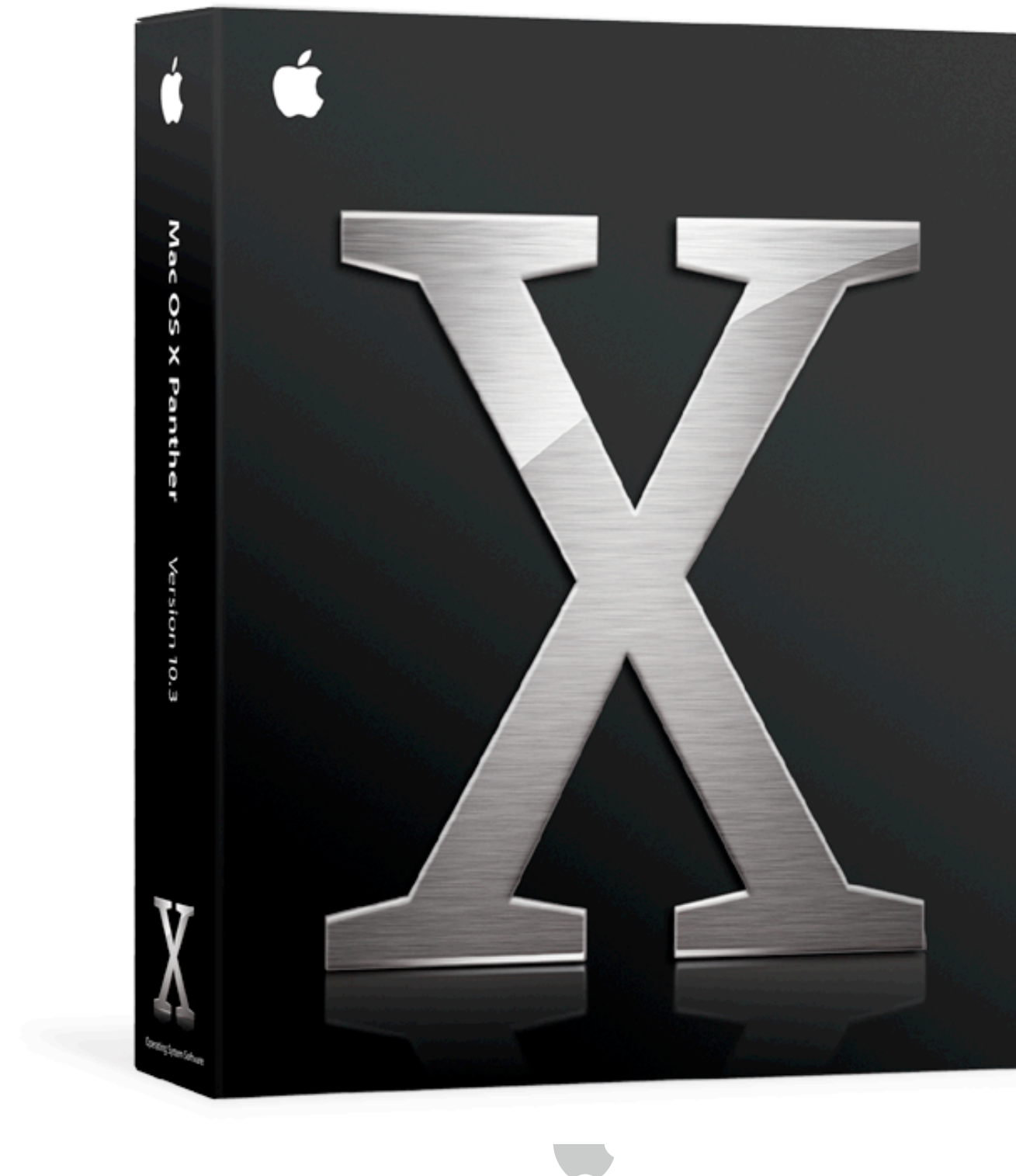


Apple in Research

Rajiv Pillai

Power of UNIX. Simplicity of Macintosh.

Mac OS X: The easy way to be open



Comand Line Interface

FreeBSD 5

Commands
and Utilities

The screenshot shows a terminal window titled "Terminal — emacs — 80x(16+8)". The window is divided into two panes. The top pane shows the output of the command `ls -v` in the directory `My-Computer:Scripts`. The output lists various files and directories: `About Scripts.txt`, `Debug`, `Public`, `Test`, `counter.php`, `debug.tcl`, `get-data.rb`, `main.c`, `matchup.py`, `profile`, `query`, `query_all`, `restore.pl`, `restore.pl~`, `setup.sh`, `status.csh`, `trials.csv`, and `僞黒 Pro.ttf`. The bottom pane shows the contents of the `restore.pl` file, which is a Perl script. The script includes a menu bar with `File Edit Options Buffers Tools Help`, a comment `#check whether the row was INSERTED`, and a conditional statement `if (!$sth) { $retval = 'false'; }`. The status bar at the bottom of the window shows `----:**-F1 restore.pl (Perl)--L346--82%----`.

```
My-Computer:Scripts apple$ ls -v
About Scripts.txt      get-data.rb           restore.pl
Debug                  main.c                restore.pl~
Public                  matchup.py            setup.sh
Test                    profile               status.csh
counter.php             query                  trials.csv
debug.tcl               query_all              僞黒 Pro.ttf
My-Computer:Scripts apple$ emacs restore.pl

File Edit Options Buffers Tools Help
  my $valuesString = &buildValueString($ipAddress);

  my $sql = qq{ INSERT into condorcet_records
                VALUES ( $valuesString ) };

  my $sth = $dbh->do($sql);

  #check whether the row was INSERTED
  if ( !$sth )
  {
    $retval = 'false';
  }

----:**-F1 restore.pl (Perl)--L346--82%----
```

Editors

Scripting
languages

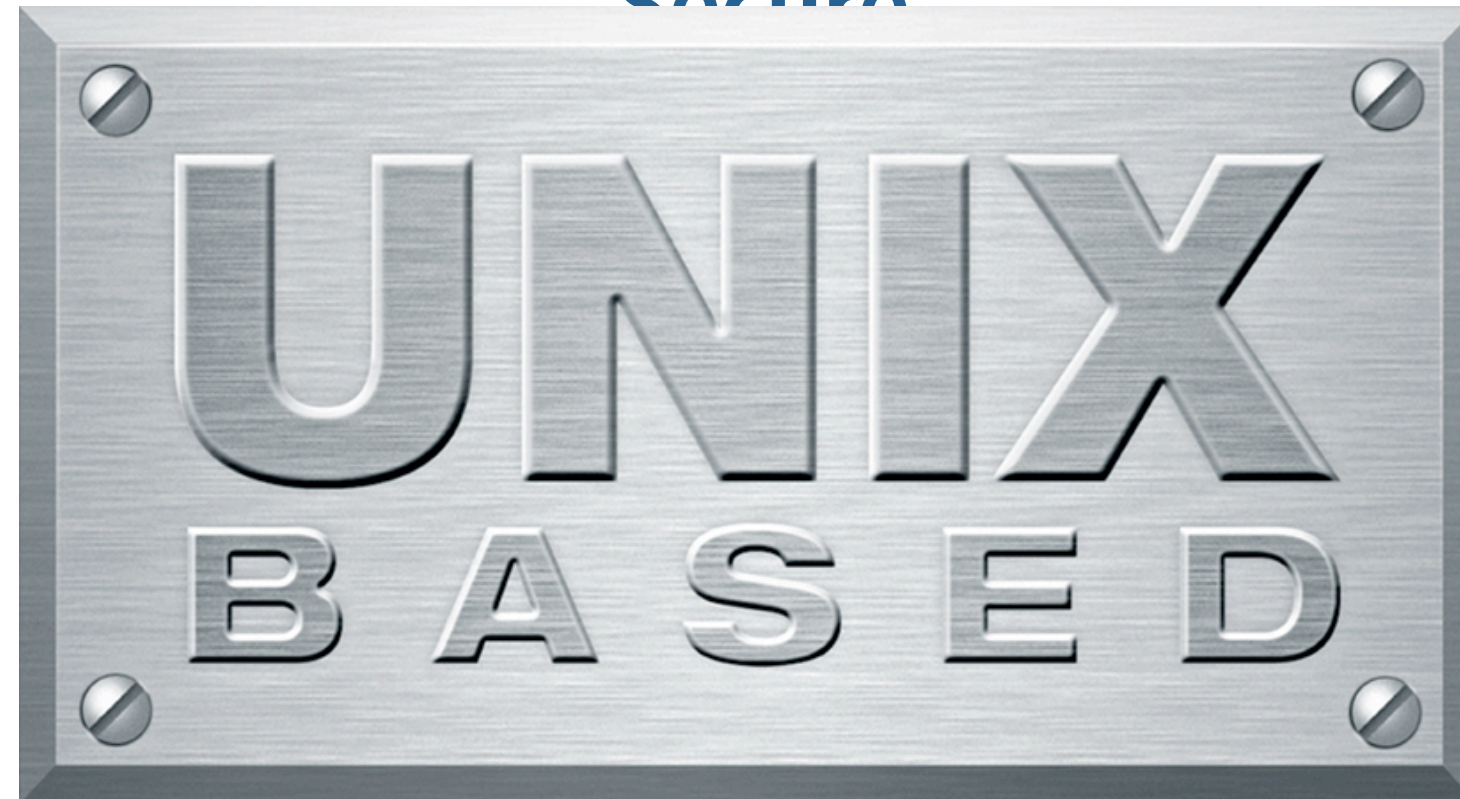
Shells

The Best Foundation



The Best Foundation

Secure










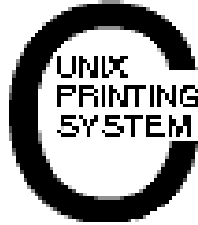








Advanced networking



Built on Open Source

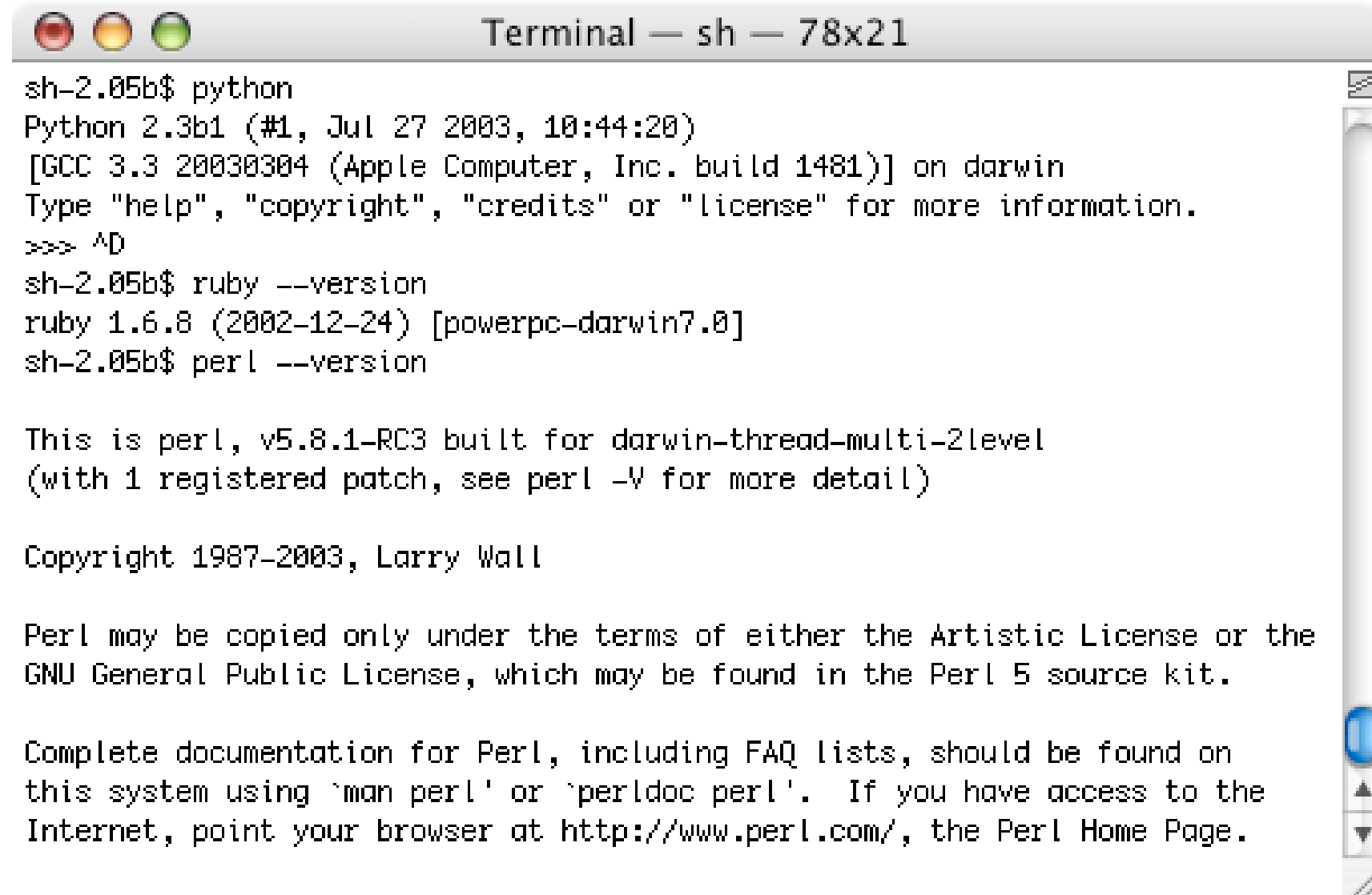
Over 100 Open Source Projects



Modern Languages

- GCC 3.3
- Perl 5.8.1
- Python 2.3
- PHP 4.3.2
- TCL 8.4.2
- Ruby 1.6.8
- Bash 2.05



```
Terminal — sh — 78x21
sh-2.05b$ python
Python 2.3b1 (#1, Jul 27 2003, 10:44:20)
[GCC 3.3 20030304 (Apple Computer, Inc. build 1481)] on darwin
Type "help", "copyright", "credits" or "license" for more information.
>>> ^D
sh-2.05b$ ruby --version
ruby 1.6.8 (2002-12-24) [powerpc-darwin7.0]
sh-2.05b$ perl --version

This is perl, v5.8.1-RC3 built for darwin-thread-multi-2level
(with 1 registered patch, see perl -V for more detail)

Copyright 1987-2003, Larry Wall

Perl may be copied only under the terms of either the Artistic License or the
GNU General Public License, which may be found in the Perl 5 source kit.

Complete documentation for Perl, including FAQ lists, should be found on
this system using `man perl' or `perldoc perl'.  If you have access to the
Internet, point your browser at http://www.perl.com/, the Perl Home Page.
```



Integrated X11

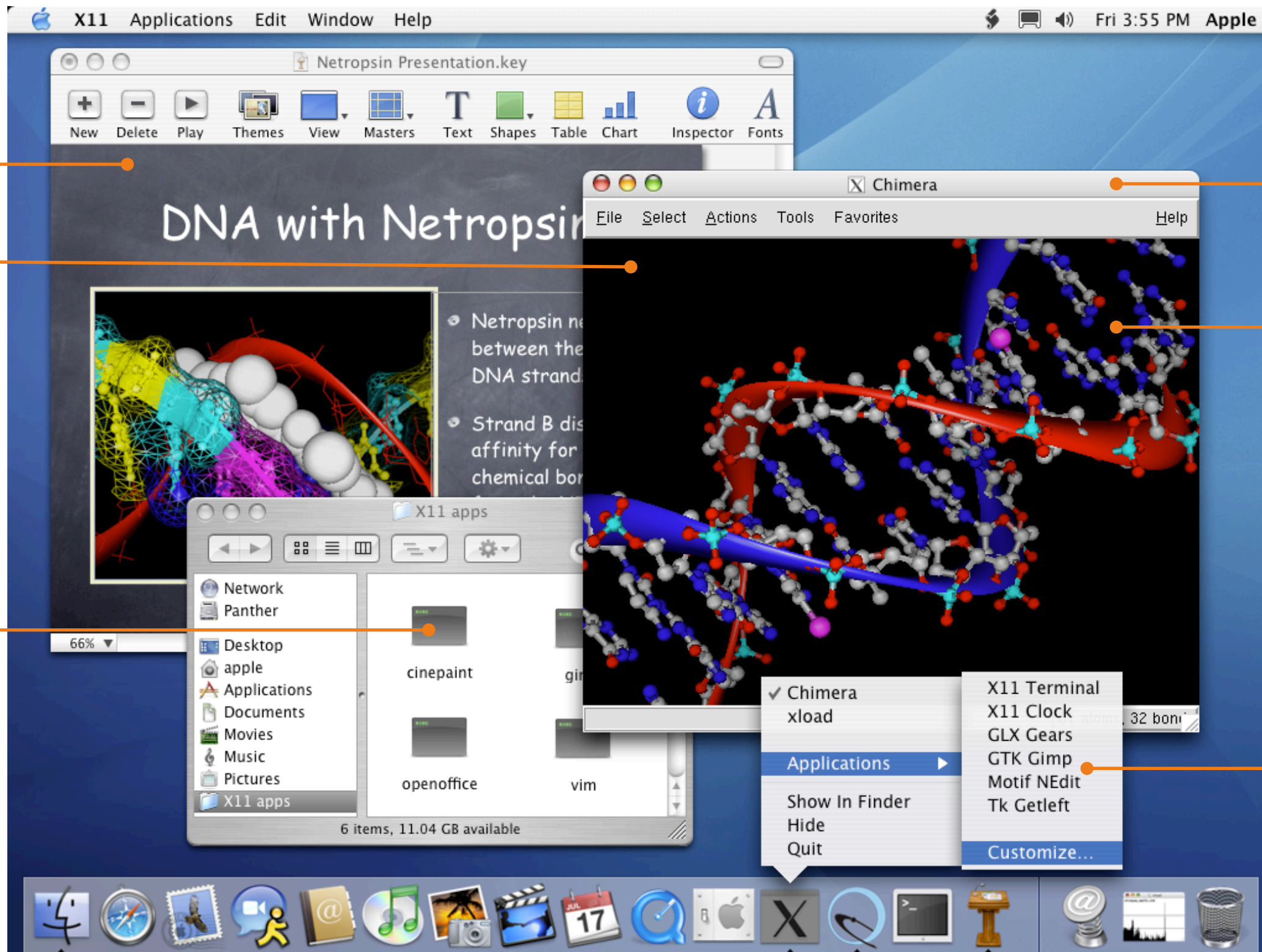
Runs side-by-side with native applications (or full screen)

Launch from Finder

Quartz window manager

Accelerated graphics

Dock menu



A Whole New World of Solutions

Bringing Mac OS X into new markets

Scientific	Distributed	Enterprise
Mathematica	Platform LSF	Oracle 10g
MATLAB	Globus	Sybase
BLAST	Sun Grid Engine	HP OpenView
HMMER	MPI	SAP client
GROMACS	PBS	SAS
GeneSpring	Myrinet	JBoss (J2EE)
PyMol	Infiniband	Tomcat (JSP)
IBM XL Fortran	iNquiry	Axis (SOAP)



Mac OS X

The Best of Both Worlds

Open Like Linux

Convenient Like Windows

Open Source

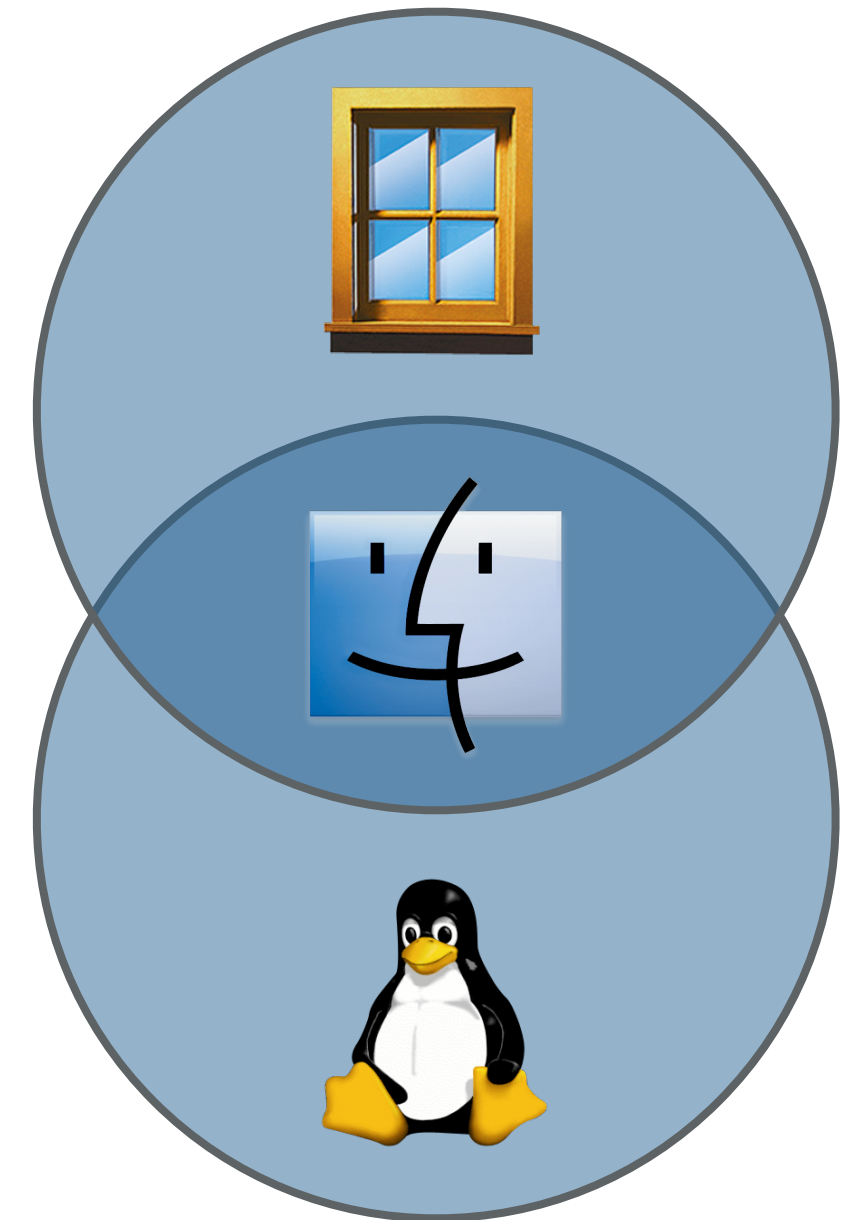
Shrink-wrap solutions

Open Standards

Fits in to existing networks

Open APIs & Applications

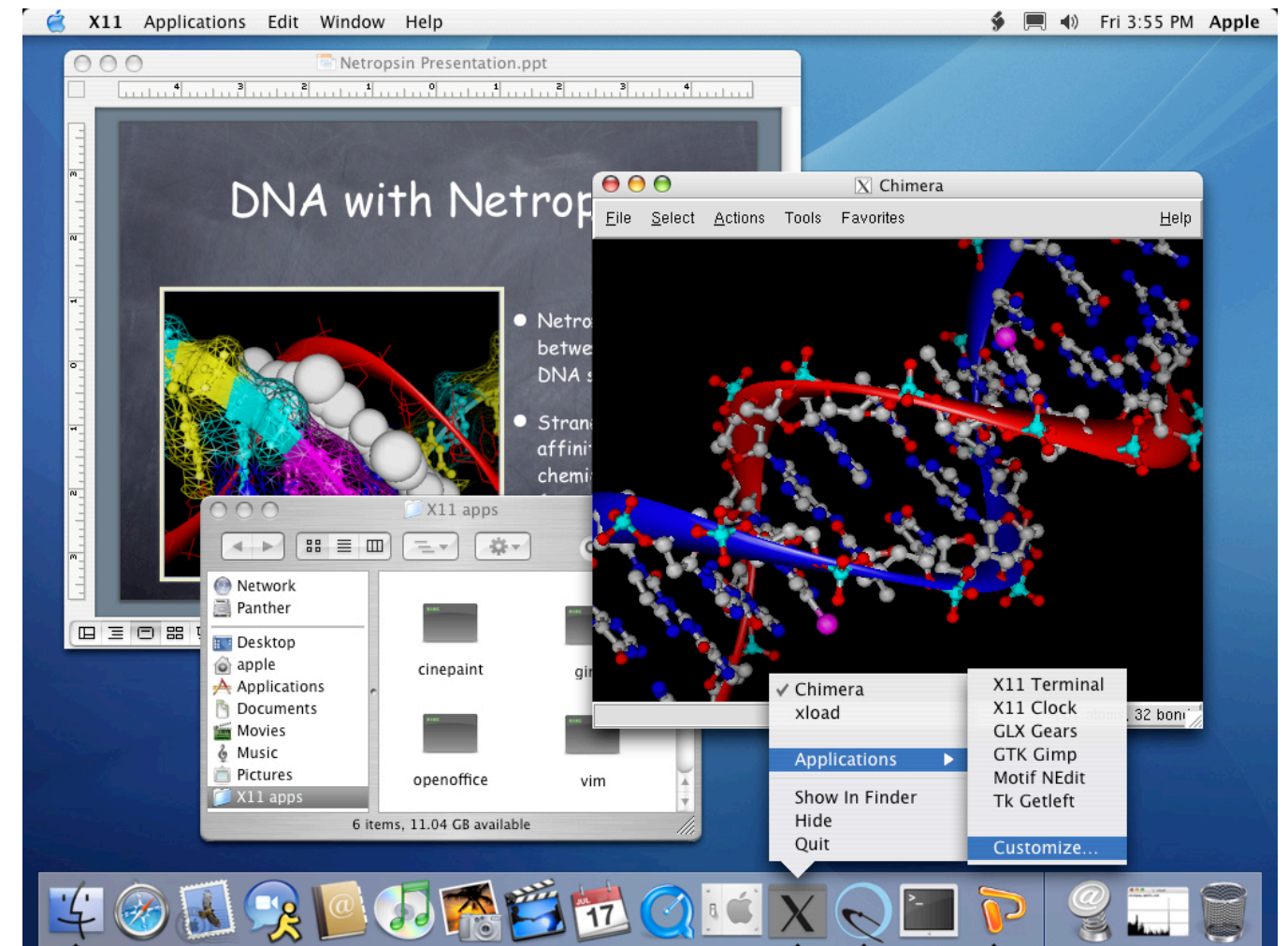
Single point of support



Runs all the Apps a Scientist Needs

A single system on their desk

- Their favorite GUI applications (e.g. Mathematica, Gaussian, Vector NTI, TurboWorx, more)
- *And* their favorite UNIX applications (e.g. Phred/Phrap, HMMer, BLAST, Smith-Waterman, more)
- *And* their favorite productivity tools (e.g. Photoshop, Microsoft Office, Outlook email client)
- All run simultaneously on Mac OS X (Yes! Side by side)



Over 100 installations since March

Academic	Government and Commercial	
Harvard University	Naval Medical Research Center	Isis Pharmaceuticals
Stanford University	Scripps Research Institute	Cincinnati Children's Hospital
Cornell University	Children's Mercy Hospital	U.S. Dept. of Agriculture
Yale University	Dana Farber Cancer Institute	Oakland Children's Hospital
McGill University	Beth Israel Cancer Center	Many private companies





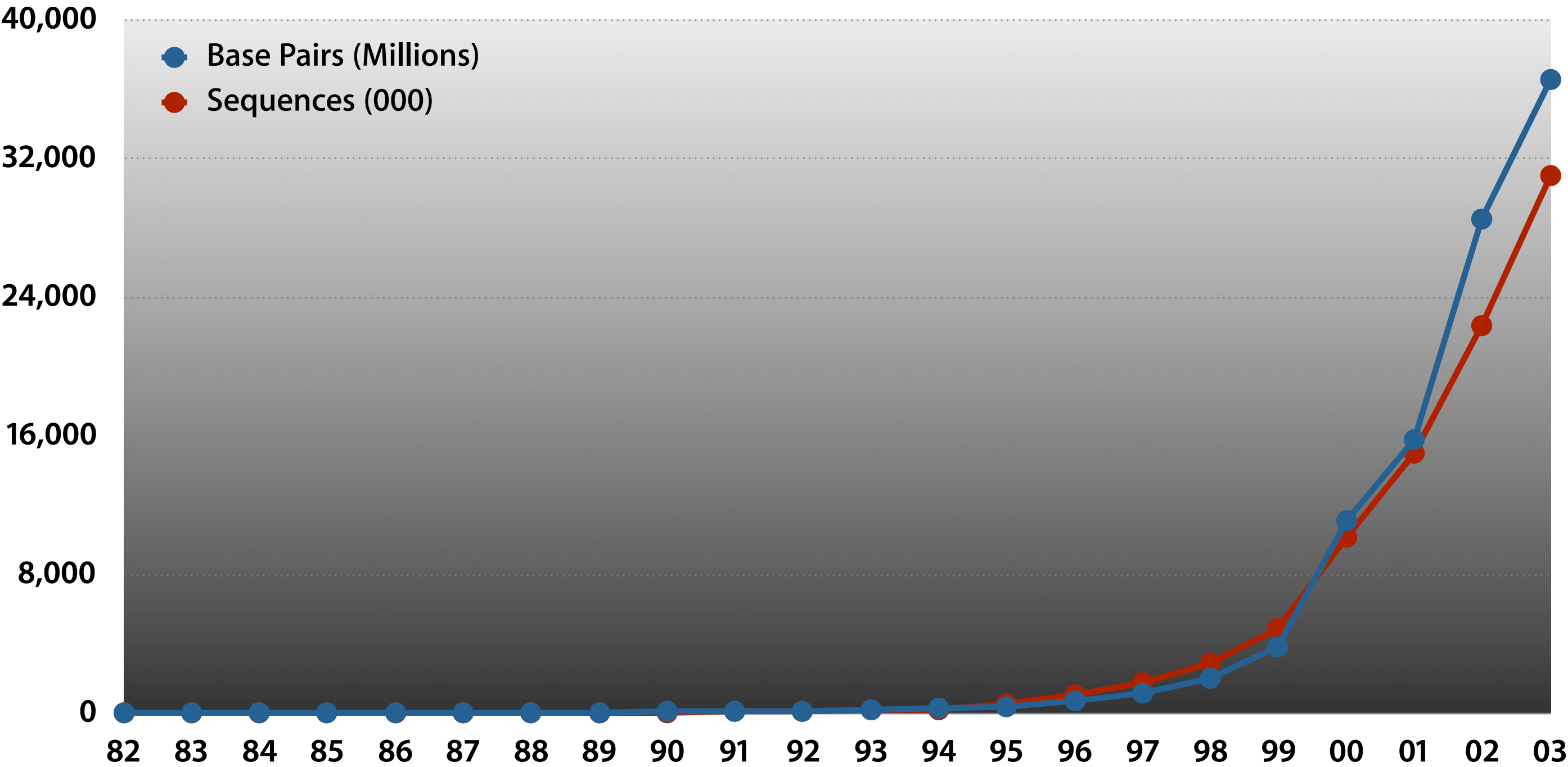
Clustering made Easy

Why discuss Clusters ??



Exponential Growth of GenBank

Researchers face a data explosion

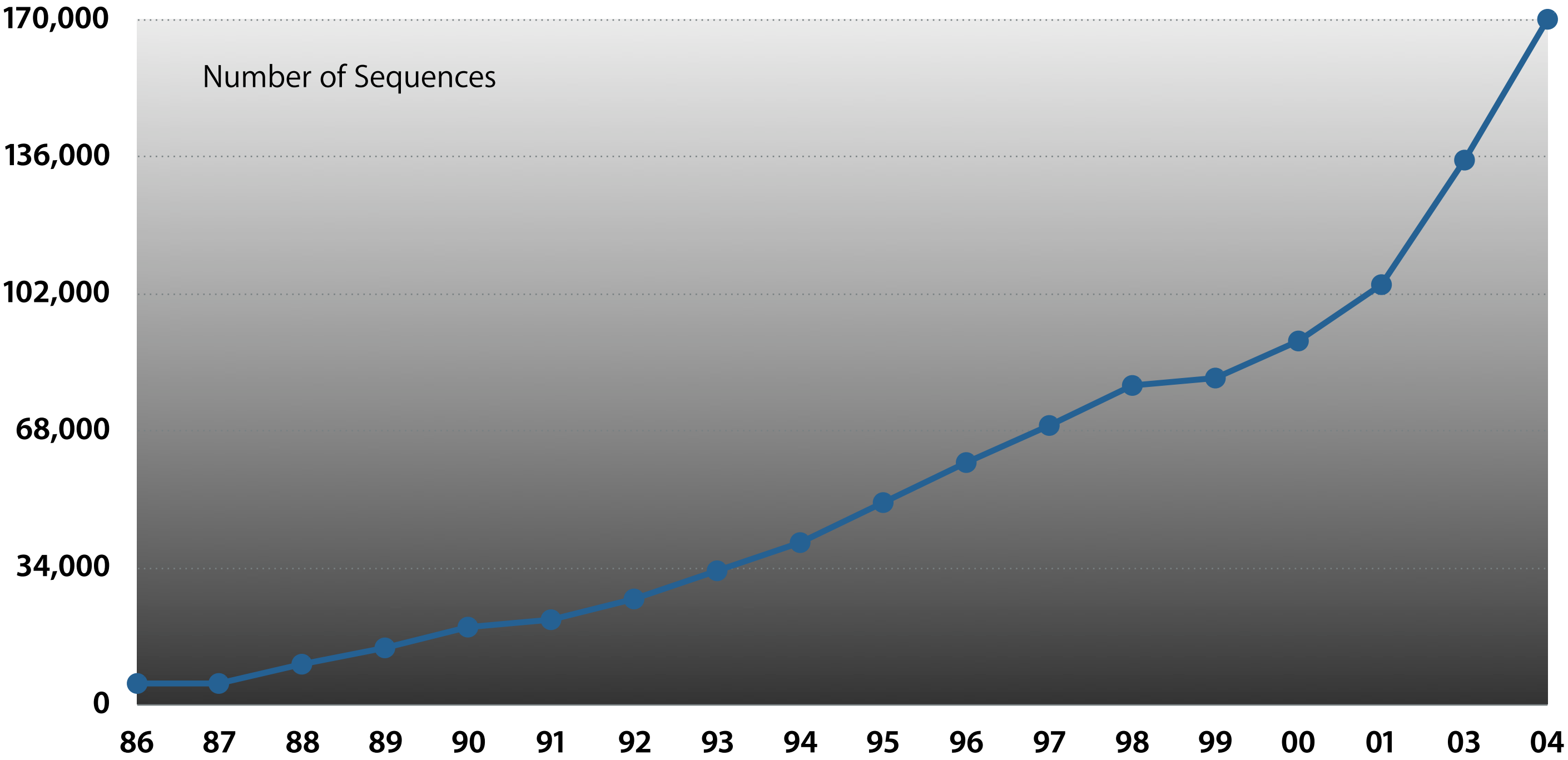


Source: National Center for Biotechnology Information



Protein Database Growth

Swiss-Prot Database



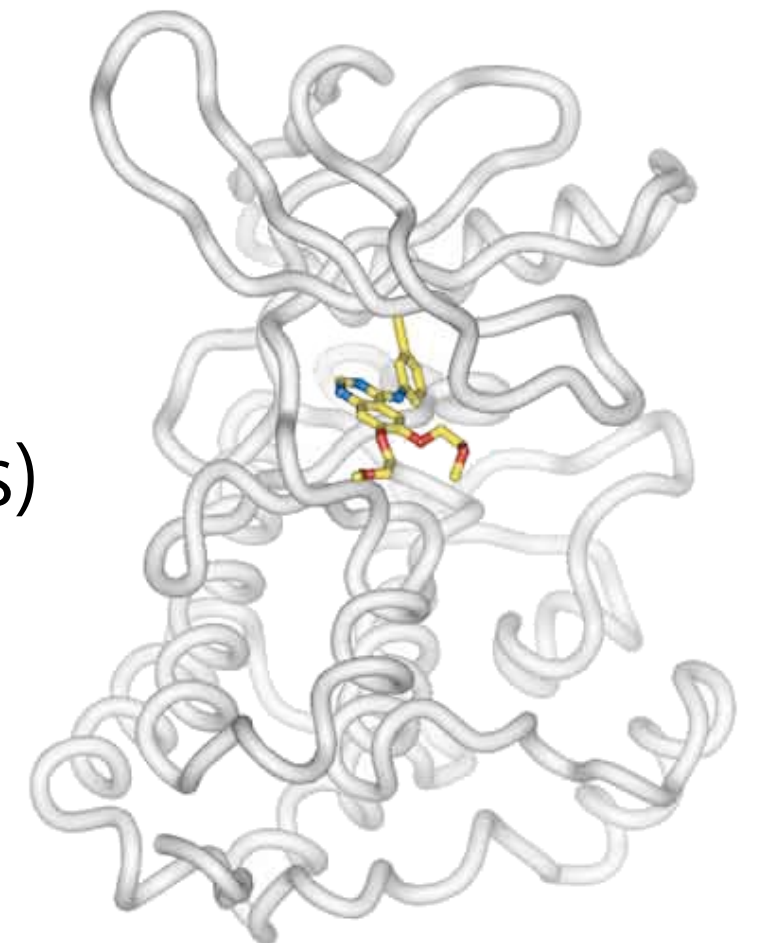
Source: SIB SWISSPROT EBI



Benefits of Clustering in Life Sciences

Immense data processing power

- Accelerates data processing
 - Maintain pace with quickly-growing genome and protein databases
- Faster turnaround time on large computations or searches
 - Reduced time to insight and discovery
 - Better depth of exploration for higher-quality results
- Enables difficult/time consuming computations
 - Large word size BLAST searches
 - Parametric studies (same problem, different parameters)
- Sharing resources allows a lower cost per gigaflop



Cluster Applications

Classes of applications common on clusters

- Bioinformatics
- Business intelligence/data warehousing
- Computational biology
- Computational chemistry
- Computational fluid dynamics
- Data analysis and visualization
- Numerics and statistics
- Simulation



The HPC Landscape is Changing

Smarter, more efficient approaches

- Use off-the-shelf systems whenever possible
 - Cheapest is not always best
 - Price-performance cannot be the only criterion
- Methods are becoming mainstream
 - Clusters are becoming critical components of the research workflow
 - Dependence yields higher standards
- Scientists are realizing there's no "free lunch"



Barriers to Clustering

Why aren't more researchers using their own clusters?

- Complex installation and management
 - Difficult to choose appropriate hardware
 - Complex software presents substantial technical barriers
 - Management resource requirements offset research benefits
- Barriers within the IT organization
 - Funding or logistical barriers to collocating the hardware
 - Lack of human resources to manage additional infrastructure
- Cost
 - Not just hardware, but also operating and maintenance costs
 - Indirectly associated cost - TIME !!



What makes clustering complex ??



Hardware Selection Considerations

- Computational requirements
 - RAM
 - Storage
 - Number of nodes
- Power
- Network
- Cooling
- Noise
- Setup and maintenance
- Security



“We are scientists, not IT professionals. And we wish to remain so.”



What we need

Ready to use clusters

Open source based solution

Low or Zero Maintenance



How does Apple help ?





Apple Workgroup Cluster for Bioinformatics

Apple Workgroup Cluster for Bioinformatics

The freedom to focus on your research

- Easy, do-it-yourself cluster setup
- All-inclusive turnkey solution
- Blazing speed of the G5 processor
- Powerful UNIX-based platform
- Ultraquiet enclosure
- More than 200 preconfigured bioinformatics applications
- Affordable, all-inclusive pricing
- Power- and space-efficient design



Web-Based Tool Access

Extensible and modifiable

All tools have an advanced form and a simple form

Tools are organized in folders by function

The active tool is boldfaced

Applications can be viewed in a flat list

The screenshot shows a web browser window titled "iNquiry Bioinformatics Portal" with the URL "http://inquiry.flybase.harvard.edu/". The page header includes "The BioTeam" logo and navigation links: "Home", "Admin", "About", and "Logoff". A "Welcome admin" message is displayed. On the left, a sidebar lists various applications in a flat list, with "btblastall" highlighted in bold. The main content area is titled "BTBLASTALL : Altschul, Madden, Schaeffer, Zhang, Miller, Lipman". It features a "Submit btblastall" button, an "Email:" field with "user@domain.com", and a "Description:" field with "ecoli vs drosoph--august". Below these is a "View Simple Form" link. The main form area is titled "blastn: nucleotide query / nucleotide db" and includes a "Blast program" dropdown. It has two input sections: "1. Filename:" with a "Choose File" button and "no file selected" text, and "2. or Actual data:" with a text area containing a DNA sequence. Below the text area are two input fields for "Start of required region in query sequence (-L)" (value 353) and "End of required region in query sequence (-L)" (value 23). There are also dropdown menus for "drosoph.aa" (protein db) and "drosoph.nt" (nucleotid db). At the bottom, there are links for "Filtering and masking options" and "Selectivity options".

Results are emailed to user (and displayed in the web browser)

Quick access to simple forms for standard searches

Data entry via file upload

Direct data entry

Quick access to installed databases

All command-line options are available in the web interface

Web-Based Results



Simple User Management

The screenshot shows a web browser window titled "iNquiry Bioinformatics Portal" with the URL "http://inquiry.flybase.harvard.edu/". The browser's address bar and search bar are visible. Below the browser window, the portal's header includes the "The BioTeam" logo and navigation links: "Home", "Admin", "About", and "Logoff". The "Admin" section is active, showing sub-links: "Usage Reports", "User Administration", and "Menu Regeneration". A sidebar on the left lists various applications: "profile", "alignment", "phylogeny", "feature tables", "utils", "unclassified", "edit", "search", "nucleic", "display", "protein", "enzyme kinetics", "util", and "information". The main content area is titled "Add a User" and contains a form with fields for "Username", "Password", "Email", and "Verify". A "Group" dropdown menu is set to "USER", and a "Submit" button is present. Below this, the "Remove a User" section shows a "Username" dropdown set to "admin", a "Delete" checkbox, and a "Submit" button. Three orange lines with dots point to specific elements: one to the "Add a User" title, one to the "Group" dropdown, and one to the "Submit" button in the "Remove a User" section.

iNquiry Bioinformatics Portal

[Home](#) [Admin](#) [About](#) [Logoff](#)

[Usage Reports](#) [User Administration](#) [Menu Regeneration](#)

Add a User

Username: Password: Group:

Email: Verify:

Remove a User

Username: ☐ Delete

Minimal effort to create a new user

Choose between regular user and administrator

Single-click user disabling or deletion



Usage Reporting

Quickly see results and user statistics

The screenshot shows a web browser window titled "iNquiry Bioinformatics Portal" with the URL <http://inquiry.flybase.harvard.edu/>. The browser's address bar and search bar are visible. Below the browser window, the portal's header includes the "The BioTeam" logo and navigation links: [Home](#), [Admin](#), [About](#), and [Logoff](#). A sidebar on the left contains a "Welcome admin" message and a list of applications: [profile](#), [alignment](#), [phylogeny](#), [feature tables](#), [utils](#), [unclassified](#), [edit](#), [search](#), [nucleic](#), [display](#), [protein](#), [enzyme kinetics](#), and [util](#). The main content area is titled "Usage Reports" and displays a table of usage data for the user "thomass" with the action "history". The table has columns for Submit Time, Job, Exit, Clock, CPU, Jobs, and Results. The data shows four entries for August 2003, with the last entry for August 18, 2003, being partially cut off.

Welcome **admin**

[View Simple Forms](#)

[Applications](#)

- [profile](#)
- [alignment](#)
- [phylogeny](#)
- [feature tables](#)
- [utils](#)
- [unclassified](#)
- [edit](#)
- [search](#)
- [nucleic](#)
- [display](#)
- [protein](#)
- [enzyme kinetics](#)
- [util](#)

Usage Reports

Username: Action:

Submit Time	Job	Exit	Clock	CPU	Jobs	Results
Tue Aug 26 02:32:47 2003	251	0	3	0	3	A19149106187956
Wed Aug 20 07:21:38 2003	234	0	2	0	3	A18072106137849
Wed Aug 20 06:44:15 2003	233	1	1	0	1	A17656106137625
Wed Aug 20 01:43:08 2003	230	0	9	1	3	A14244106135818
Mon Aug 18 11:14:56						

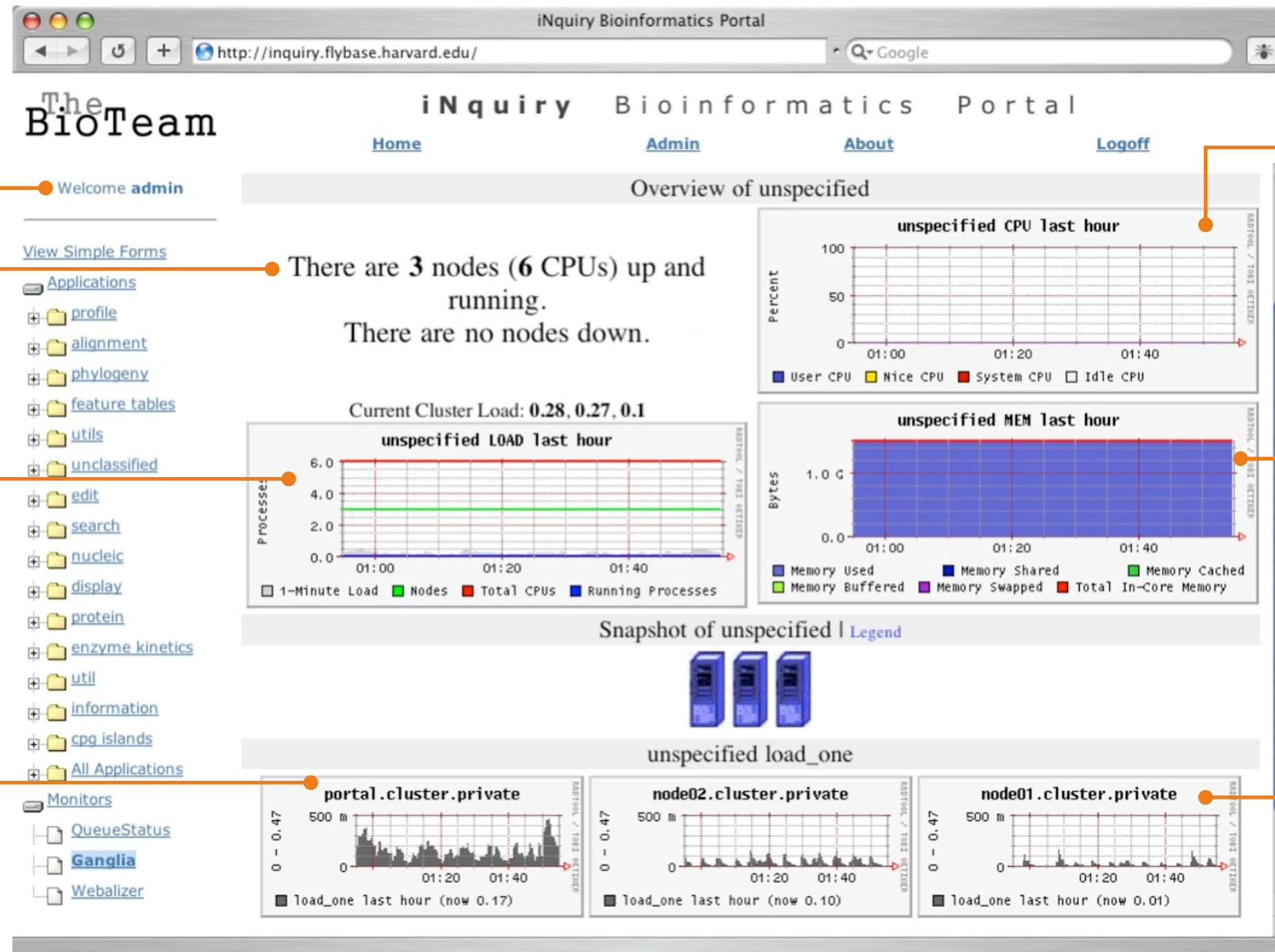
Cluster Monitoring

Only admin users have access to management tools

Instantly see if any cluster nodes are offline

See load statistics for the entire cluster

See load statistics for individual cluster nodes, including the portal (head) node



Histograms of CPU utilization by percentage

Histograms of memory usage by gigabyte

Load histograms for individual cluster nodes

Key Points

- Simple setup process – up and running in 30 minutes
 - approximately two man-weeks of labor and/or \$40k professional services of consulting
- Self-sufficiency – minimum IT dependency
- Access to UNIX applications via rich web GUI
- No compiling of tools – optimized versions already installed
- Keeps research data in-house – no outside resources required
- Reduced TCO by simplifying setup and minimizing administration required

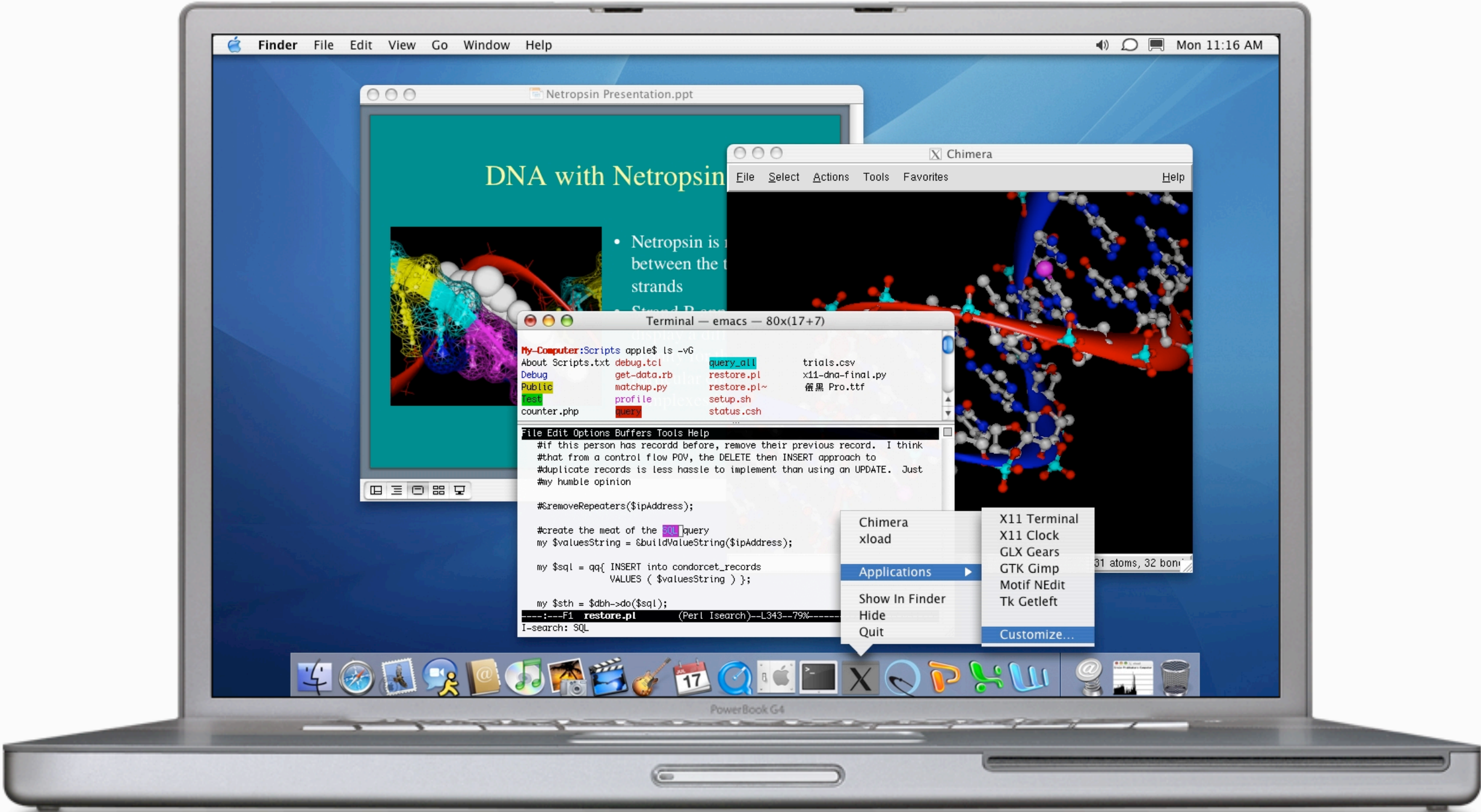


Key Advantages

- Everything included – *complete cluster solution*
- Easy to setup, easy to administer, easy to use – *produce results!*
- Over 200 bioinformatics applications – *optimized, ready to go*
- Xserve G5 performance – *results fast!*
- Support included – *no worries!*
- UPS, noise deadening rack – *put it anywhere*



Mobile Super-Computing !!!



Xserve G5 in the Workgroup Cluster

Portal



Two G5 processors at 2.3GHz
Three drive bays for up to 1200GB storage
Up to 8GB PC3200 ECC DDR SDRAM

CD-RW/DVD drive
Mac OS X Server unlimited-client license

Compute Nodes



Two G5 processors at 2.3GHz
One drive bay with 80GB module
Up to 8GB PC3200 ECC DDR SDRAM



Breakthrough Performance in a 1U Server

Dual PCI-X slots at
up to 133MHz

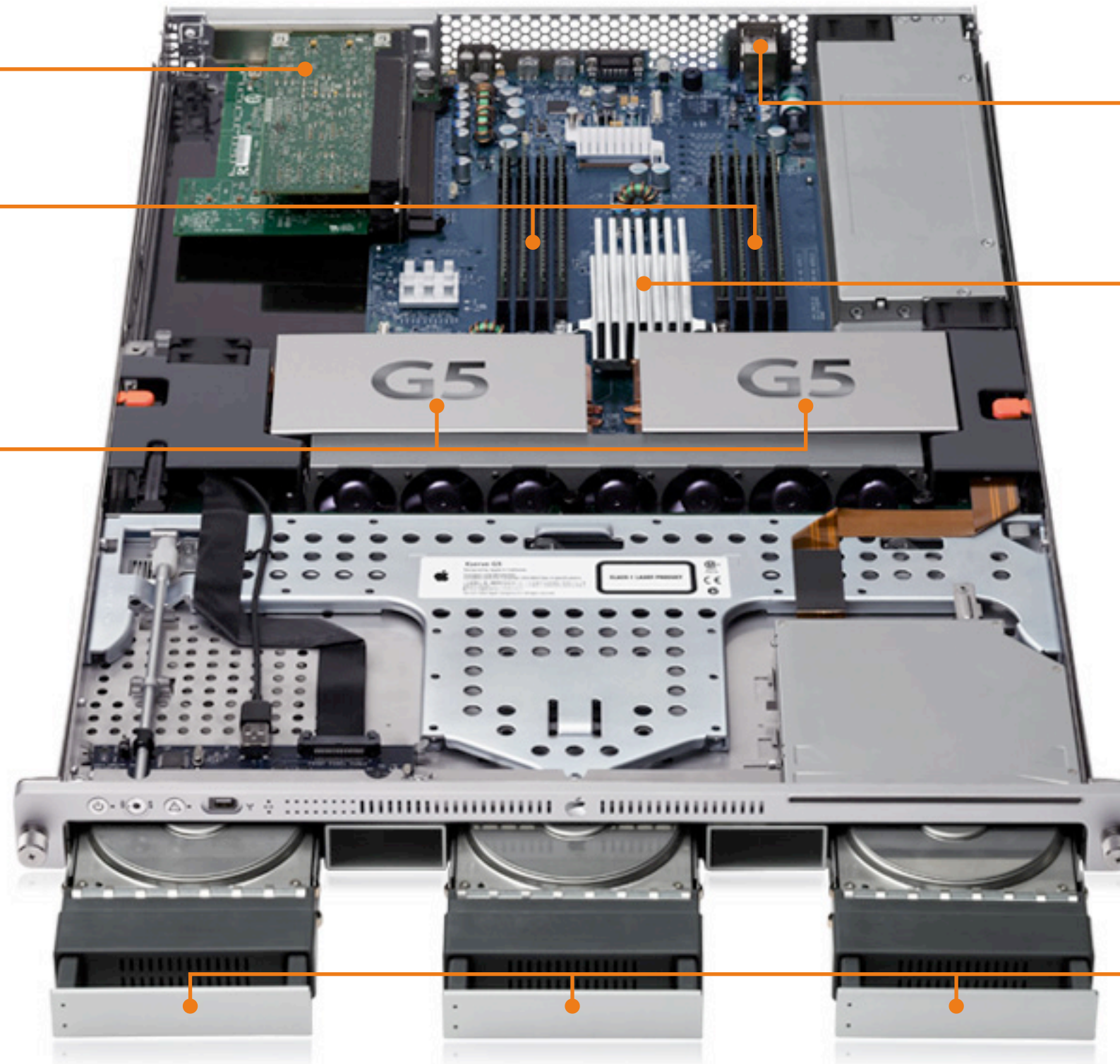
Up to 8GB ECC DDR
main memory

Dual 2.3GHz PowerPC
G5 processors

Dual onboard Gigabit
Ethernet ports

Advanced system
controller with dual
1.15GHz system buses

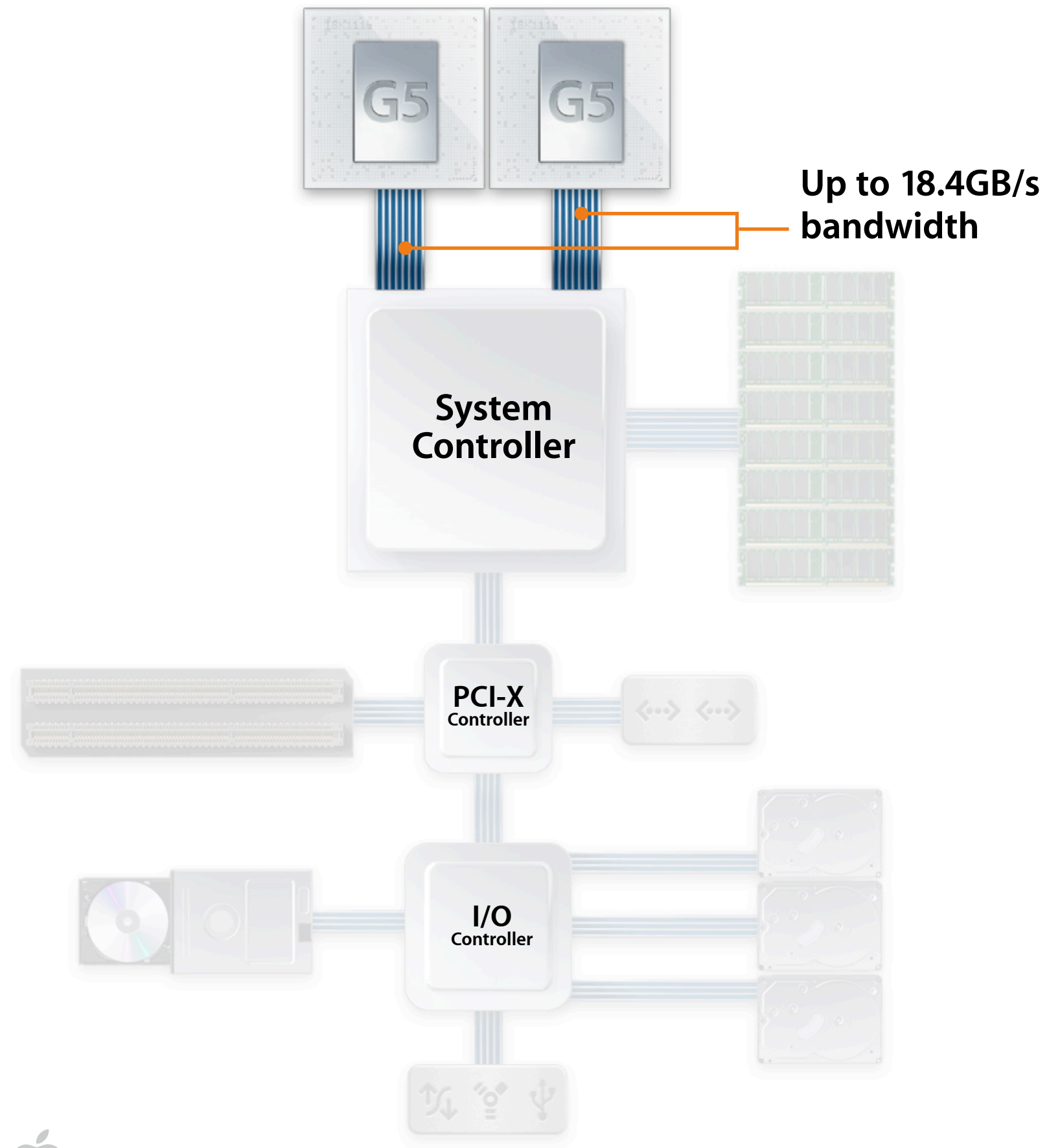
Up to three 400GB drive
modules—1.2TB in 1U



1.15GHz Frontside Bus

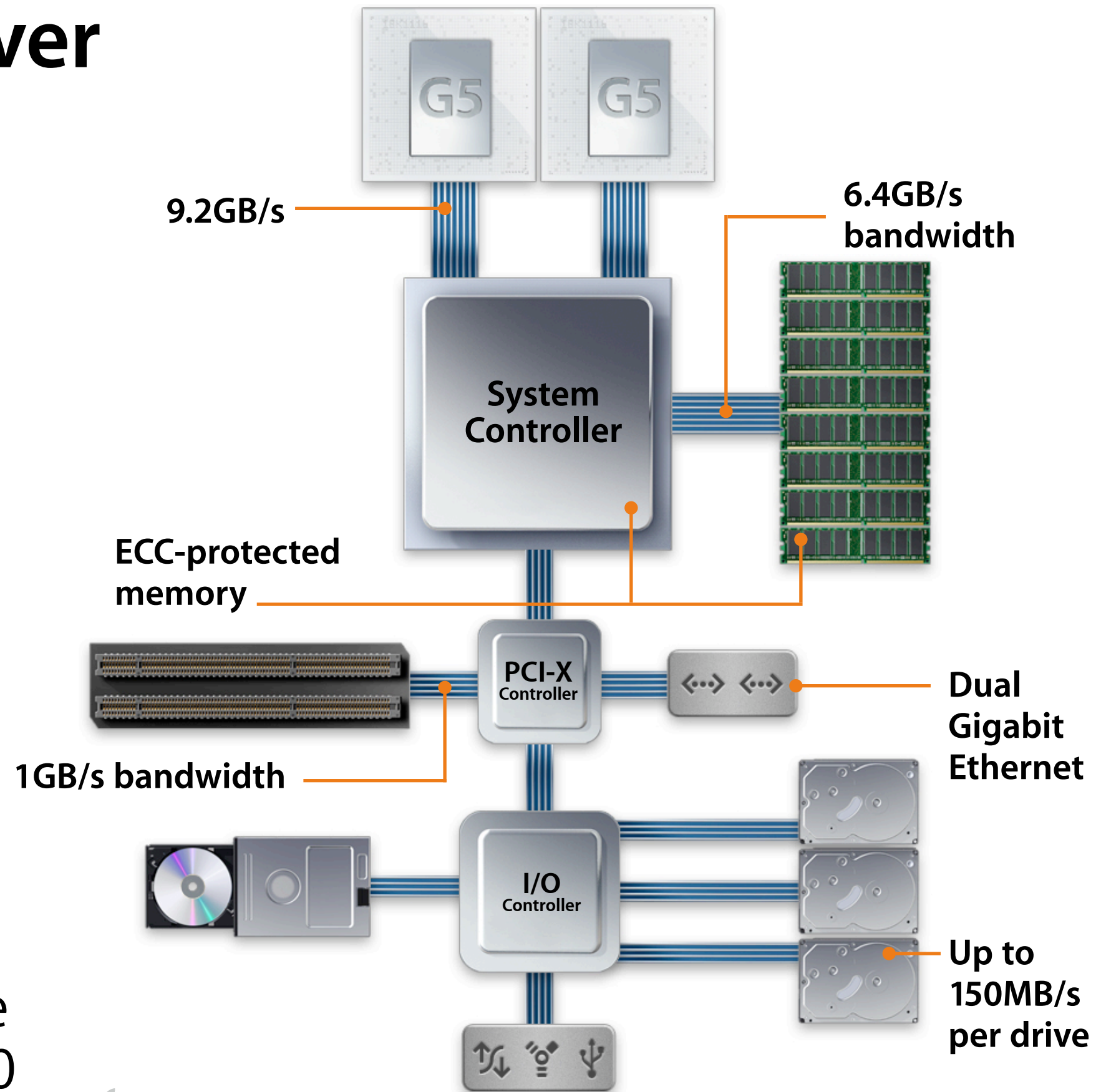
Fastest frontside bus in the industry

- 64-bit DDR bus for massive bandwidth up to 8GB/s
- Dual-channel bus for continuous flow of data
- Superior to standard bus, which negotiates direction
- Elastic interface self-tunes during startup for optimal signal quality



High-Bandwidth Server Architecture

- Apple-designed system controller
 - Dual 1.15GHz frontside buses with 18.4GB/s combined bandwidth
 - 128-bit PC3200 ECC DDR SDRAM with 6.4GB/s bandwidth
- Two PCI-X expansion slots
- Dual Gigabit Ethernet on dedicated internal PCI-X bus
- Three 150MB/s Serial ATA drive bays, FireWire 800, and USB 2.0



Dual 2.3GHz G5 Processing Power

Dual scalar floating-point units plus Velocity Engine deliver tremendous computational capability

**Double-Precision
Floating Point**

10.35

Gigaflops



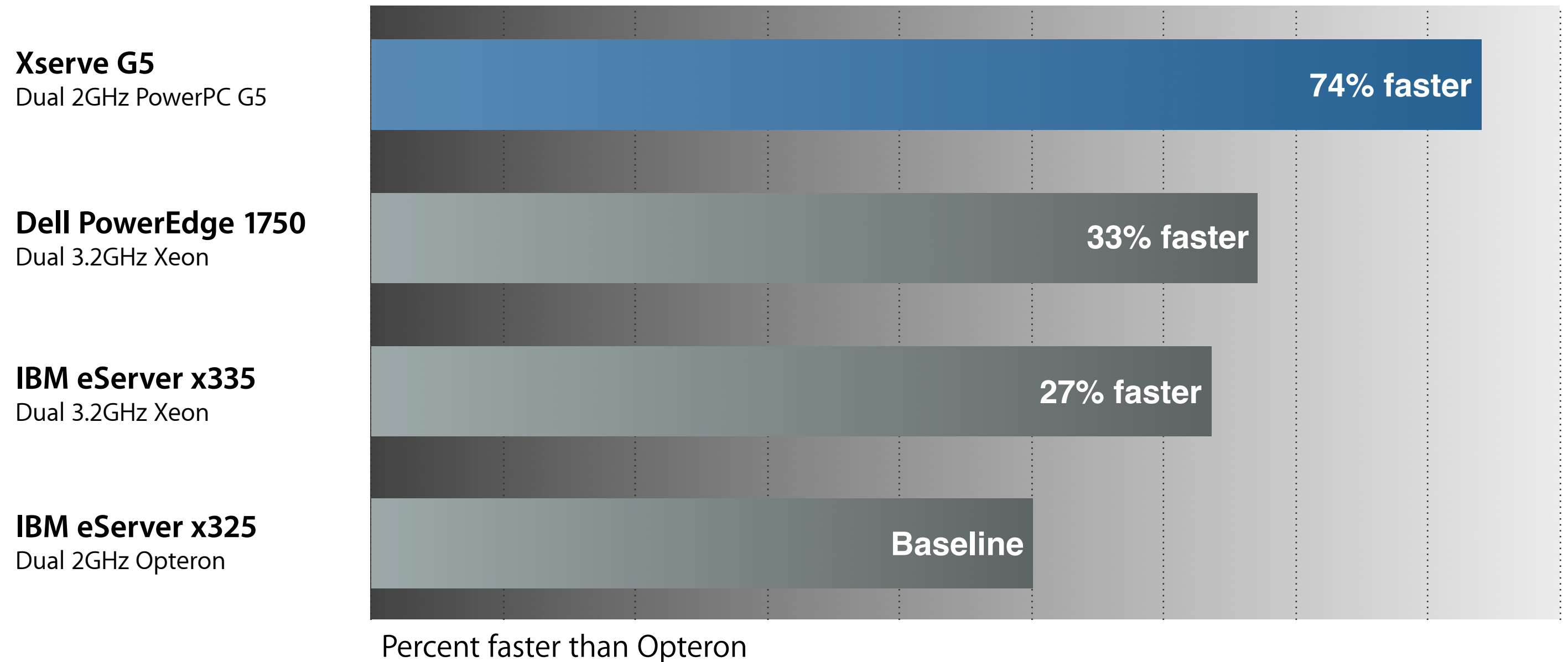
**Single-Precision
Floating Point**

35.22

Gigaflops

HMMer Results

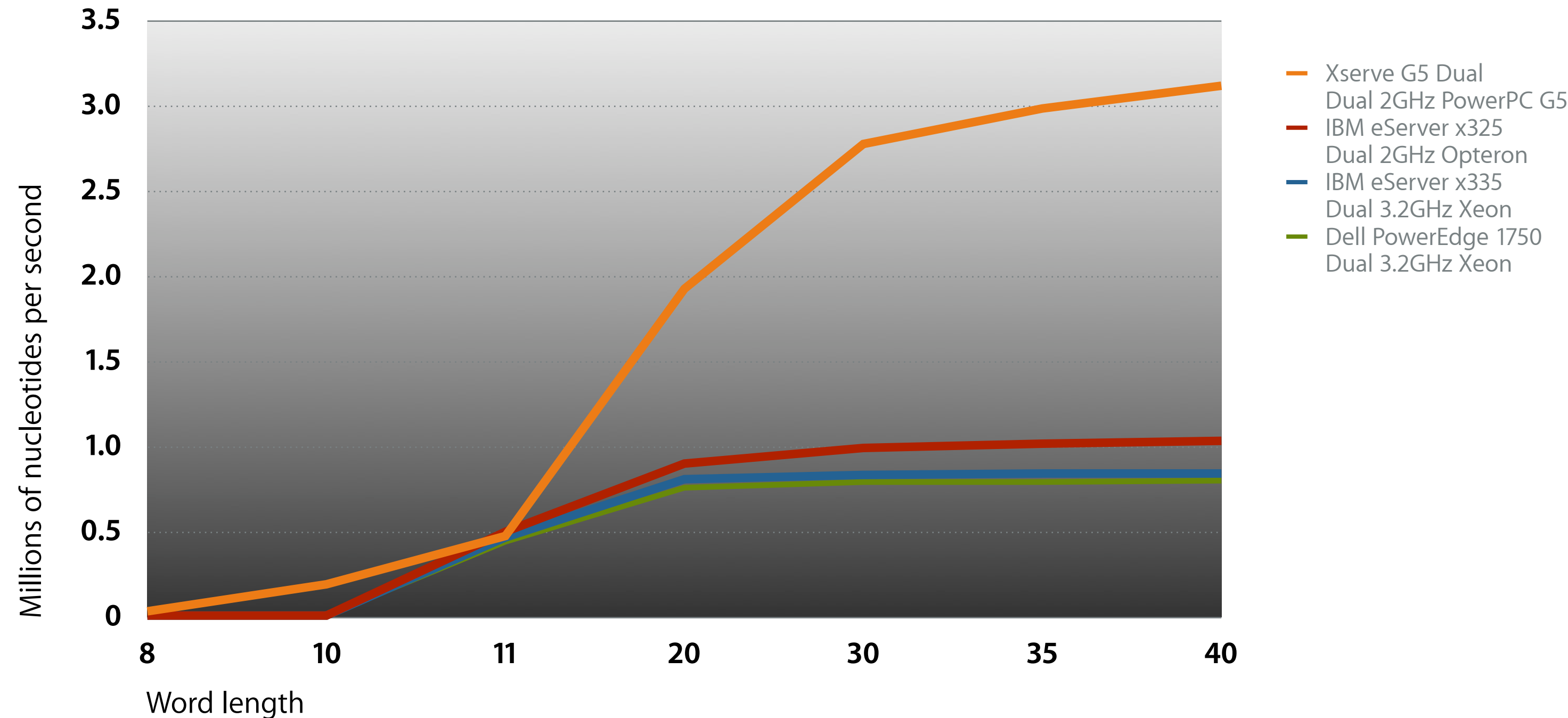
Genome sequence matching



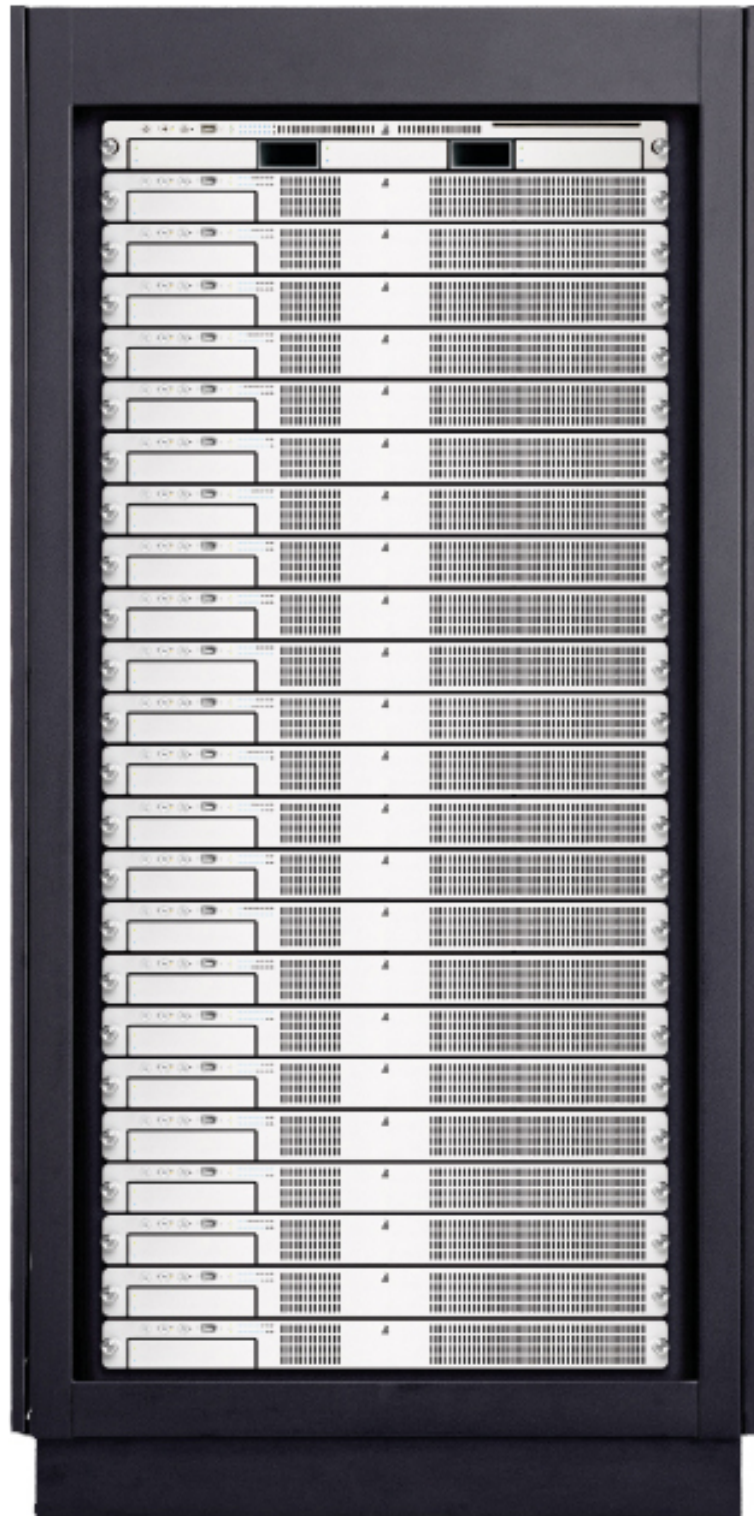
Testing conducted by Apple in January 2004 using preproduction dual 2GHz Xserve G5 units; all other systems tested were shipping units. All Xserve G5 systems were tested using Mac OS X Server v10.3.2. The IBM eServer x335 and Dell PowerEdge 1750 tested using Red Hat Linux 9.0; IBM eServer x325 used Red Hat Enterprise Linux 3.

BLAST Results

DNA sequence matching



Testing conducted by Apple in January 2004 using preproduction dual 2GHz Xserve G5 units; all other systems tested were shipping units. All Xserve G5 systems were tested using Mac OS X Server v10.3.2 and A/G BLAST. The IBM eServer x335 and Dell PowerEdge 1750 ran NCBI BLAST on Red Hat Linux 9.0. IBM eServer x325 ran NCBI BLAST on Red Hat Enterprise Linux 3.



Making your customized cluster



What is a Cluster?

Varied components with a common goal

- 1 Some number of independently operable computers



Xserve G5 in the Workgroup Cluster

Portal



Two G5 processors at 2.3GHz
Three drive bays for up to 1200GB storage
Up to 8GB PC3200 ECC DDR SDRAM

CD-RW/DVD drive
Mac OS X Server unlimited-client license

Compute Nodes



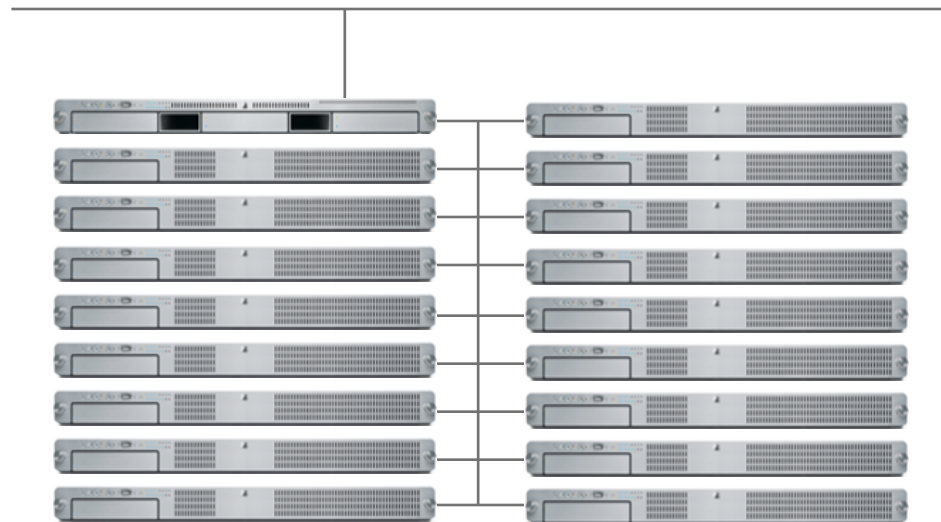
Two G5 processors at 2.3GHz
One drive bay with 80GB module
Up to 8GB PC3200 ECC DDR SDRAM



What is a Cluster?

Varied components with a common goal

- 1 Some number of independently operable computers
- 2 Interconnection network





Interconnects

Choosing the Right Interconnect

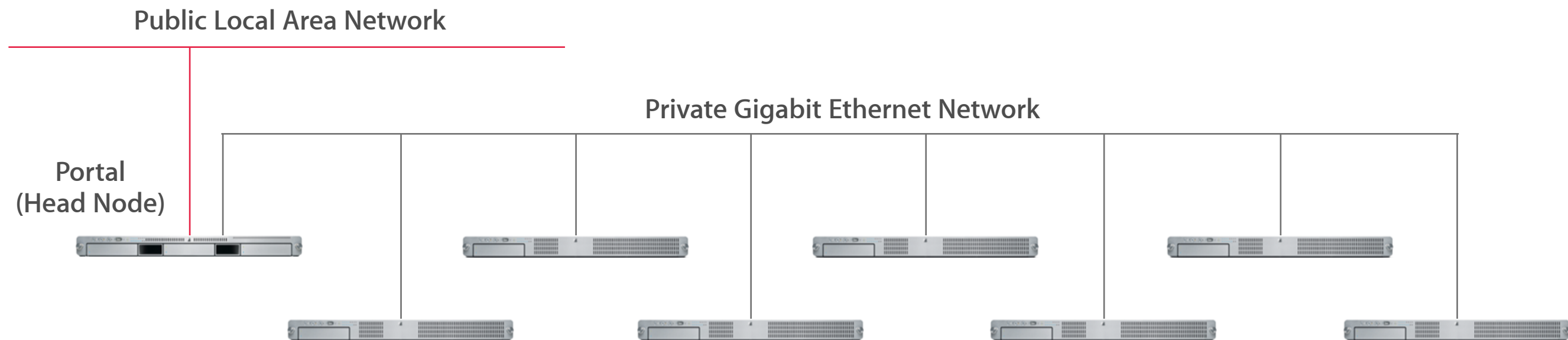
Let the application drive the selection process

- Type of problem
 - Embarrassingly parallel or tightly coupled
- Type of cluster
 - High performance or high throughput
- Faster interconnect or more nodes
 - Evaluation of the algorithm should determine the choice
- Interaction of cluster software stack with interconnect
 - OS/DRM/MPI/compilers/libraries/developer tools
- Don't hesitate to ask for help or look for consultative expertise



Loosely Coupled Cluster

- Some number of computers on a private Ethernet network
- TCP/IP routes communications between nodes
- A 'portal' acts as the primary point of contact for people using the cluster
- Example: The Apple Workgroup Cluster for Bioinformatics



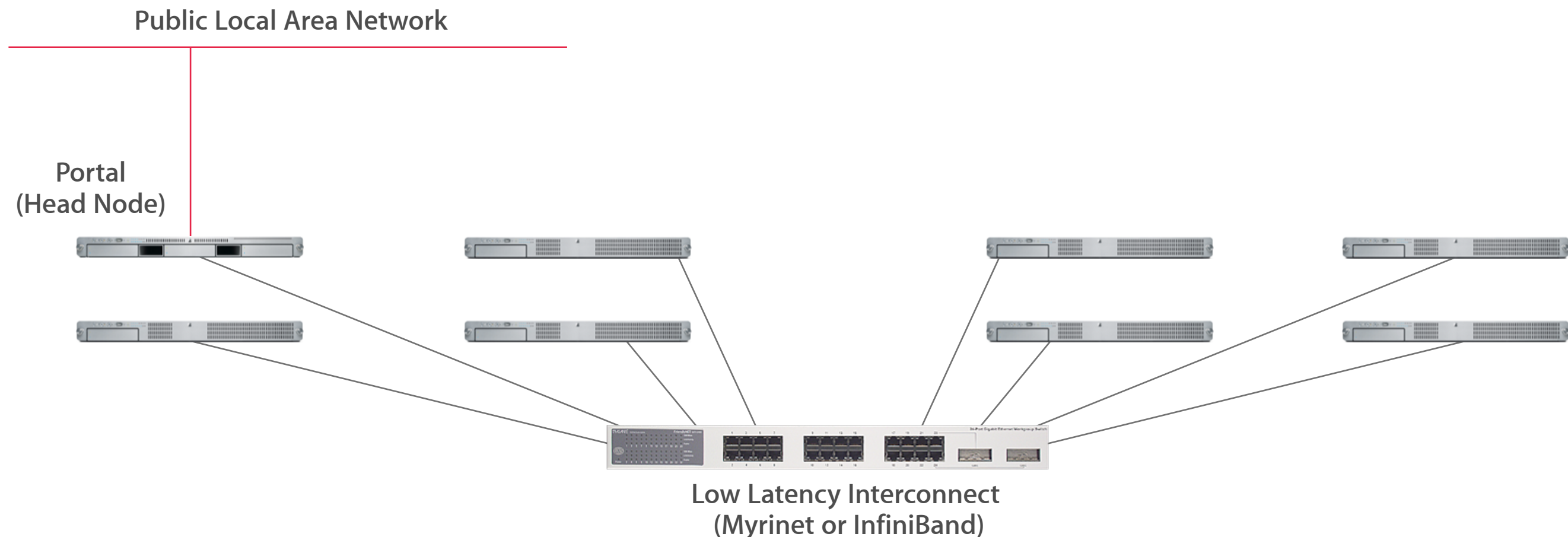
Gigabit Ethernet



Tightly Coupled Cluster

Uses low latency, high bandwidth interconnect

- Some number of computers connected by Myrinet or InfiniBand
- Proprietary protocol handles message passing, may implement MPI directly
- Required by 'tightly coupled' applications such as AMBER
- A 'portal' acts as the primary point of contact for people using the cluster



Myrinet (Myricom) InfiniBand



High-performance Interconnects

- Myrinet
 - Very well tested and highly reliable
 - Mature driver stack
- Infiniband
 - Open standard
 - Prices expected to drop precipitously



Comparing Interconnects

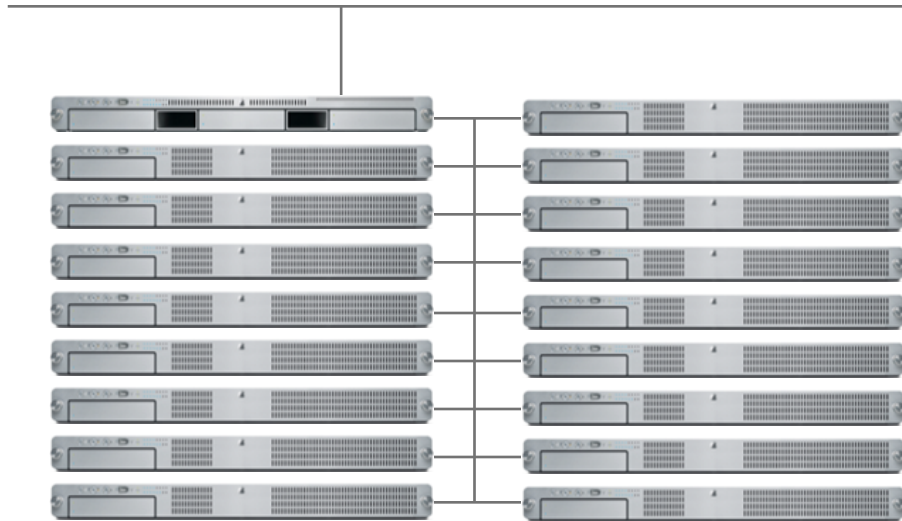
	GbE	Myrinet	Voltaire InfiniBand
Bandwidth	1 Gb	2.5 Gb	10 Gb
Latency	50 uSec	6 uSec	5 uSec
Linpack Network Efficiency	50%	60%	80%
Storage Connectivity	✗	✗	✓

What is a Cluster?

Varied components with a common goal

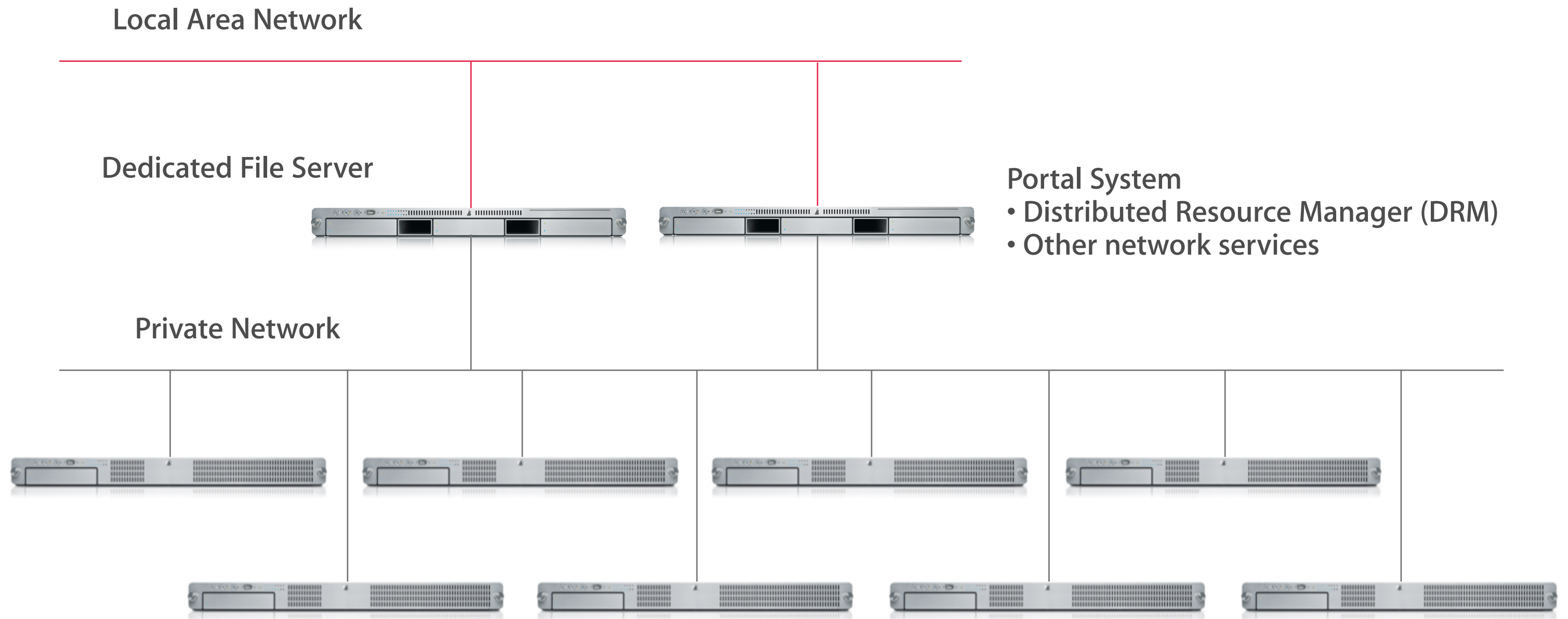
- 1 Some number of independently operable computers
- 2 High performance interconnection network
- 3 Software for controlling concurrent tasks (DRM)

Distributed Resource Manager (DRM)



Distributed Resource Management Software

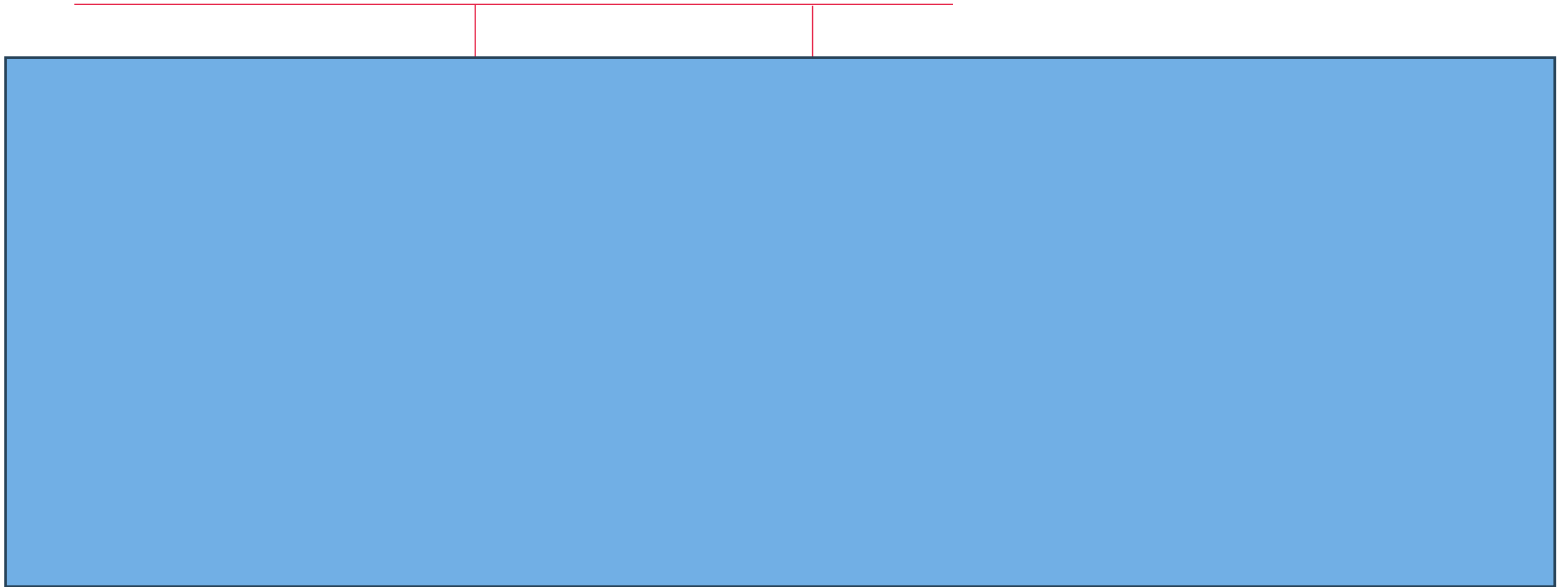
Turns a collection of cluster components...



Distributed Resource Management Software







Into a single virtual resource...

Local Area Network



Distributed Resource Management Software

Products available for Mac OS X

	Platform LSF	Powerful and flexible workload management software for deploying high-performance computing solutions.
	Sun Grid Engine	Sun's open source DRM software for deploying powerful compute farm solutions.
	OpenPBS	The Portable Batch System (PBS) is a flexible open source batch queueing and workload management system originally developed for NASA.
	PBS Pro by Altair	Commercial version of PBS goes beyond OpenPBS with additional features, such as enhanced fault tolerance, reliability and superior cluster support.
	iNquiry	Created by The BioTeam, this fully provisioned informatics cluster solution is installed on Xserve G5 systems in minutes from an Apple iPod.
	Xgrid	Apple's grid tool that supports both dedicated clusters and idle cycle utilization deployment. Supports basic batch scheduling.



Distributed Resource Management

Queueing and Scheduling

- Xgrid
- Sun Grid Engine
- OpenPBS and PBS Pro
- Pooch
- Platform LSF
- MAUI
- Condor

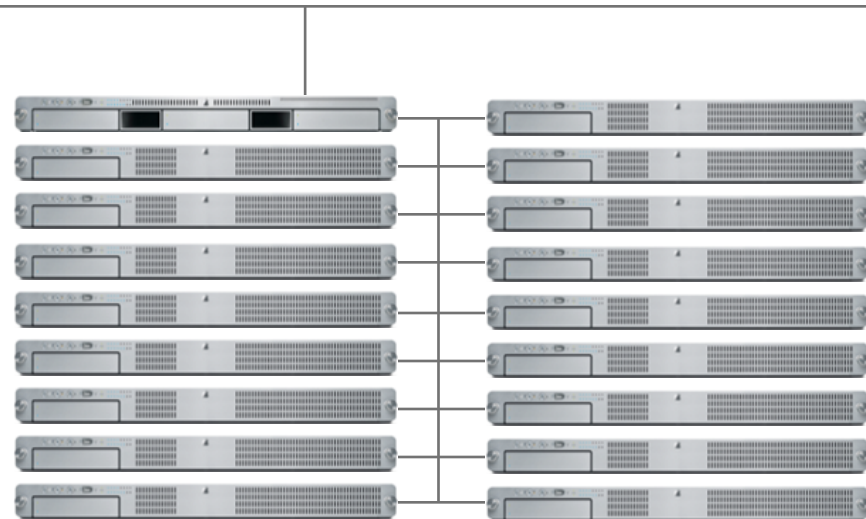


What is a Cluster?

Varied components with a common goal

Message Passing Interface (MPI)

Distributed Resource Manager (DRM)



- 1 Some number of independently operable computers
- 2 High performance interconnection network
- 3 Software for controlling concurrent tasks (DRM)
- 4 API for parallel application development (MPI)





Message Passing Interface (MPI)

MPI Basics






Enables parallel computing by allowing an app running across a cluster to pass results between nodes

- Has become the de-facto standard cluster savvy API
- Generally implemented as a library for use by developers
- Supports simple or complex application development schemes
- Provides access to parallel (cluster, grid, other) hardware for:
 - End users
 - Library writers
 - Tool developers



MPI and Other Parallel Computing Tools

Products available for Mac OS X

	MPICH	Open source, portable implementation of MPI, the standard for message-passing libraries.
	MPI Pro by MPI Software Technology	Commercial MPI solution with performance and feature enhancements.
	LAM/MPI	Local Area Multicomputer (LAM) MPI programming environment and development system for heterogeneous computers on a network.
	Linda and Paradise by Scientific Computing Associates	Proven and flexible tools for parallel and distributed computing.
	Pooch by Dager Research	Cluster management software for creating easy-to-use, high-performance parallel computers.



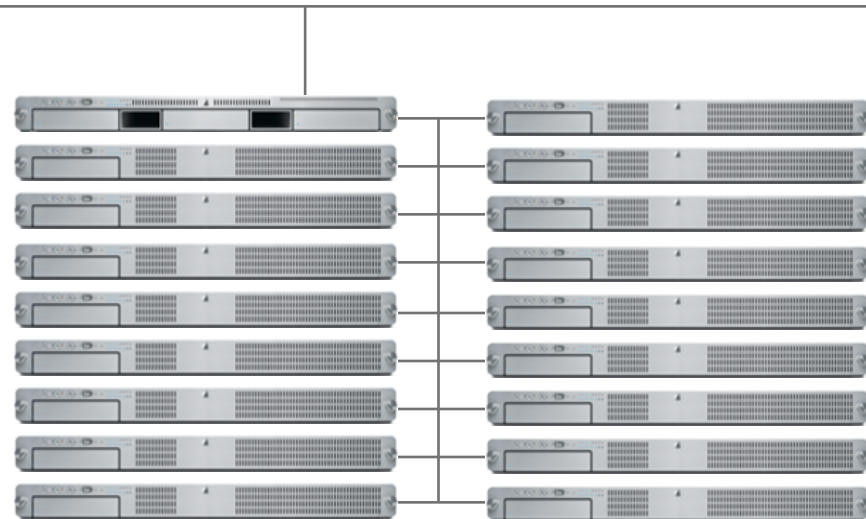
What is a Cluster?

Varied components with a common goal



Message Passing Interface (MPI)

Distributed Resource Manager (DRM)



- 1 Some number of independently operable computers
- 2 High performance interconnection network
- 3 Software for controlling concurrent tasks (DRM)
- 4 API for parallel application development (MPI)
- 5 Development tools for cluster-aware applications

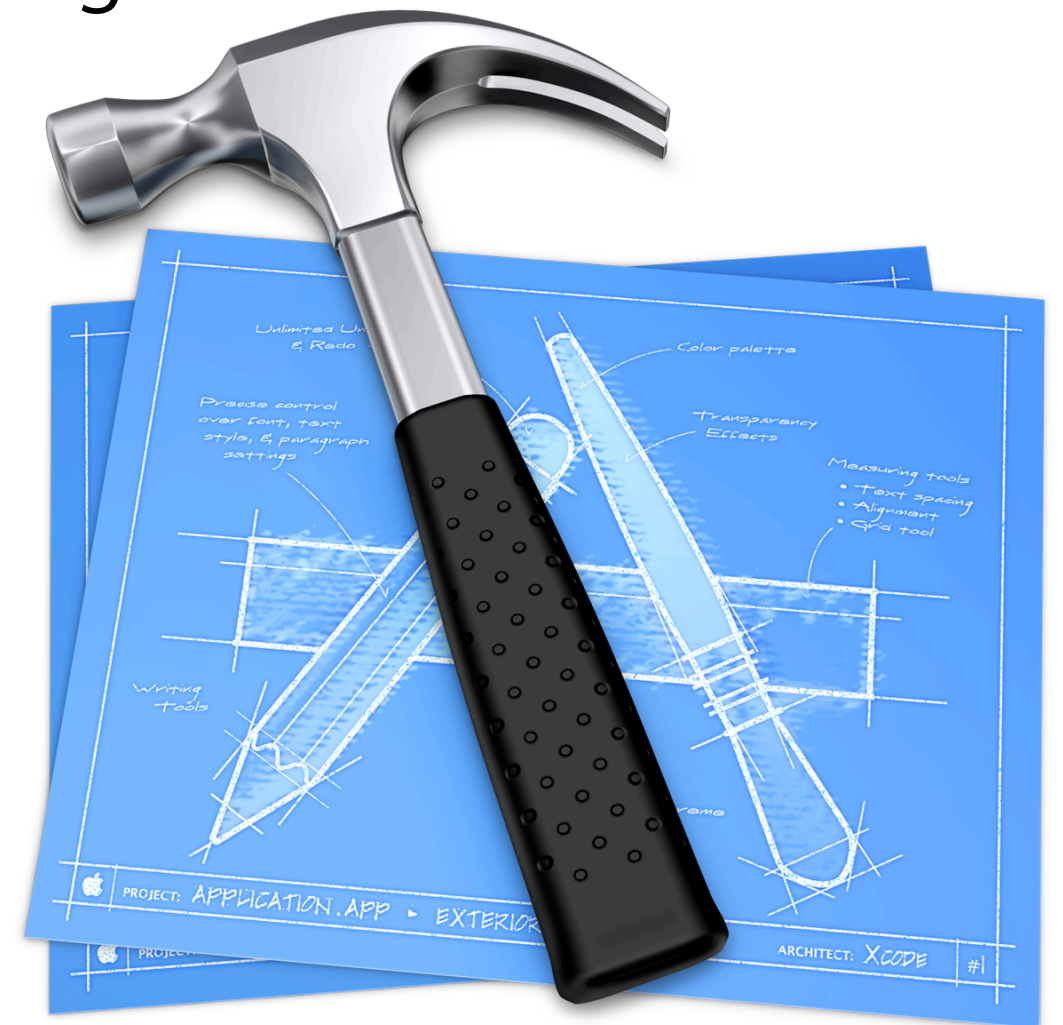


Xcode

The fastest way to create Mac OS X applications

- GCC 3.3
- Excellent support for C99, ANSI C++, and the C++ STL
- Includes GDB source-level debugger
- Works with C, C++, Objective-C, and other languages

FREE !!!



Compilers and Languages Courses

- Java
 - Standards-compliant optimized implementation
 - Included virtual machine, compiler, and debugger
- Legacy languages
 - Multiple implementations of Fortran F77 and F95
 - ANSI Common LISP and other LISP implementations
 - PowerPC assembly, plus multiple MIPS, x86, and other assembly virtual machines



Compilers

- Numerical Algorithms Group (NAG) f95
- Absoft F77, F90, and F95 compilers
- Veridian
 - VAST-F/AltiVec
- GNU Software Project
 - G77 for GCC 3.1
- IBM
 - XL Fortran
 - XL C/C++
- Auto-vectorizing GCC 4 in Mac OS X v10.4 !!



NAGWare f95
Compiler



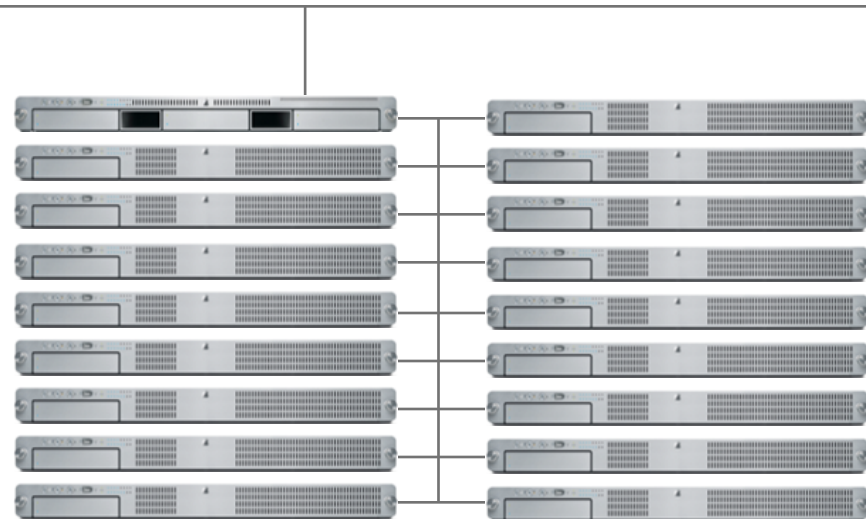
What is a Cluster?

Varied components with a common goal



Message Passing Interface (MPI)

Distributed Resource Manager (DRM)

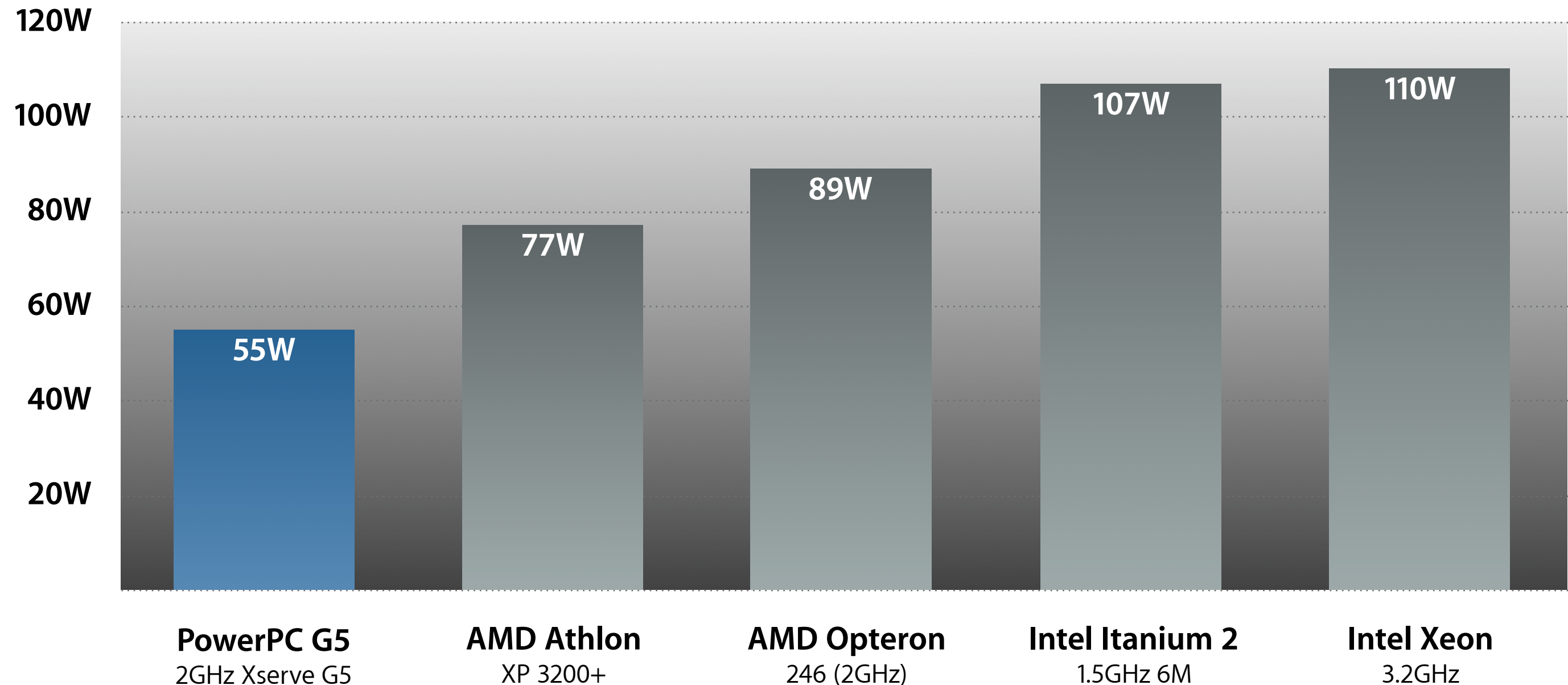


- 1 Some number of independently operable computers
- 2 High performance interconnection network
- 3 Software for controlling concurrent tasks (DRM)
- 4 API for parallel application development (MPI)
- 5 Development tools for cluster-aware applications
- 6 Physical infrastructure (space, power, HVAC)



Superior Power Efficiency

PowerPC G5 provides outstanding performance with low power consumption



*Maximum power draw. Information from manufacturers' data sheets as of January 3, 2004.

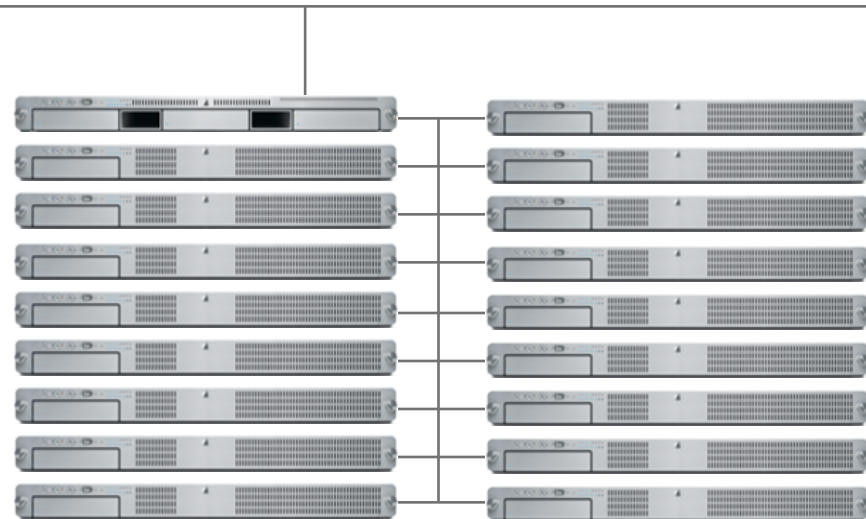
What is a Cluster?

Varied components with a common goal



Message Passing Interface (MPI)

Distributed Resource Manager (DRM)



- 1 Some number of independently operable computers
- 2 High performance interconnection network
- 3 Software for controlling concurrent tasks (DRM)
- 4 API for parallel application development (MPI)
- 5 Development tools for cluster-aware applications
- 6 Physical infrastructure (space, power, HVAC)
- 7 Administrative and diagnostic tools





Third-party Scientific Software

Open Source Applications

Emacs OpenOffice Tcl/Tk Fink xTools LaTeX
SPICE Staden Package GRASS CUVIEWER XEphem
Glimmer2 Perl SeqIO Artemis SEMPHY EMBOS Gammes
Ghostscript MUMmer NCBI BLAST Phred-Phrad/Swat/CrossMatch
DOE 2000 Elect Notebook Pine ClustalW MOLMOL
MPI FASTA HMMer WU BLAST PyMOL
OmniGene/OmniView Wise2.2.0 Apollo Genome Browser
NOMAD Apache Jakarta "R" "O"
BioPerl/Java/Python/DAS MySQL NCBI Toolkit
RasMOL Primer 3.09 PAUP XML/Ruby/TeX/CORBA
MolPro ACT Phylip 3.5c SIDB
xFree86 XCluster ARB Sun GRID Engine
GIMP Sequence Analysis Java TreeView



Productivity and Scientific Applications

Dev Tools

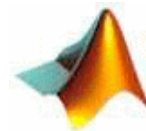
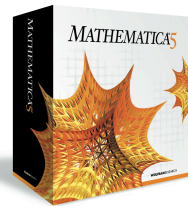


XL Fortran

absoft
development tools and languages



Math/Stat



MATLAB

SPSS®



Visualization



LabVIEW 7 Express



Instrumentation



 **Molecular Devices**

 **NATIONAL
INSTRUMENTS™**

 **StereoGraphics**



Productivity and Scientific Applications

Informatics



Vector **NTI**[®] Suite

 Silicon Genetics


 **Daylight**
Chemical
Information
Systems, Inc.

 **accelrys**

HPC

*TURBO*WORX




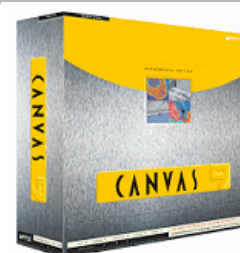
 **Sun**
microsystems
Sun Grid Engine

Platform[™]

Publishing

EndNote[®]

 Office v. X
for Mac



 **OpenOffice.org**
Source Project

Databases

ORACLE[®]



 **SYBASE**[®]

MySQL[™]



UNIX Sequence Analysis

BLAST, A/G-BLAST

HMMER

Smith-Waterman

EMBOSS

FASTA

ClustalW

Phylip, PAUP

UNIX 3D Structural Analysis

Chimera
AutoDock
FADE, PADRE
PyMOL
VMD
GROMACS

Commercial: Sequence Analysis

Accelrys: MacVector

InforMax[®]: VectorNTI

GeneCodes: Sequencher

Textco: GeneConstruction Kit

Gene Expression

Silicon Genetics: GeneSpring

Invitrogen: Pathways

BioDiscovery: Imagene

Image Analysis

- NIH: ImageJ
- Improvion: Volocity
- Scanalytics: IPLab
- QImaging
- QED Imaging





Some Clusters



Virginia Tech

“I’d never used a Mac before in my life. Within three days I’d made up my mind that Mac OS X and the new Macintosh G5 were the tools I wanted to use.”

Dr. Srinidhi Varadarajan, Associate Professor of Computer Science
and Terascale Computing Center Director, Virginia Tech





Top 3 Supercomputers*



Rank	#1	#2	#3
Name	Earth Simulator	ASCI Q	System X
Location	Yokohama, Japan	Los Alamos, USA	Blacksburg, USA
Rmax/Rpeak	35.86/40.96 TF	13.88/20.48 TF	10.28/17.60 TF
# Processors	5,120	8,192	2,200
CPU Type	500MHz NEC (NEC)	1.25GHz Alpha (Compaq)	2GHz PowerPC G5 (Apple)
Cost	\$300M	\$215M	\$7.5M
Manufacturer	NEC	HP	Self-made
Cost/GigaFlop	\$ 8366	\$ 15490	\$ 730

* TOP500 List for November, 2003. Please see www.top500.org for additional details.



COLSA, Corp. (U.S. Army)

1,566 nodes



Node Details

- Head Nodes—4 dual 2.0 GHz Xserve G5 units
 - Dual mirrored 80 GB HDD
 - 8 GB RAM
 - 1 CD-RW
 - 1 video card
- Compute Nodes—1562 dual 2.0 GHz Xserve G5 units
 - Single 80 GB HDD
 - 3.5 GB RAM
 - No CD-ROM or video card
- Total of 3132 CPUs, 8 Gflop/s per CPU = 25.056 Tflop/s



TM and © 2003 Apple Computer, Inc. All rights reserved.



Contact Info :

**Jatinder Bharadwaj -
jatinder.b@asia.apple.com**

**Rajiv Pillai -
rajiv@asia.apple.com**