

Introduction to BioHPC Lab

BioHPC Lab Workshop

Jaroslav Pillardy

Bioinformatics Facility
Institute of Biotechnology
Cornell University

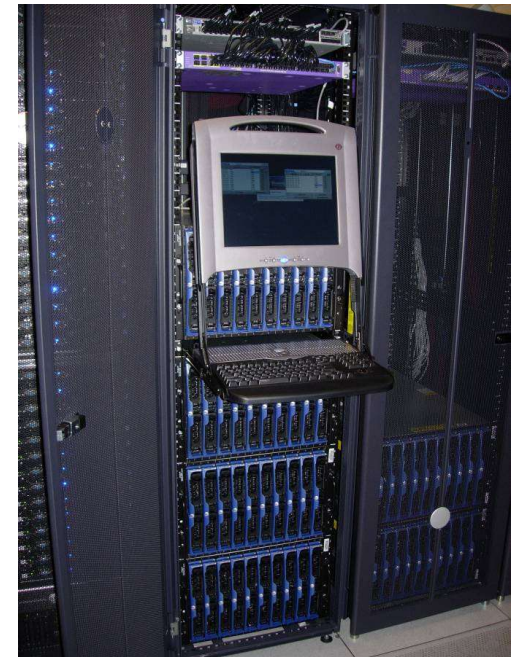
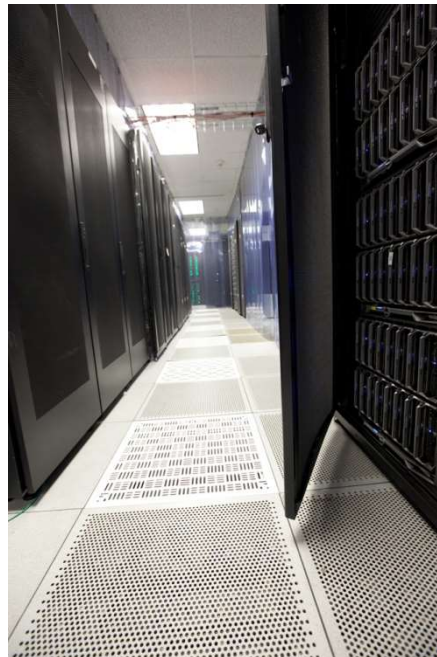
<http://cbsu.tc.cornell.edu/lab/lab.aspx>

[http://cbsu.tc.cornell.edu/lab/doc/Introduction to BioHPC Lab v3c.pdf](http://cbsu.tc.cornell.edu/lab/doc/Introduction%20to%20BioHPC%20Lab%20v3c.pdf)

BioHPC Laboratory

BioHPC Laboratory is a computational resource configured and optimized for the needs of computational biology and bioinformatics

- Available to Cornell and external users
- Provides access to computing, storage and software (over 300 titles)
- Located in Rhodes Hall and accessible remotely and on-site



BioHPC Lab

Renting computing resources

Hosting computing resources

Storage

Consulting and education

BioHPC Lab: computing

Two ways of using BioHPC Lab computing resources:

- Buy hours and run computations on BioHPC Lab workstations/servers

Only pay for the hours you need, avoid problems with maintaining your own hardware, software and resource allocation.

- Buy your own hardware (or better ask us to buy it for you) and host it in BioHPC Lab

If you need a special hardware, or you expect to use it 24/7, you can still avoid problems related to maintaining your own hardware, software and resource allocation by hosting the machine with the Lab

BioHPC Lab: hosting

Buy your own hardware and host it in BioHPC Lab

- Fully customizable hardware – buy just what needed
- Access to all software and storage – same as rental
- Machine usage restricted to group: usage may be regulated internally (all have access) or by reservations (users need to reserve machine)
- No root access – installations that require full admin rights may be done by us or in a customized Docker container
- Annual fee (\$1,039.17)
- Use Lab scheduler or install scheduler per request
- Storage servers can also be hosted

BioHPC Lab: multi-machine hosting

- Annual fee is smaller for following identical hosted servers (first server \$1,039.17 following ones \$611.75).
- Machines can be joined together using SGE scheduler as desired
- We can host a separate cluster storage (Lustre or Gluster)

BioHPC Lab: storage

- 1013TB of networked storage available in two volumes: 700TB Lustre volume and 313TB Gluster volume
- Very robust and scalable architecture: cluster storage based on RAID6/RAID7 servers connected by Lustre or Gluster, new servers can be added to expand storage.
- Very affordable! \$91.35 per TB per year is lower than even Amazon archival storage
- Users get free storage allocations with the accounts

BioHPC Lab: Lustre storage

- High performance scalable parallel storage system
- Metadata (file names and other information) separated from storage itself
- Storage servers use ZFS raidz2 (RAID6 equivalent) file system
- Main system for fast access – home directories, storage groups

BioHPC Lab: Backup service

- We are going to introduce a backup service soon (Feb 2017)
- Users will be able to choose backup options using Lab website (what to backup, how many versions etc)
- Backup servers (currently 270TB) are located in different building (Weill Hall)

BioHPC Lab: software

- BioHPC Lab is pre-configured for bioinformatics with software and related software infrastructure (libraries, development tools etc.).
- All software installed as a response to our or our users computing needs.
If you need a program that is not installed, ask us. We may install it, it depends on possible usage level and time investment required to deploy.
- 326 titles as of 1/6/2017
- Common genomic data is available locally in the Lab: sequence and annotation databases, preformatted for common programs

BioHPC Lab hardware infrastructure



interactive workstations with nice consoles (“general”):

4 4-core, 24GB RAM, 4TB HDD
(cbsuwrkst1,2,3,4 – can be used directly in 625 Rhodes)



“general” remote workstations:

32 8-core, 16GB RAM, 1TB HDD
(cbsum1c1b0NN, cbsum1c2b0NN)



“medium memory” remote workstations

1 16-core, 64GB RAM, 1TB HDD
16 12-core, 128GB RAM, 4TB HDD, 1TB SSD
(cbsummNN)



“large memory” remote workstations

6 64-core, 512GB RAM, 12TB HDD
2 96-core, 512GB RAM, 12TB HDD, 1TB SSD
2 112-core, 512GB RAM, 12TB HDD, 1TB SSD
(cbsulmNN)
1 64-core, 1024GB RAM, 9TB HDD, 1TB SSD
(cbsuem01)



BioHPC Lab hardware infrastructure



networked storage: total 1013TB available in two volumes

313TB Gluster cluster (5 servers)

700TB Lustre cluster (12 servers)



login machines (cbsulogin, cbsulogin2)

2 12-core, 64GB RAM, 1.5TB HDD



Setting up an account

- In order to get an account fill out account request form online
<https://cbsu.tc.cornell.edu/NewUserRequest.aspx>
- All Cornell employees, students and alumni are eligible
- Any collaborators of Cornell employees, students and alumni are eligible
- External users requests are considered on case-by-case basis, depending on Lab overall usage.

File Edit View History Bookmarks Favorites Tools Help

Bioinformatics Internal Sit... X +

https://cbsu.tc.cornell.edu/Default.aspx Search

CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search ☐ Cornell Pages ☐ Cornell People

Home BRC Services **BioHPC Lab** NGS Data Contact Us Login

institute of biotechnology >> brc >> bioinformatics >> internal >> bioinformatics

BIOINFORMATICS INTERNAL HOME

Welcome to the internal website of **Biotechnology Resource Center** (BRC). Bioinformatics Facility is Cornell University core facility.

This website integrates dynamic computational and training resources for the **Computational Biology Service Unit** (CBSU). BRC Bioinformatics.

Workshops
Office Hours
BioHPC Computing Lab
BioHPC NGS

If you would like to...

- BioHPC Lab
- Announcements
- User Guide
- Software
- Hardware
- Pricing
- Reservations
- My Reservations
- Office Hours
- Request New User Account

BIOINFORMATICS FACILITY


You can manage all your Lab resources and find answers to many questions on Lab website


<http://cbsu.tc.cornell.edu/lab/lab.aspx>

← → http://cbsu.tc.cornell.edu/lab/userguide.aspx

BioHPC Lab: User Guide

File Edit View Favorites Tools Help


 CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search  ☒ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab BioHPC Web Contact Us Login

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: user guide

BIOHPC LAB: USER GUIDE

 BIOINFORMATICS FACILITY

Overview Quick Start Guide Accounts Access Storage Storage Space Databases Software Workflows FAQ

Workstations

There are several types of workstations available in the BioHPC Laboratory: *interactive remote (general medium memory large memory)* valid research workstation documents are especially workstation configurations

Reservations

Only reservations can be made during business hours. If a reservation has expired, it can be renewed by logging in. Please remember to remove any reservations you do not need to avoid blocking access for others and losing your Lab Credit Account hours. Only actually used hours are charged, if you cancel your reservation before it starts nothing is charged, if you cancel before it ends, only the actual hours between start and end are charged. NOTE: "time used" is defined as the wall clock time

There is lots of information in "User Guide", including some useful workflows (like "RNA-Seq" workflow)

<http://cbsu.tc.cornell.edu/lab/userguide.aspx>

100%

File Edit View History Bookmarks Favorites Tools Help

Bioinformatics Internal Sit... X +

https://cbsu.tc.cornell.edu/Default.aspx Search

CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search ☐ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab NGS Data Contact Us Login

institute of biotechnology >> brc >> bioinformatics >> internal >> bioinformatics internal site home

BIOINFORMATICS INTERNAL SITE

HOME

If you have an account you can login here

Welcome to the internal website of [Biotechnology Resource Center Bioinformatics Facility](#) (Computational Biology Service Unit, CBSU). BRC Bioinformatics Facility is Cornell University core facility for computational biology and bioinformatics.

This website integrates dynamic computational and training resources of the facility.
For more information about the facility please go to the [facility main website](#).

developments please join our [mailing list](#).

BioHPC Lab Login
BioHPC Lab Password Reset
BioHPC Request New User


Forgot password? Reset it here – it will be sent to your registered e-mail. All you need to remember is your Lab id – usually same as your Cornell Netid.

Need an account – fill the form

← → <http://cbsu.tc.cornell.edu/Default.aspx> 🔍 🏠 ☆ ⚙️

Bioinformatics Internal Site ... x

File Edit View Favorites Tools Help



CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search ☒ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab BioHPC Web Contact Us User: jarekp

[institute of biotechnology](#) >> [brc](#) >> [bioinformatics](#) >> [internal](#) >> [bioinformatics internal site home](#)

BIOINFORMATICS HOME

Keep your data, especially e-mail up to date! All communications depend on e-mail ...

Welcome to the internal website of [Biotechnology Resource Center Bioinformatics Facility](#) (Computational Biology Service Unit, CBSU). Bioinformatics Facility is Cornell University core facility for computational biology and bioinformatics.

This website integrates dynamic computational and training resources of the facility.
For more information about the facility please go to the [main website](#).

Workshops

Office Hours

BioHPC Computing Lab

BioHPC Web Computing

If you would like to receive notifications about facility events, services and new developments please join our [mailing list](#).

Manage Credit Accounts

My Storage

Profile

Reservations

My Reservations

My Groups

Change Password

Logout

[Change your password](#)

<http://cbsu.tc.cornell.edu/lab/projects.aspx> 100%

Getting started with a new account

- You need hours: create and fund your own Lab Credit Account or get added to one
- Get extra storage if needed – all users get free storage allocations, but it may not be enough
- Verify that your software is available and read instructions
- Transfer data to your Lab storage
- Make reservation(s)
- Connect to reserved workstations
- *Compute!*

Lab Credit Accounts

In order to reserve workstations you need to have hours available in your Lab Credit Account.

Multiple users can be assigned to the same Lab Credit Account, but only one person (owner) can manage it: add hours, add/remove users, view usage etc.

If your group already has a Lab Credit Account you can ask the owner to be added to it, and get instant access to its hours.

You can set up your own Lab Credit Account and buy hours using Cornell Account or a credit card.

Lab Credit Accounts

There are **3 types of workstations publicly available** linked to **3 types of hours**:

- **general**
cbsum1c1*, cbsum1c2*, cbsuwrkst*
- medium memory (**cbsum01**)
cbsum01, cbsumm*
- large memory (**cbsum02**)
cbsum*, cbsuem01

[We are working on GPU computing and special database computing]

<http://cbsu.tc.cornell.edu/Lab/Pricing.aspx>

File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: Pricing

https://cbsu.tc.cornell.edu/Lab/Pricing.aspx

cbsulm01
This pricing applies to all medium memory generally accessible workstations, i.e. cbsulm01(16 cores; 64GB RAM; 1TB HDD) and cbsummXX machines (24 cores; 128GB RAM; 4TB HDD; 1TB SSD).

unit	hours	unit cost (Cornell)	cost per hour (Cornell)		unit cost (external)	cost per hour (external)	
			server	core		server	core
200 hours	200 hours	\$158.76	\$0.79	\$0.05 (16 cores) \$0.03 (24 cores)	\$190.51	\$0.95	\$0.06 (16 cores) \$0.04 (24 cores)
1 month	730 hours	\$463.57	\$0.64	\$0.04 (16 cores) \$0.03 (24 cores)	\$556.28	\$0.76	\$0.05 (16 cores) \$0.03 (24 cores)
6 months	4,380 hours	\$2,225.15	\$0.51	\$0.03 (16 cores) \$0.02 (24 cores)	\$2,670.18	\$0.61	\$0.04 (16 cores) \$0.03 (24 cores)
1 year	8,760 hours	\$3,560.23	\$0.41	\$0.03 (16 cores) \$0.02 (24 cores)	\$4,272.28	\$0.49	\$0.03 (16 cores) \$0.02 (24 cores)

cbsulm02
This pricing is for access to large memory machines: cbsulm02-07 machines [64 cores, 512GB RAM and 13TB HDD]; cbsulm08-10 [64 cores, 512GB RAM, 9TB HDD, 1TB SSD]; cbsulm12-13 [96 cores, 512GB RAM, 12TB HDD, 1TB SSD].

unit	hours	unit cost (Cornell)	cost per hour (Cornell)		unit cost (external)	cost per hour (external)	
			server	core		server	core
200 hours	200 hours	\$300.18	\$1.50	\$0.02 (96 cores) \$0.02 (64 cores) \$0.01 (112 cores)	\$360.22	\$1.80	\$0.02 (96 cores) \$0.03 (64 cores) \$0.02 (112 cores)
1 month	730 hours	\$876.53	\$1.20	\$0.01 (96 cores) \$0.02 (64 cores) \$0.01 (112 cores)	\$1,051.84	\$1.44	\$0.02 (96 cores) \$0.02 (64 cores) \$0.01 (112 cores)
6 months	4,380 hours	\$4,207.35	\$0.96	\$0.01 (96 cores) \$0.02 (64 cores) \$0.01 (112 cores)	\$5,048.82	\$1.15	\$0.01 (96 cores) \$0.02 (64 cores) \$0.01 (112 cores)
1 year	8,760 hours	\$6,731.77	\$0.77	\$0.01 (96 cores) \$0.01 (64 cores) \$0.01 (112 cores)	\$8,078.12	\$0.92	\$0.01 (96 cores) \$0.01 (64 cores) \$0.01 (112 cores)

Up-to-date price list is always online. Prices are updated at the end of June, if they change at all.


The more time you buy at a time the cheaper it gets.


BioHPC Lab hours NEVER expire, so you can buy a large block cheap and use them in a long term.

← → http://cbsu.tc.cornell.edu/Default.aspx

Bioinformatics Internal Site ... x

File Edit View Favorites Tools Help

 CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search  ☒ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab BioHPC Web Contact Us User: jarekp

institute of biotechnology >> brc >> bioinformatics >> internal >> bioinformatics internal site home

BIOINFORMATICS INTERNAL HOME

manage your Lab Credit Accounts

Welcome to the internal website of [Biotechnology Resource Center Bioinformatics Facility](#) (Computational Biology Service Unit, CBSU). The Bioinformatics Facility is Cornell University core facility for computational biology and bioinformatics.

This website integrates dynamic computational and training resources of the facility.
For more information about the facility please go to the [facility main website](#).

[Workshops](#)
[Office Hours](#)
[BioHPC Computing Lab](#)
[BioHPC Web Computing](#)

If you would like to receive notifications about facility events, services and new developments please join our [mailing list](#).

- Manage Credit Accounts
- My Storage
- Profile
- Reservations
- My Reservations
- My Groups
- Change Password
- Logout

http://cbsu.tc.cornell.edu/lab/projects.aspx 100%


http://cbsu.tc.cornell.edu/Lab/projects.aspx

BioHPC Lab: My Lab Credit ... BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: my lab credit accounts

BIOHPC LAB: MY LAB CREDIT ACCOUNTS



Filter by:

Name: * Description: *

☐ Show inactive accounts

Order by

#	Name	Owner	Type	Hours Available	Hours Used	Hours Reserved	Other Users	Active?	Created	Description	Action
7	jarekpp_general	jarekpp	general	624.96	142.04	0.00	3	yes	11/29/2011 2:49:15 PM		Edit Credit Account Credit Account Users Reservations Add Hours Purchase History Deactivate Account
11	cbsulm02_jarekpp	jarekpp	cbsulm02	1137.00	0.00	0.00	0	yes	11/29/2011 5:34:55 PM		Edit Credit Account Credit Account Users Reservations Add Hours Purchase History Deactivate Account
154	cbsulm01	jarekpp	cbsulm01	0.00	0.00	0.00	0	yes	7/23/2013 12:49:18 PM		Edit Credit Account Credit Account Users Reservations Add Hours Purchase History Deactivate Account

3 Records found. Show

100%


http://cbsu.tc.cornell.edu/Lab/project.aspx

BioHPC Lab: Lab Credit Account x BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: lab credit account

BIOHPC LAB: LAB CREDIT ACCOUNT



New

Credit Account #	TBD
Name	Jarek's general account
Type	<div><div>cbsulm01:Medium memory general workstations.; e.g. cbsulm01</div><div>cbsulm02:512GB RAM workstations; e.g. cbsulm03</div><div>general:Interactive and remote workstations; e.g. cbsum1</div></div>
Active	Yes <input type="checkbox"/>
Description	<div>For testing</div>

Website credentials: user: jarekpp [BioHPC Lab]
[logout](#)

100%

Choose type of hours
(workstations)

You may need an account
for each type

Browser window showing the BioHPC Lab: My Lab Credit Accounts page. The URL is <http://cbsu.tc.cornell.edu/Lab/projects.aspx>. The page title is "BIOHPC LAB: MY LAB CREDIT ACCOUNTS".

Navigation links: [institute of biotechnology](#) >> [brc](#) >> [bioinformatics](#) >> [internal](#) >> [biohpc lab: my lab credit accounts](#)

BIOHPC LAB: MY LAB CREDIT ACCOUNTS

Filter by:

Name: * Description: *

☐ Show inactive accounts

Order by: Created Ascending

#	Name	Owner	Type	Hours Available	Hours Used	Hours	Other	?	Created	Description	Action
7	jarekpp_general	jarekpp	general	624.96	142.04	0.00	3	yes	11/29/2011 2:49:15 PM		Edit Credit Account Credit Account Users Reservations Add Hours Purchase History Deactivate Account
11	cbsulm02_jarekpp	jarekpp	cbsulm02	1157.00	0.00	0.00	0	yes	11/29/2011 5:34:55 PM		Edit Credit Account Credit Account Users Reservations Add Hours Purchase History Deactivate Account
154	cbsulm01	jarekpp	cbsulm01	0.00	0.00	0.00	0	yes	7/23/2013 12:49:18 PM		Edit Credit Account Credit Account Users

3 Records found. Show

Annotations:

- manage users (points to the "Credit Account Users" link in the Action column)
- purchase hours (points to the "Purchase History" link in the Action column)
- transfer hours, you can convert them any time (points to the "Transfer hours between accounts" button)


http://cbsu.tc.cornell.edu/Lab/labacctu.aspx?indx=7

BioHPC Lab: Credit Account... x BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: credit account users management

BIOHPC LAB: CREDIT ACCOUNT USERS MANAGEMENT



Credit Account 'jarekpp_general'

Filter by:

Lab ID * go

Last name * go

Cornell ID * go

Created >= MM/DD/YYYY and < MM/DD/YYYY go

Email * go

Order by Created Descending

First Name	Last Name	Lab ID	Cornell ID	E-mail	Institution	Department	Created	Action
Jarek	Pillardy	jarekpp		jarekpp@yahoo.com	Cornell University	CBSU	6/22/2011 1:32:12 PM	
Qi	Sun	qisun	qs24	qs24@cornell.edu	Cornell University	CBSU	5/20/2011 3:06:00 PM	Delete
Robert	Bukowski	bukowski	rb299	bukowski@cornell.edu	Cornell University	Biotech	11/18/2010 5:14:47 PM	Delete
Jaroslav	Pillardy	jarekp	jp86	jp86@cornell.edu	Cornell University	Biotech	11/18/2010 5:11:35 PM	Delete

4 Records found. Show 1-4

Add user with labid to the Lab credit account Add


add users, can be comma-separated list of Lab id's

delete user

http://cbsu.tc.cornell.edu/Lab/transfer.aspx

BioHPC Lab: Transfer hours... x BioHPC Lab: Pricing

File Edit View Favorites Tools Help


 CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search ☐ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab BioHPC Web Contact Us User: jarekpp

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: transfer hours between lab credit accounts

BIOHPC LAB: TRANSFER HOURS BETWEEN LAB CREDIT ACCOUNTS

 BIOINFORMATICS FACILITY

FROM: 'cbsulm02_jarekpp' (cbsulm02) 1157.00 hrs left 100 hours

TO: 'jarekpp_general' (general) 624.96 hrs left 344 hours

conversion factor: 1 hr => 3.440 hr

[Transfer](#)

Website credentials: user: jarekpp [BioHPC Lab]
[logout](#)

hours are converted using their price ratios, so no gain/loss of value

100%

Getting started with a new account

- ✖ You need hours: create and fund your own Lab Credit Account or get added to one
- Get extra storage if needed – all users get free storage allocations, but it may not be enough
- Verify that your software is available and read instructions
- Transfer data to your Lab storage
- Make reservation(s)
- Connect to reserved workstations
- *Compute!*

http://cbsu.tc.cornell.edu/Lab/labres.aspx

BioHPC Lab: Reservations x BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: reservations

BIOHPC LAB: RESERVATIONS

Interactive Workstations
Remote Workstations (general)
Remote Workstations (medium memory)
Remote Workstations (large memory)
Restricted Workstations

at. Lab Credit Account of type "cbsulm02" is required.
Total of 6 workstations available

choose type of machines

choose credit account – only compatible accounts are listed

Display reservations from February 17, 2014 for 30 days Go!

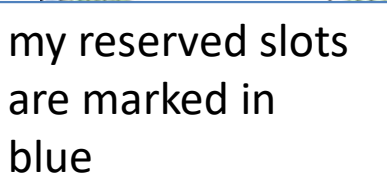
New reservation from February 17, 2014 3:00pm to February 17, 2014 3:00pm for machine cbsulm03 with Lab credit account 'cbsulm02_jarekpp' owner:jarekpp 1,157.0hrs left Reserve!

You can delete your reservations by clicking on [x], you can modify your reservations by clicking on them, you can add a new reservation by clicking on the appropriate "AVAILABLE" text or in the box above.

choose machine

click on "available" link to start in time slot you would like to use

	cbsulm05 Linux (RedHat 6.4) Red Barn Server 2 64 cores; 512GB RAM; 13TB HDD; VM supported Credit account: cbsulm02	cbsulm08 Linux (RedHat 6.4) Red Barn Server 3 64 cores; 512GB RAM; 9.4TB HDD; 1TB SSD; VM supported Credit account: cbsulm02	cbsulm09 Linux (RedHat 6.4) Red Barn Server 3 64 cores; 512GB RAM; 9.4TB HDD; 1TB SSD; VM supported Credit account: cbsulm02	cbsulm10 Linux (RedHat 6.4) Red Barn Server 3 64 cores; 512GB RAM; 9.4TB HDD; 1TB SSD; VM supported Credit account: cbsulm02
Mon Feb 17 2014	jaw358 ALL DAY	zehong ALL DAY	keh233 ALL DAY	keh233 ALL DAY
Tue Feb 18 2014	jaw358 ALL DAY	zehong ALL DAY	keh233 ALL DAY	keh233 ALL DAY
Wed Feb 19 2014	jaw358 ALL DAY	zehong UNTIL 05:00 PM	keh233 ALL DAY	keh233 ALL DAY
Thu Feb 20	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Fri Feb 21	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Sat Feb 22	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Sun Feb 23	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Mon Feb 24	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Tue Feb 25	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Wed Feb 26	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE
Thu Feb 27 2014	AVAILABLE	AVAILABLE	AVAILABLE	AVAILABLE



available slots are
marked in green

reserved slots are
marked in red

http://cbsu.tc.cornell.edu/Lab/labresman.aspx?indx=29076&cuid=jarekpp

BioHPC Lab: My Reservations x BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: my reservations

BIOHPC LAB: MY RESERVATIONS

adjust dates and times

Change Reservation

Proposed reservation is shown in black. You have to click "Reserve!" button in order to finalize

[Manage all my active reservations](#)

Display reservations from February 17, 2014 for 30 days Go!

Modify reservation #29076 from February 20, 2014 12:00am to February 27, 2014 12:00am for cbsulm09 in remote workstations (large memory) with Lab credit account 'cbsulm02_jarekpp' owner:jarekpp 989.0hrs left Preview Reserve!

preview new dates/times

You can delete your reservations by clicking on [x], you can modify your reservations by clicking on them, you can add a new reservation by clicking on the appropriate "AVAILABLE" text or in the box above.

	cbsulm09 Linux [CBSU]
Mon Feb 17 2014	1g356 UNTIL 03:30 PM AVAILABLE
Tue Feb 18 2014	AVAILABLE
Wed Feb 19 2014	AVAILABLE
Thu Feb 20 2014	jarekpp 12:00 AM - EOD
Fri Feb 21 2014	jarekpp ALL DAY
Sat Feb 22 2014	jarekpp ALL DAY
Sun Feb 23 2014	jarekpp ALL DAY
Mon Feb 24 2014	jarekpp ALL DAY
Tue Feb 25 2014	jarekpp ALL DAY

current (edited)
reservation in black

←

→

Ⓢ

http://cbsu.tc.cornell.edu/Lab/labresman.aspx?cntrl=635282463175003644&cuid=jarekpp


🔍 ↻ 🏠 ☆ ⚙

BioHPC Lab: My Reservations × BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: my reservations

BIOHPC LAB:
MY RESERVATIONS

BIOINFORMATICS FACILITY

change dates/times or account

Manage My Reservations

My active reservations (reservations starting in future are marked in red):

Res #	Start	End	Computer	OS	System info	Other users	Credit Account	Action	VNC port #
29076	2/20/2014 12:00:00 AM	2/27/2014 12:00:00 AM	cbsulm09	Linux	Red Barn Server 3 64 cores; 512GB RAM; 9.4TB HDD; 1TB SSD; VM supported		cbsulm02_jarekpp	Change Cancel	

Other active reservations I can access (reservations starting in future are marked in red):
None

You can connect to your Linux reserved workstations using VNC protocol at from this page, for more on VNC please read "Access with VNC" in the Lab's [User Guide](#).


Add user with labid to my reservation #


New reservation from to for the first available computer in with

Go To Main Reservations Page:

Website credentials: user: jarekpp [BioHPC Lab]
[logout](#)

©2013 Institute of Biotechnology

Cornell University

NYSTAR[®] designated
Center For
Advanced Technology

http://cbsu.tc.cornell.edu/lab/labresman.aspx?cntrl=635282467832466622&cuid=jarekpp

BioHPC Lab: My Reservations x BioHPC Lab: Pricing

File Edit View Favorites Tools Help

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: my reservations

BIOHPC LAB: MY RESERVATIONS

reservations I own

Manage My Reservations

My active reservations (reservations starting in future are marked in red):

Res #	Start	End	Computer	OS	System info	Other users	Credit Account	Action	VNC port #
29079	2/17/2014 3:13:01 PM	2/19/2014 3:00:00 PM	cbsum1c2b009	Linux	Dell PowerEdge M600 8 cores; 16GB RAM; 1TB HDD; VM supported		jarekpp_general	Change Cancel Connect VNC Reset VNC	

Other active reservations I can access (reservations starting in future are marked in red):

Res #	Start	End	Computer	OS	System info	Owner	Other users	Credit account	Action	VNC port #
29078	2/17/2014 3:10:22 PM	2/21/2014 3:00:00 PM	cbsum1c2b015	Linux	Dell PowerEdge M600 8 cores; 16GB RAM; 1TB HDD; VM supported	jarekpp	jarekpp bukowski qisun	CBSU Collaboration	Connect VNC Reset VNC	

You can connect to your Linux reserved workstations using VNC protocol at 1280x800 from this page, for more on VNC please read "Access with VNC" in the Lab's [User Guide](#).

other users' reservations I am allowed to use

Add user with labid to my reservation # Add!

New reservation from February 17, 2014 3:00pm to February 17, 2014 3:00pm for the first available computer in inter Go!

Go To Main Reservations Page: Inter allow other users to use my reserved machine My Reservations History

100%

Reservations

You can only make reservation if you have enough hours of appropriate type.

Your hours will be “reserved” when you make the reservation so you cannot use them twice – but not immediately deducted.

Only actually used hours are charged, if you cancel your reservation before it starts nothing is charged, if you cancel before it ends only the actual hours between start and cancel are charged.

NOTE: “Time used” is defined as the wall clock time elapsed when your reservation is active - it has nothing to do with how much you actually used the CPU/RAM during this time. "Time used" reflects the span for which you had the workstation reserved.

Reservations: new options

We are redesigning reservation system to improve user experience

- One type of hours to buy, consumed at different rate depending on hardware
- Annual membership allowing unlimited capped usage. Unlimited hours, but limited number of concurrent reservations. Cost will vary depending on membership hardware bias.

Reservations

What happens when a reservation ends, but you are still working?

- You will not be able to login to the machine anymore.
- If you are logged in you will stay logged in until the user from the next reservation logs in.
- Your programs will continue to run, as long as the machine is not used – this is to give you time to extend reservation if you need it.
- When a person that has the next reservation (now current) logs in all your programs and processes will be killed and you will be logged out.

Reservations

What if I am running a program and need to end the reservation immediately when the program ends?

- Run the program from a *script* – more about scripting on “Linux for Biologists”.
- After a line with program name add the following command
/programs/bin/labutils/endres.pl

```
#!/bin/bash
```

```
/home/myid/myprogram [options]
```

```
/programs/bin/labutils/endres.pl
```

Getting started with a new account

✖ You need hours: create and fund your own Lab Credit Account or get added to one

- Get extra storage if needed – all users get free storage allocations, but it may not be enough
 - Verify that your software is available and read instructions
 - Transfer data to your Lab storage
- ✖ Make reservation(s)
- Connect to reserved workstations
 - *Compute!*

Storage

- **Networked storage**

Very large storage (700TB+313TB), access limited by network speed, much slower than local storage. *Unsuitable for direct computing*. Very good for storing data long-term or sharing data between workstations – networked storage is the same on all machines.

- **Local storage**

Fast storage, especially on large memory and medium memory workstations. Small – between 1TB (general) and 12TB (large memory). *Designed to be used for computations*.

Storage

Linux directory structure is *continuous*, i.e. regardless of the physical location of storage it all seems to be part of one directory tree starting from root (/).

Not easy to tell which storage is local and which global just by a name.

/home/jarekp

/usr/local

/workdir/jarekp

/shared_data

/local_data

Storage

If in doubt “df -h” lists all storage devices

```
jarekp@cbsudesktop01:~  
login as: jarekp  
jarekp@cbsudesktop01's password:  
Last login: Tue Oct 11 16:52:18 2016 from clownfish.tc.cornell.edu  
-----  
Welcome to BRC Bioinformatics Facility BioHPC Lab  
server information: localhost, 2 cores, 8GB RAM, RedHat 7.1  
-----  
[jarekp@cbsudesktop01 ~]$ df -h
```

Filesystem	Size	Used	Avail	Use%	Mounted on
/dev/mapper/rhel-root	250G	28G	222G	12%	/
devtmpfs	3.4G	0	3.4G	0%	/dev
tmpfs	3.4G	80K	3.4G	1%	/dev/shm
tmpfs	3.4G	362M	3.0G	11%	/run
tmpfs	3.4G	0	3.4G	0%	/sys/fs/cgroup
/dev/sda1	497M	127M	371M	26%	/boot
/dev/mapper/rhel-home	441G	5.5G	436G	2%	/local
tmpfs	682M	16K	682M	1%	/run/user/42
cbsugfs1:/home	313T	227T	78T	75%	/glusterfs/home
tmpfs	682M	0	682M	0%	/run/user/0
128.84.3.177@tcp1:128.84.3.176@tcp1:/lustre1	702T	483T	220T	69%	/home
tmpfs	682M	0	682M	0%	/run/user/516

```
[jarekp@cbsudesktop01 ~]$
```

These are network devices – starting with “computername:/”

Storage

```
jarekp@cbsudesktop01:~  
login as: jarekp  
jarekp@cbsudesktop01's password:  
Last login: Tue Oct 11 16:52:18 2016 from clownfish.tc.cornell.edu  
-----  
Welcome to BRC Bioinformatics Facility BioHPC Lab  
server information: localhost, 2 cores, 8GB RAM, RedHat 7.1  
-----  
[jarekp@cbsudesktop01 ~]$ df -h  
Filesystem                                Size  Used Avail Use% Mounted on  
/dev/mapper/rhel-root                     250G   28G  222G   12% /  
devtmpfs                                 3.4G     0  3.4G    0% /dev  
tmpfs                                     3.4G   80K  3.4G    1% /dev/shm  
tmpfs                                     3.4G  362M  3.0G   11% /run  
tmpfs                                     3.4G     0  3.4G    0% /sys/fs/cgroup  
/dev/sda1                                497M  127M  371M   26% /boot  
/dev/mapper/rhel-home                     441G   5.5G  436G    2% /local  
tmpfs                                     682M   16K  682M    1% /run/user/42  
cbsugfs1:/home                           313T  227T   78T   75% /glusterfs/home  
tmpfs                                     682M     0  682M    0% /run/user/0  
128.84.3.177@tcp1:128.84.3.176@tcp1:/lustre1 702T  483T  220T   69% /home  
tmpfs                                     682M     0  682M    0% /run/user/516  
[jarekp@cbsudesktop01 ~]$
```

/home/jarekp	networked
/usr/local	local
/workdir/jarekp	local
/shared_data	networked
/local_data	local

Storage

- **Networked storage**

/home

/shared_data

/programs

- **Local storage**

/workdir

/SSD

Home directories

Each Unix (Linux) user has a personal storage space called home directory usually referred as /home/userid.

All home directories on BioHPC Lab are networked.

DO NOT RUN ANY COMPUTATIONS IN YOUR HOME DIRECTORY!

Copy your files to /workdir/mylabid first and run computations there!


Space available for each user in home directory is limited by a quota, which depends on type of the user and his resources.


You can always see your current limits and storage under “My Storage” menu. The storage info is updated daily during the night.

← → http://cbsu.tc.cornell.edu/Default.aspx

Bioinformatics Internal Site ... x

File Edit View Favorites Tools Help

 CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search  ☒ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab BioHPC Web Contact Us User: jarekp

institute of biotechnology >> brc >> bioinformatics >> internal >> bioinformatics internal site home


BIOINFORMATICS INTERNAL HOME

Welcome to the internal website of [Biotechnology Resource Center Bioinformatics Facility](#) (Computational Biology Service Unit, CBSU). The Bioinformatics Facility is Cornell University core facility for computational biology and bioinformatics.

This website integrates dynamic computational and training resources of the facility.
For more information about the facility please go to the [facility main website](#).

[Workshops](#)
[Office Hours](#)
[BioHPC Computing Lab](#)
[BioHPC Web Computing](#)

If you would like to receive notifications about facility events, services and new developments please join our [mailing list](#).

 BIOINFORMATICS

"My Storage"

- Manage Credit Accounts
- My Storage
- Profile
- Reservations
- My Reservations
- My Groups
- Change Password
- Logout

http://cbsu.tc.cornell.edu/lab/projects.aspx 100%

Home storage quotas

If user DOES NOT have access to paid storage

- User is associated with an active Lab Credit Account. Home directory storage limit is 200 GB.
- User is associated with an active hosted hardware resource. Home directory storage limit is 200 GB.
- User is NOT associated with an active Lab Credit Account or hosted hardware. Home directory storage limit is 20 GB.

Free storage quotas cannot be combined, added to purchased storage or used for multiple accounts. They are just to make sure users can carry out common computations without purchasing extra storage.

File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: My Storage

https://cbsu.tc.cornell.edu/Lab/mystorage.aspx

CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search

search ☒ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab NGS Data Contact Us User: jarekpp

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: my storage

BIOHPC LAB: MY STORAGE

my home directory location

This page provides detailed view of your storage. Your data can be stored in your home directory or in any of the group storage directories you may have access to. Your home directory may in turn be a part of a storage group. For detailed explanation of BioHPC Lab storage system [please click here](#).

[Storage purchase history](#)

HOME DIRECTORY

Your home directory location is /home/jarekpp

Current disk usage:	24.8GB	current usage
Storage system:	Lustre	
Number of files:	454	
Number of directories:	92	current limit
Disk usage updated:	10/24/2016 7:01:01 PM	
Current disk quota:	200.0GB	limit type
Quota type:	automatic - user associated with an active Lab Credit Account	

[Update home directory storage info](#) (may take long time)

[Add or modify home directory storage](#)

add more storage or change quota

You are not part of any storage groups.

BIOINFORMATICS FACILITY

File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: My Storage X +

https://cbsu.tc.cornell.edu/lab/mystorage.aspx Search

CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search ☒ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab NGS Data Contact Us User: jarekpp

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: my storage

BIOHPC LAB: MY STORAGE

my home directory location

This page provides detailed view of your storage. Your data can be stored in your home directory or in any of the group storage directories you may have access to. Your home directory may in turn be a part of a storage group. For detailed explanation of BioHPC Lab storage system [please click here](#).

[Storage purchase history](#)

HOME DIRECTORY

Your home directory location is /home/jarekpp

Current disk usage:	24.8GB	current usage
Storage system:	Lustre	
Number of files:	454	
Number of directories:	92	
Disk usage updated:	10/24/2016 7:01:01 PM	current limit
Current disk quota:	512.0GB	limit type
Quota type:	purchased storage	
Purchased storage expiration date:	10/25/2018 5:07:40 PM	expiration (for purchased storage)

[Update home directory storage info](#) (may take long time)

[Add or modify home directory storage](#)

add more storage or change quota

You are not part of any storage groups.

Storage

Extra storage can be purchased for \$91.35 per TB per year.

Extra storage can be applied to user's home directory.

Extra storage can be shared among group of users in a **storage group**

Users can have their home directories placed in a storage group, their combined storage limit is then equal to the limit of the storage group.

Please contact us to create a storage group, once created it can be managed online under “My Groups” and “My Storage”

http://cbsu.tc.cornell.edu/Lab/mystorage.aspx

BioHPC Lab: My Storage x BioHPC Lab: Pricing

File Edit View Favorites Tools Help

This page provides detailed view of your storage. Your data can be stored in your home directory or in any of the group storage directories you may have access to. Your home directory of BioHPC Lab storage system [please click here](#).

[Storage purchase history](#)

HOME DIRECTORY

Your home directory location is `/home/jarekp`

Current disk usage:	354.2GB
Disk usage updated:	2/17/2014 5:01:06 AM
Current disk quota:	5,000.0GB
Quota type:	fixed

[Update home directory storage info](#) (may take long time)

[Add or modify home directory storage](#)

You have access to the following storage groups:

QISUN_C4

Group storage location: `/home/qisun_c4`

Current group disk usage:	174.0GB
Group disk usage updated:	2/17/2014 5:01:06 AM
Current group disk quota:	2,048.0GB
Group storage expiration date:	12/29/2439 12:43:48 PM

[Update qisun_c4 storage info](#) (may take long time)

[Add or modify qisun_c4 storage](#)

Website credentials: user: jarekp [BioHPC Lab]
[logout](#)

100%

my home directory location is still under /home so it does not belong to a storage group

but now I have access to another directory, /home/qisun_c4 where I can store my files too

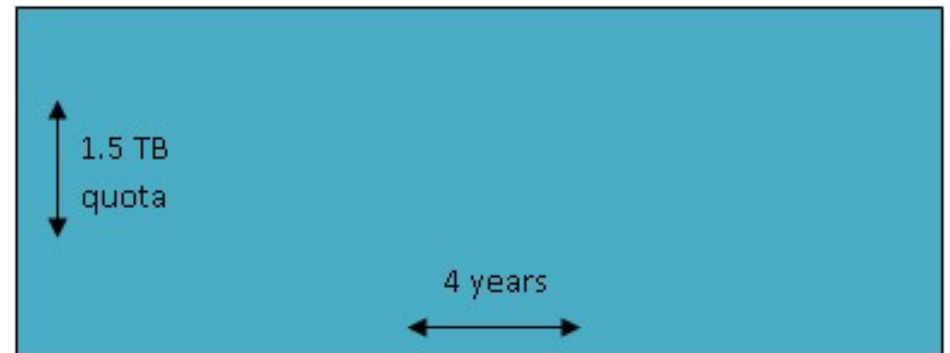
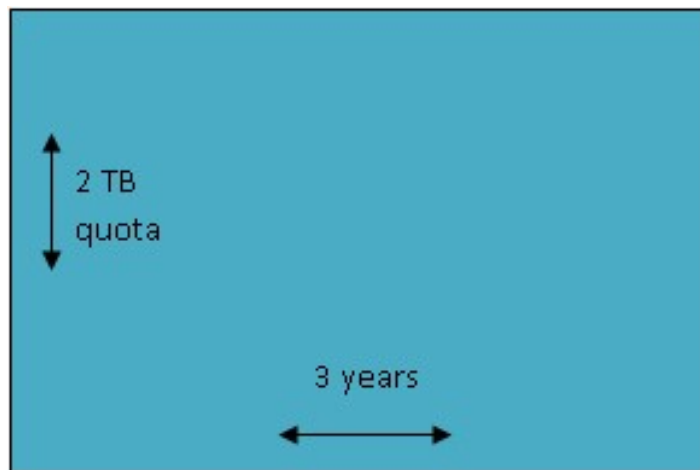
Storage

- The storage can be only purchased in 1 TB-year chunks, it needs to be done up front, and you can set your quota to an appropriate size, which in turn will decide the expiration date.
- You can buy as many of the 1TB-year chunks as you want and then set the quota at the level you want, the expiration date will be computed as the result.

Storage: TB-years

Storage in TB-years represents an *area* and it is always preserved, but either of the rectangle sides can be changed resulting in the other one adapting: lower quota extends expiration time, higher quota shortens time span.

Both rectangles represent the same purchase: 6 TB-years.



File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: Add Storage

https://cbsu.tc.cornell.edu/lab/pstorage.aspx?dir=home

Purchase # TBD

Storage home

Payment type Cornell Account

Cornell Account Number (XXXXXXX):

Cornell Account Owner Name:

Cornell Account Owner Cornell NetID:

Purchasing options:

Current used storage	24.8GB
Purchased storage left	1,025.4GB-year
Add 1 units of 1.0 TB-year at \$91.35 each	1.0TB-year for \$91.35
Quota	512.0GB (0.5TB) (current 512.0GB)
Expiration date	10/24/2020 5:09:46 PM
Description (optional)	

Submit Reset

adding 1TB-year

this is left over from past

limit is kept at 0.5TB

expiration date will be 10/24/2020

File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: Add Storage

https://cbsu.tc.cornell.edu/lab/pstorage.aspx?dir=home

Purchase # TBD

Storage home

Payment type Cornell Account

Cornell Account Number (XXXXXXX):

Cornell Account Owner Name:

Cornell Account Owner Cornell NetID:

Purchasing options:

Current used storage	24.8GB
Purchased storage left	1,025.4GB-year
Add 1 units of 1.0 TB-year at \$91.35 each	1.0TB-year for \$91.35
Quota	2,048.0GB (2.0TB) (current 512.0GB)
Expiration date	10/25/2017 5:11:55 PM
Description (optional)	

Submit Reset

now quota is 2TB

... and new expiration date will be 10/26/2017

File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: Add Storage X +

https://cbsu.tc.cornell.edu/lab/pstorage.aspx?dir=home

Search

Services BioHPC Lab NGS Data Contact Us User: jarekpp

Services >> internal >> biohpc lab: add storage

BIOINFORMATICS FACILITY

Purchase # TBD

Storage home

Payment type Quota Change

Purchasing options:

Current used storage	24.8GB
Purchased storage left	1,025.4GB-year
Add 0 units of 1.0 TB-year at \$91.35 each	0.0TB-year for \$0.00
Quota	3,072.0GB (3.0TB) (current 512.0GB)
Expiration date	2/23/2017 5:16:06 PM
Description (optional)	

Submit Reset

Choose payment type
"Quota Change" and you
can change quota without
buying

now quota is 3TB

... and new expiration
date will be 2/23/2017

set number of units to 0
and you can change
quota without buying

Storage

Similarly as with Lab Credit Accounts computing hours you are charged for *reservation* of storage, i.e. your TB-year storage purchased is used and subtracted based on your *quota*, NOT the amount of actually stored data.

Local Storage Notes

Your local storage on a machine (in /workdir or /SSD) is **NOT** persistent!

It will be deleted some time after your reservation ends, so you must copy all the files back to your home directory if you want to keep them.

Local directories are cleaned at 3am every night.

If the machine is not used the files may stay up to 5 days.

If the machine is used by other users, the files will be deleted on the first night ...

Getting started with a new account

- ✘ You need hours: create and fund your own Lab Credit Account or get added to one
- ✘ Get extra storage if needed – all users get free storage allocations, but it may not be enough
 - Verify that your software is available and read instructions
 - Transfer data to your Lab storage
- ✘ Make reservation(s)
 - Connect to reserved workstations
 - *Compute!*

Connecting to BioHPC Lab machines

Text-based connection: ssh (Secure SHell)

GUI (graphical) connection: X-Windows or VNC

Logging in to a Linux machine

- ❑ On any Linux machine, you need
 - **network name** of the machine (e.g. cbsumm10.tc.cornell.edu)
 - an account, i.e., **user ID** and **password**
 - on your local computer: remote access software (typically: **ssh client**)

- ❑ Linux is a multiple-access system: multiple users may be logged in and operate on one machine at the same time

Logging in to a Linux machine

❑ Remotely from a PC (Windows) via **ssh client**

- Install and configure remote access software (**PuTTY**).
- Use **PuTTY** to open a terminal window on the reserved workstation using **ssh** protocol;
- You may open several terminal windows, if needed.

Logging in to a Linux machine

❑ Remotely from other Linux machine or Mac via native **ssh client**

➤ Launch the Mac's or Linux terminal window. Type

ssh jarekp@cbsuwrkstX.tc.cornell.edu

(replace the “**cbsuwrkstX**” with the workstation that you just reserved, and “**jarekp**” with your own user ID). Enter the lab password when prompted.

➤ You may open several terminal windows, if needed, and log in to the workstation from each of them.

Logging in to CBSU machines from outside of Cornell

Two ways to connect from outside:

- ❑ Install and run the CIT-recommended VPN software (<http://www.it.cornell.edu/services/vpn>) to join the Cornell network, then proceed as usual
- ❑ Log in to `cbsulogin.tc.cornell.edu` (or `cbsulogin2.tc.cornell.edu`):

`ssh jarekp@cbsulogin.tc.cornell.edu` (using PuTTY or other ssh client program)

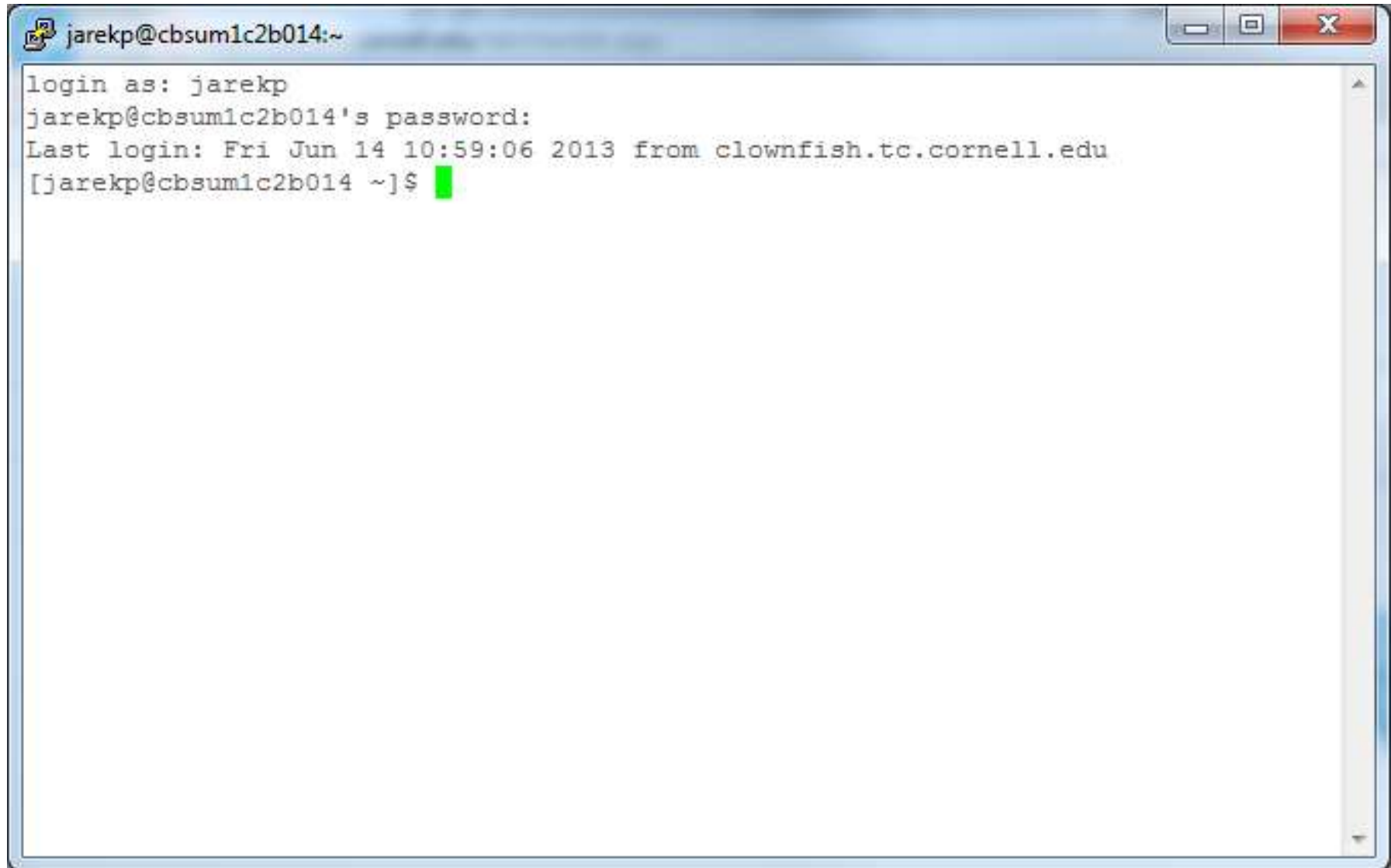
Once logged in to `cbsulogin`, ssh further to your reserved machine

`ssh jarekp@cbsuwrkst3.tc.cornell.edu`

Backup login machine is `cbsulogin2.tc.cornell.edu`

<https://cbsu.tc.cornell.edu/lab/doc/BioHPCLabexternal.pdf>

Terminal window

A screenshot of a terminal window. The title bar at the top shows a small icon and the text 'jarekp@cbsum1c2b014:~'. On the right side of the title bar are three window control buttons: minimize, maximize, and close. The main area of the terminal contains the following text: 'login as: jarekp', 'jarekp@cbsum1c2b014's password:', 'Last login: Fri Jun 14 10:59:06 2013 from clownfish.tc.cornell.edu', and '[jarekp@cbsum1c2b014 ~]\$' followed by a green cursor. A vertical scrollbar is visible on the right side of the terminal area.

```
jarekp@cbsum1c2b014:~  
login as: jarekp  
jarekp@cbsum1c2b014's password:  
Last login: Fri Jun 14 10:59:06 2013 from clownfish.tc.cornell.edu  
[jarekp@cbsum1c2b014 ~]$
```

Terminal window

- ❑ User communicates with the machine via **commands** typed in the terminal window
 - Commands are interpreted by a program referred to as **shell** – an interface between Linux and the user. Usually shell called **bash** is used (another popular shell is **tcsh**).
 - Typically, each command is typed in one line and “**entered**” by hitting the **Enter** key on the keyboard.
 - Commands deal with **files** and **processes**, e.g.,
 - request information (e.g., list user’s files)
 - launch a simple task (e.g., rename a file)
 - start an application (e.g., Firefox web browser, BWA aligner, IGV viewer, ...)
 - stop an application

Logging out of a Linux machine

- ❑ While in terminal window, type **exit** or **Ctrl-D** - this will close the current terminal window

Exercise: connect to your assigned workstations using ssh

- Find your assigned machine on the list on workshop page
<https://cbsu.tc.cornell.edu/ww/machines.aspx?i=81>
- Windows: open PuTTY program, enter your workstation name and connect. Provide your user name and password when prompted.
- Linux or Mac: Open terminal window and type ssh command “ssh labid@workstation.tc.cornell.edu”. Provide your user name and password when prompted.

Connecting to BioHPC Lab

GUI (graphical) connection: VNC

Logging in to a Linux workstation via VNC client (GUI)

In web browser, navigate to <http://cbsu.tc.cornell.edu/>, log in (if not yet logged in), click on **User:your_id**, select tab **My Reservations**

The screenshot shows the 'MY RESERVATIONS' page in a web browser. The browser address bar shows the URL: <http://cbsu.tc.cornell.edu/lab/labresman.aspx?cntrl=635071561019933150&cuid=jarekpp>. The page title is 'BioHPC Lab: My Reservations'. The main heading is 'MY RESERVATIONS' followed by 'Manage My Reservations'. A text box with an arrow points to the 'Connect VNC' link in the 'Action' column of the first reservation table, containing the text: 'Click "Connect VNC", to initialize VNC connection, or "Reset VNC" re-initialize'. Below this is a table of 'My active reservations (reservations starting in future are marked in red):'. The table has columns: Res #, Start, End, Computer, OS, System info, Other users, Credit Account, Action, and VNC port #. The first row shows reservation 20194 for a Dell PowerEdge M600. Below this is another table for 'Other active reservations I can access (reservations starting in future are marked in red):'. This table has columns: Res #, Start, End, Computer, OS, System info, Owner, Other users, Credit account, Action, and VNC port #. The first row shows reservation 20137, also for a Dell PowerEdge M600. A text box with an arrow points to the resolution dropdown menu, containing the text: 'Select resolution you want'. Below the tables, there is a text input field for 'Add user with labid' and a dropdown for 'to my reservation #'. At the bottom, there is a form for 'New reservation from' with date and time pickers, and a 'Go!' button. There are also buttons for 'Go To Main Reservations Page:', 'Interactive Workstations', and 'My Reservations History'. The footer shows 'user: jarekpp [BioHPC Lab]'.

Click "Connect VNC", to initialize VNC connection, or "Reset VNC" re-initialize

Res #	Start	End	Computer	OS	System info	Other users	Credit Account	Action	VNC port #
20194	6/18/2013 12:41:41 PM	6/19/2013 12:30:00 PM	cbsum1c1b011	Linux	Dell PowerEdge M600 8 cores; 16GB RAM; 1TB HDD; VM supported		jarekpp_general	Change Cancel Connect VNC Reset VNC	

Other active reservations I can access (reservations starting in future are marked in red):

Res #	Start	End	Computer	OS	System info	Owner	Other users	Credit account	Action	VNC port #
20137	6/19/2013 12:00:00 AM	6/22/2013 12:00:00 AM	cbsum1c2b003	Linux	Dell PowerEdge M600 8 cores; 16GB RAM; 1TB HDD; VM supported	jarekpp	jarekpp ly86 dbm222 gtb7 njk63 hc556	CBSU Collaboration		

Select resolution you want

You can connect to your Linux reserved workstations using VNC protocol at 1280x800 from this page, for more on VNC please read "Access with VNC" in the Lab's [User Guide](#).

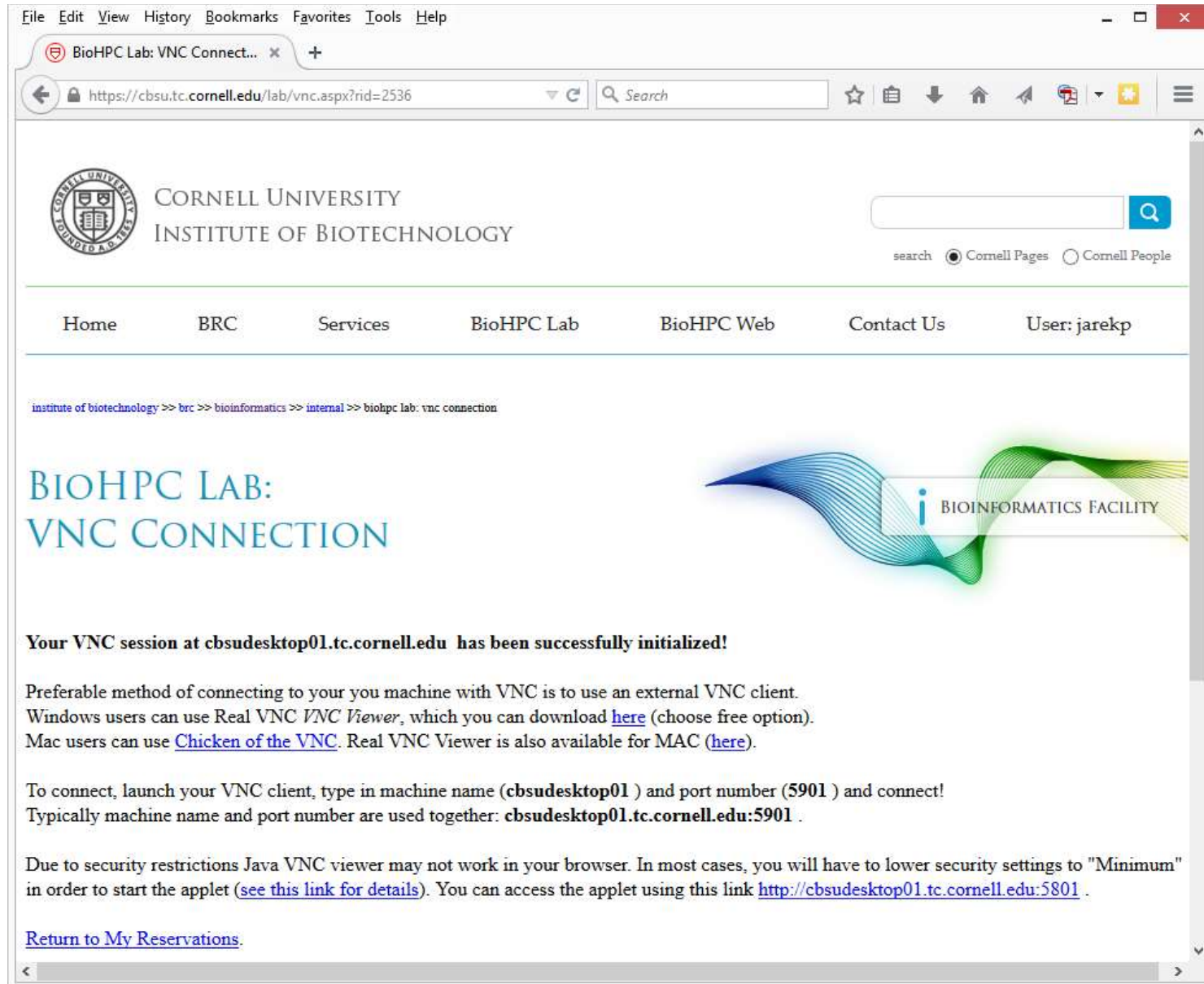
Add user with labid to my reservation # Add!

New reservation from June 18, 2013 12:30pm to June 18, 2013 12:30pm for the first available computer in interactive workstations with Linux Go!

Go To Main Reservations Page: Interactive Workstations My Reservations History

user: jarekpp [BioHPC Lab]

Logging in to a Linux workstation (GUI)



File Edit View History Bookmarks Favorites Tools Help

BioHPC Lab: VNC Connect... x +

https://cbsu.tc.cornell.edu/lab/vnc.aspx?rid=2536


CORNELL UNIVERSITY
INSTITUTE OF BIOTECHNOLOGY

search ☐ Cornell Pages ☐ Cornell People

Home BRC Services BioHPC Lab BioHPC Web Contact Us User: jarekp

institute of biotechnology >> brc >> bioinformatics >> internal >> biohpc lab: vnc connection

BIOHPC LAB: VNC CONNECTION



Your VNC session at cbsudesktop01.tc.cornell.edu has been successfully initialized!

Preferable method of connecting to your you machine with VNC is to use an external VNC client.
Windows users can use Real VNC *VNC Viewer*, which you can download [here](#) (choose free option).
Mac users can use [Chicken of the VNC](#). Real VNC Viewer is also available for MAC ([here](#)).

To connect, launch your VNC client, type in machine name (**cbsudesktop01**) and port number (**5901**) and connect!
Typically machine name and port number are used together: **cbsudesktop01.tc.cornell.edu:5901** .

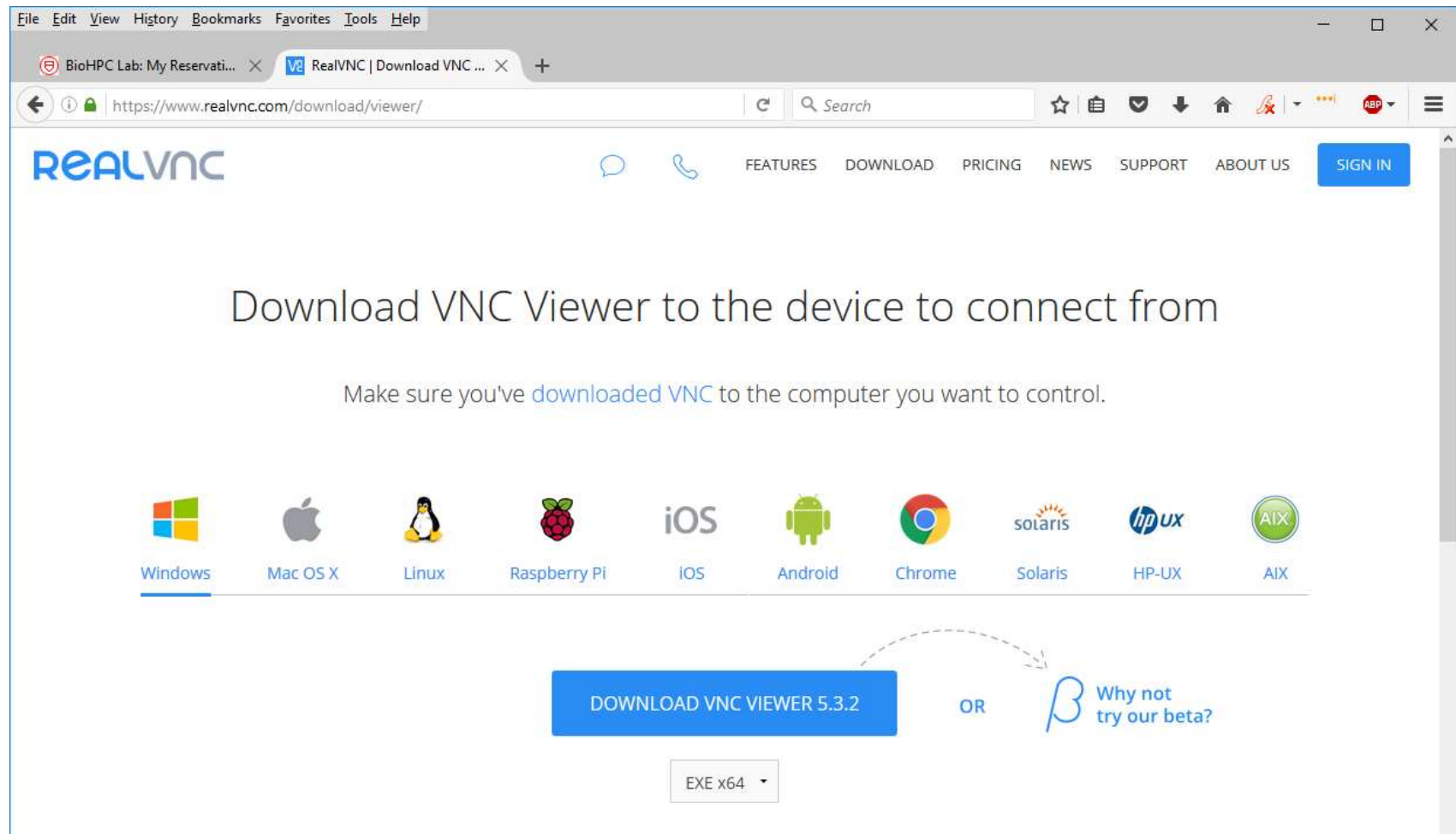
Due to security restrictions Java VNC viewer may not work in your browser. In most cases, you will have to lower security settings to "Minimum" in order to start the applet ([see this link for details](#)). You can access the applet using this link <http://cbsudesktop01.tc.cornell.edu:5801> .

[Return to My Reservations.](#)

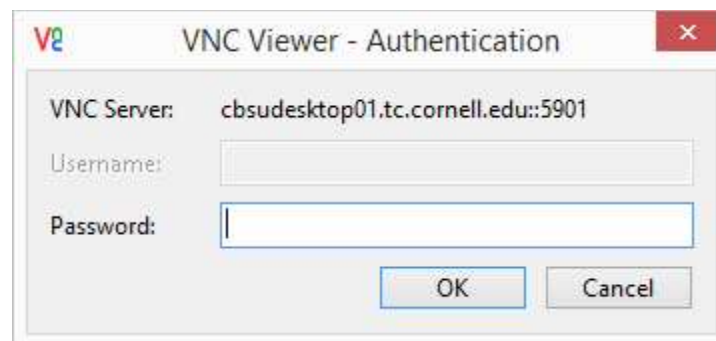
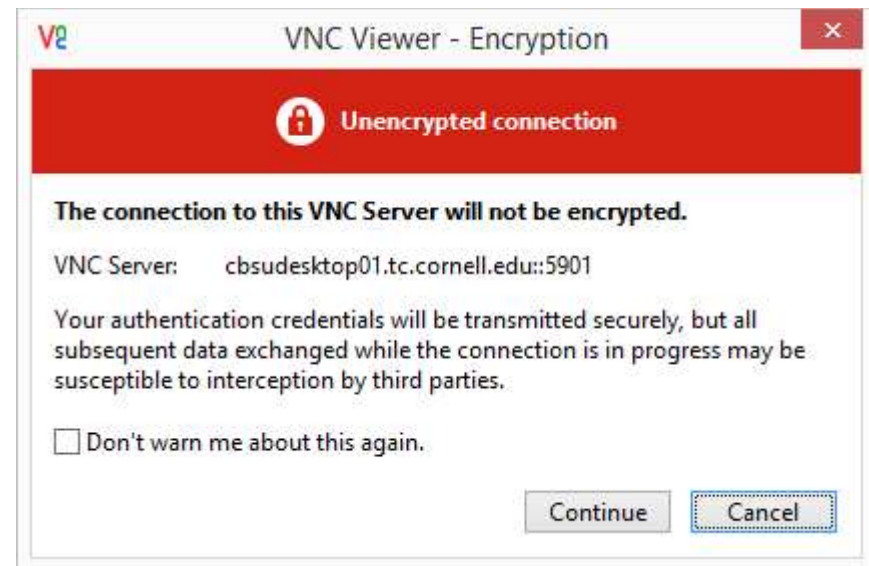
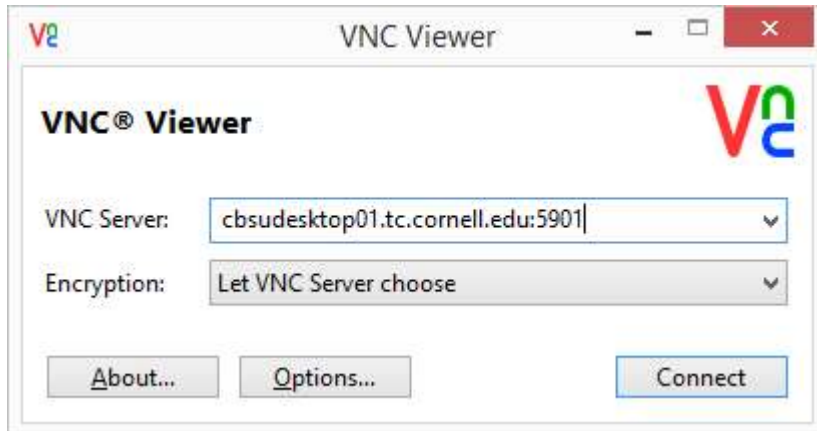
Logging in to a Linux workstation (GUI)

You need software client to connect to your machine via VNC.

We recommend RealVNC VNC Viewer for all platforms.

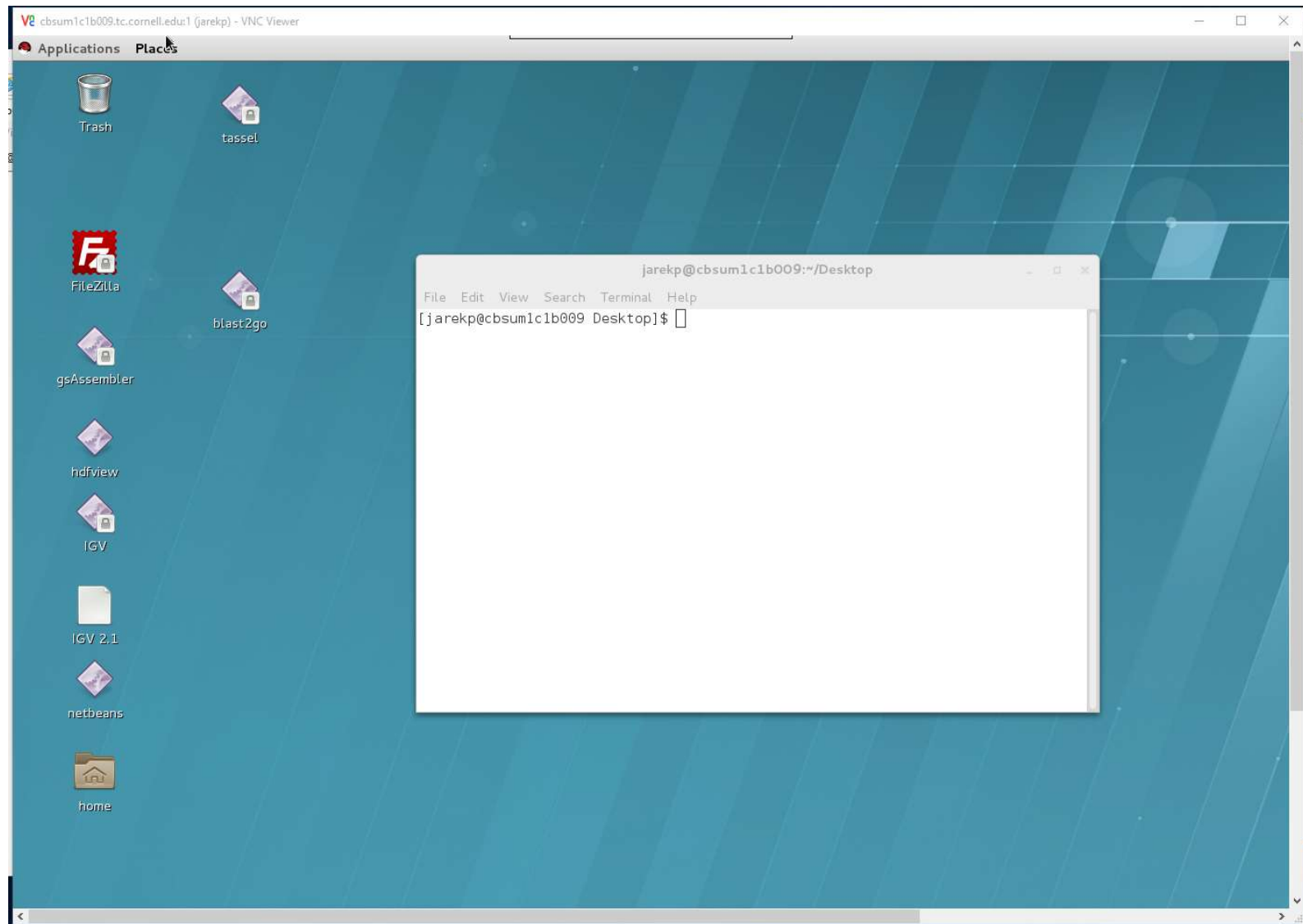


Logging in to a Linux workstation (GUI)



Logging in to a Linux workstation via VNC client (GUI)

Right-click anywhere within desktop, select **Open Terminal** or
.... click **Applications -> Accessories -> Terminal**



Exercise: connect to your assigned workstation using VNC

- Go to “My Reservations” page
<http://cbsu.tc.cornell.edu/lab/lab.aspx> , log in, click on “My Reservations” menu link
- Choose resolution (depends on your monitor)
- Click on “Connect VNC”
- Follow prompts
- Open terminal window in the VNC desktop by right-click on the desktop background and choosing “Open Terminal”.
- Disconnect (close browser windows) and then reconnect. Is the session still alive?

Connecting to BioHPC Lab: VNC

VNC sessions are *persistent*.

They run even when the client is disconnected.

If you need to reset the session you need to use “Reset VNC” link.

Equivalent to Windows Remote Desktop.

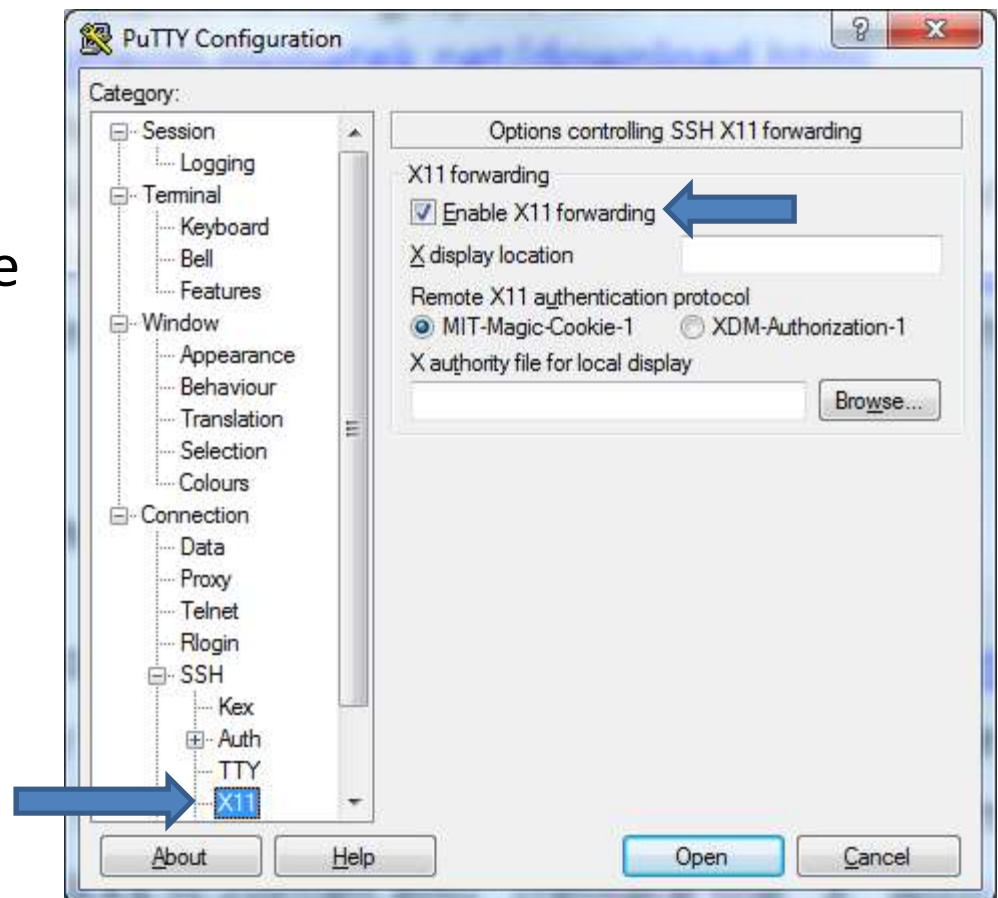
Connecting to BioHPC Lab

GUI (graphical) connection: X-Windows

Not persistent – programs will get killed when client disconnects.

Connecting to BioHPC Lab: X-Windows Windows

- Install X-Windows software on your computer. We recommend MobaXterm free (<http://mobaxterm.mobatek.net/download.html>)
- Start MobaXterm
- Connect to BioHPC Lab machine using PuTTY. Make sure X11 forwarding is enabled. X11 is a synonym for X-Windows



Connecting to BioHPC Lab: X-Windows Windows

- Start your GUI (graphical) software in terminal window. For testing you may try eog (Linux image viewer) or firefox.
- You may need to allow MobaXterm connections through Windows firewall.
- New window with your GUI program will appear. The program will physically run on the BioHPC Lab machine, but it will display graphics on your local computer.

Connecting to BioHPC Lab: X-Windows

Linux or Mac

- Connect to BioHPC Lab machine using ssh with X11 forwarding :
`ssh -X labid@workstation.tc.cornell.edu`
- Start your GUI program in remote terminal window. For testing you may try eog (Linux image viewer) or firefox.
- New window with your GUI program will appear. The program will physically run on the BioHPC Lab machine, but it will display graphics on your local computer.

Exercise: connect to your assigned workstation with X-Windows

- Connect to your workstations using ssh with X11 forwarding enabled
- Windows: start MobaXterm
- Start eog in remote terminal.

Getting started with a new account

- ✖ You need hours: create and fund your own Lab Credit Account or get added to one
- ✖ Get extra storage if needed – all users get free storage allocations, but it may not be enough
 - Verify that your software is available and read instructions
 - Transfer data to your Lab storage
- ✖ Make reservation(s)
- ✖ Connect to reserved workstations
 - *Compute!*

Transferring data

- `sftp` or `scp` (secure file transfer protocol)

Transfer can be done to and from Lab machines.

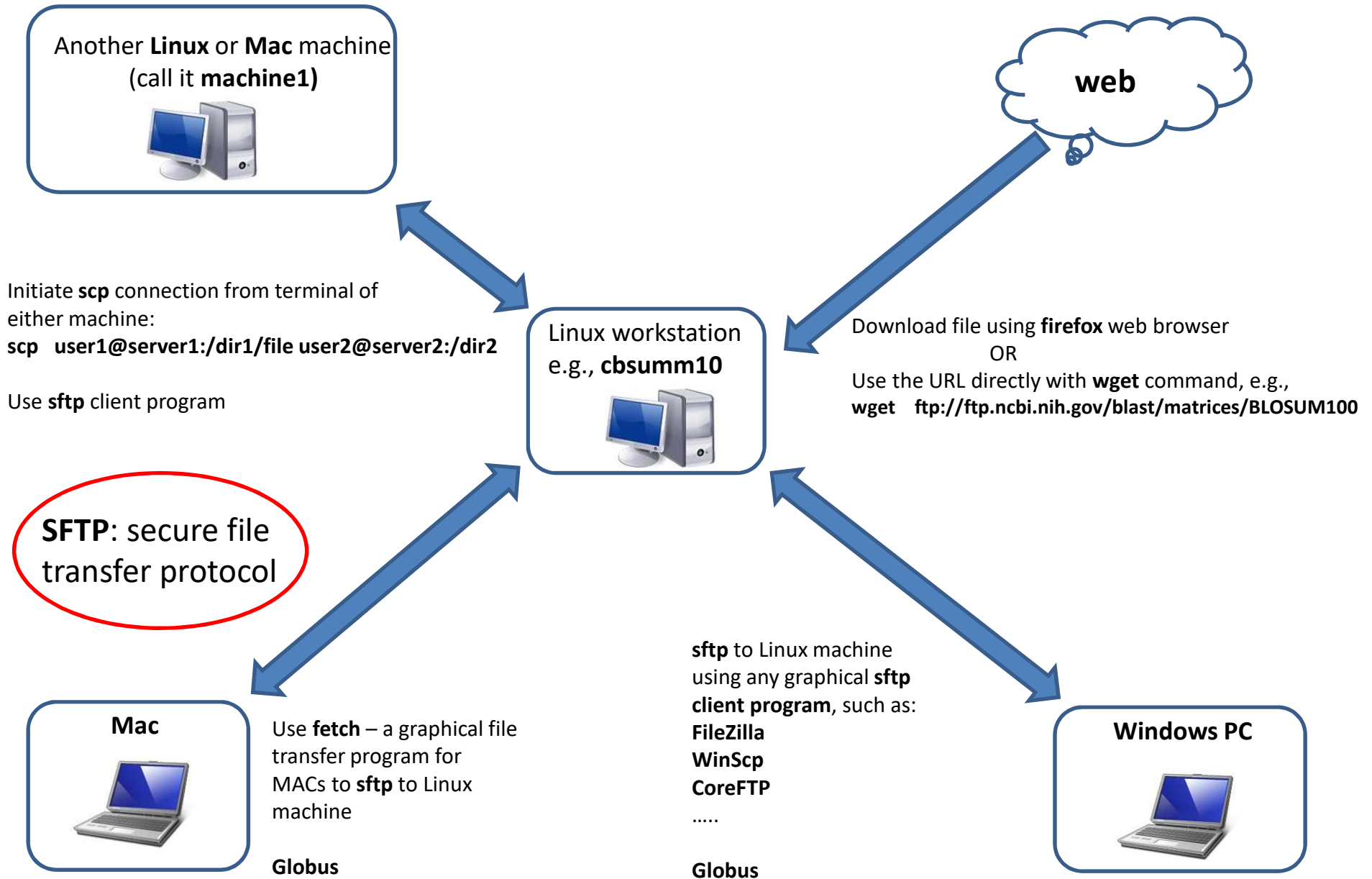
- `Globus`

Transfer can be done to and from Lab machines.

- `wget`

Transfer can be done to Lab machines only.

File Transfer: summary



File transfer: wget

from web- and ftp sites to lab workstations

Option 1: run **wget** command on the workstation (if you know the URL of the file)

- **Examples:**

```
wget ftp://ftp.ncbi.nih.gov/blast/matrices/BLOSUM100
```

(will download the file BLOSUM100 from the NCBI FTP site and deposit it in the current directory under the name BLOSUM100)

- **another Example (the following should be typed on one line):**

```
wget -O e_coli_1000_1.fq  
"http://cbsuapps.tc.cornell.edu/Sequencing/showseqfile.aspx?cntrl=646698859&laneid=487&mode=http&file=e_coli_1000_1.fq"
```

(the command above can be used to download files given by complicated URLs; note the "" marks around the link and the -O option which specifies the name you want to give the downloaded file)

Exercise: download BLOSUM100 with wget


- Connect to your workstation using ssh
- Type wget command

```
wget ftp://ftp.ncbi.nih.gov/blast/matrices/BLOSUM100
```


File transfer: sftp

between PC or Mac and a Lab workstation

On Windows PC: install and use your favorite **sftp client** program, such as

- **winscp**: <http://winscp.net/eng/index.php>
- **CoreFTP LE**: <http://www.coreftp.com/>
- **FileZilla** (client): <http://filezilla-project.org/> 
- ... others...
- When connecting to Lab workstations from a client, use the **sftp** protocol. You will be asked for your user name and password (the same you use to log in to the lab workstations).
- Transfer text file in text mode, binary files in binary mode (the “default” not always right).
- All clients feature
 - File explorer-like graphical interface to files on both the PC and on the Linux machine
 - Drag-and-drop functionality

Recommended!

On a Mac: file transfer program is **fetch** (recommended by Cornell CIT)

- http://www2.cit.cornell.edu/services/systems_support/filefetch.html#fetchinst
- graphical user interface
- Drag-and-drop functionality

File transfer: scp

between a lab workstation and another Linux machine

Suppose we want to transfer a file `/home/jarekp/test.fa` from **cbsulogin.tc.cornell.edu** (another Linux machine; substitute “your” Linux machine here) and **cbsum1c2b007** lab workstation `/workdir/jarekp` directory.

scp is a Unix command to copy files between servers

#copying file1 to dir2 on server2

```
scp user1@server1:/dir1/file1 user2@server2:/dir2
```

#copying dir2 to dir3 on server2

```
scp -r user1@server1:/dir1/dir2 user2@server2:/dir3
```

If you are logged in on cbsulogin

```
scp /home/jarekp/test.fa cbsum1c2b007:/workdir
```

If you are logged in on cbsum1c2b007

```
scp cbsulogin:/home/jarekp/test.fa /workdir
```

Option: **Filezilla** is installed on Lab workstations. Connect to Lab workstations with GUI support (VNC or X-Windows), type filezilla and connect to the other servers using sftp protocol.

**Exercise: download BLOSUM100 file from Lab machine
to your local computer**

- Connect to your workstation using sftp program (FileZilla)
- Download BLOSUM100

Transferring data: Globus

Globus Online is an online system based on GridFTP engine that supports fast and reliable data transfer and can be scheduled and controlled online in a web browser.

Data can be transferred between endpoints, which can be data servers or Globus Connect clients.

BioHPC Lab Globus endpoint servers are **biohpc#cbsulogin** and **biohpc#cbsulogin2**

You can transfer data to another server or to your computer (using Globus Connect client).

[http://cbsu.tc.cornell.edu/lab/doc/Globus at BioHPC Lab.pdf](http://cbsu.tc.cornell.edu/lab/doc/Globus_at_BioHPC_Lab.pdf)

<https://www.globusonline.org/quickstart/>

Transferring data: Globus

- Sign up for Globus online account if you don't have one (use the link above).
- Sign in to Globus online using your id and password
- Go to File Transfer, in the left panel "Endpoint" field type **biohpc#cbsulogin** and click go. Login window will pop up, you need to use your BioHPC Lab user id and password to connect to the endpoint, click Authenticate
- When authentication is successful files from your home directory will show up in the left panel.
- If you would like to connect to another **server** endpoint you can just type it in the right side "Endpoint" field and connect.
- If you want to transfer to the local laptop (which is not a server) you need to install Globus Connect (if it is already installed, just start it).

File Edit View History Bookmarks Favorites Tools Help

How To

https://docs.globus.org/how-to/ Search

globus docs APIs How To Guides Support

HOME / HOW TO

How To

- [Log In and Transfer Files with Globus](#)
- [Link a New Identity to an Existing Globus Account](#)
- [Share Data Using Globus](#)
- [Manage Globus Groups](#)
- [Install and Configure Globus Connect Personal for Mac OS X](#)
- [Install and Configure Globus Connect Personal for Windows](#)
- [Install and Configure Globus Connect Personal for Linux](#)
- [Configure Firewall Policy for Globus Connect Personal](#)
- [Create a Globus Amazon S3 Endpoint](#)

© 2010-2016 The University of Chicago Legal

Transferring data: Globus

- Sign up for Globus online account if you don't have one (use the link above).
- Sign in to Globus online using your id and password
- Go to File Transfer, in the left panel “Endpoint” field type **biohpc#cbsulogin** and click go. Login window will pop up, you need to use your BioHPC Lab user id and password to connect to the endpoint, click Authenticate
- When authentication is successful files from your home directory will show up in the left panel.
- If you would like to connect to another **server** endpoint you can just type it in the right side “Endpoint” field and connect.
- If you want to transfer to the local laptop (which is not a server) you need to install Globus Connect (if it is already installed, just start it).

FileEditViewHistoryBookmarksFavoritesToolsHelp

Transfer Files | Globus

https://www.globus.org/app/transfer

Search

☆📅🔒⬇️🏠🔗🔴🔴🔴🔴🔴

g globus

Manage DataPublishGroupsSupportAccount

Transfer FilesActivityEndpointsBookmarksConsole

Transfer Files

RECENT ACTIVITY000

EndpointStart here...☆◀▶EndpointPathGo

Start by selecting an endpoint.

EndpointPathGo

Start by selecting an endpoint.

Label This Transfer

This will be displayed in your transfer activity.

Transfer Settings

☐ sync - only transfer new or changed files ?

☐ delete files on destination that do not exist on source ?

☐ preserve source file modification times ?

☒ verify file integrity after transfer ?

☐ encrypt transfer ?

[Get Globus Connect Personal](#)
Turn your computer into an endpoint.

© 2010–2016 The University of Chicago legal

BioHPC Lab endpoint name

File Edit View History Bookmarks Favorites Tools Help

Transfer Files | Globus

https://www.globus.org/app/transfer?origin_id=d20e623c-6d04-11e1

g globus Manage Data Publish Groups Support Account

Transfer Files Activity Endpoints Bookmarks Console

RECENT ACTIVITY 0 0 0

Endpoint biohpc#cbsulogin Path Go

Endpoint Path Go

Please authenticate to access this endpoint

Login Server cbsulogin.tc.cornell.edu Username Password advanced Authenticate

BioHPC Lab endpoint name

cbsulogin is our server

enter you Lab id and password

Label This Transfer This will be displayed in your transfer activity.

Transfer Settings

- ☐ sync - only transfer new or changed files
- ☐ delete files on destination that do not exist on source
- ☐ preserve source file modification times
- ☒ verify file integrity after transfer
- ☐ encrypt transfer

Get Globus Connect Personal Turn your computer into an endpoint.

© 2010–2016 The University of Chicago legal

Transferring data: Globus

- Sign up for Globus online account if you don't have one (use the link above).
- Sign in to Globus online using your id and password
- Go to File Transfer, in the left panel "Endpoint" field type **biohpc#cbsulogin** and click go. Login window will pop up, you need to use your BioHPC Lab user id and password to connect to the endpoint, click Authenticate
- When authentication is successful files from your home directory will show up in the left panel.
- If you would like to connect to another **server** endpoint you can just type it in the right side "Endpoint" field and connect.
- If you want to transfer to the local laptop (which is not a server) you need to install Globus Connect (if it is already installed, just start it).


FileEditViewHistoryBookmarksFavoritesToolsHelp

Transfer Files | Globus

https://www.globus.org/app/transfer?origin_id=d20e623c-6d04-11e1

Search

☆📁📌📄🏠🔗🔴🔴🔴

Manage DataPublishGroupsSupportAccount

Transfer FilesActivityEndpointsBookmarksConsole

Transfer Files

RECENT ACTIVITY000

Endpointbiohpc#pbslogin

Path/~/Go

select allup one folderrefresh list

Buckler-RNASeqFolder

DesktopFolder

DocumentsFolder

DownloadsFolder

EventsManagerFolder

KerryFolder

MixMapperFolder

MusicFolder

PASTECFolder

PicturesFolder

PublicFolder

TemplatesFolder

TestFilesFolder

VideosFolder

ViennaRNAFolder

VirtualBox VMsFolder

arabidopsisFolder

atestFolder

billieFolder

birdsuiteFolder

Endpoint

PathGo

Start by selecting an endpoint.

Label This Transfer

This will be displayed in your transfer activity.

Transfer Settings

☐ sync - only transfer new or changed files

☐ delete files on destination that do not exist on source

☐ preserve source file modification times

☒ verify file integrity after transfer

☐ encrypt transfer

Get Globus Connect Personal

Turn your computer into an endpoint.

Transferring data: Globus

- Sign up for Globus online account if you don't have one (use the link above).
 - Sign in to Globus online using your id and password
 - Go to File Transfer, in the left panel “Endpoint” field type **biohpc#cbsulogin** and click go. Login window will pop up, you need to use your BioHPC Lab user id and password to connect to the endpoint, click Authenticate
 - When authentication is successful files from your home directory will show up in the left panel.
- If you would like to connect to another **server** endpoint you can just type it in the right side “Endpoint” field and connect.
 - If you want to transfer to the local laptop (which is not a server) you need to install Globus Connect (if it is already installed, just start it).

Start Transfer | Transfer | Gl... x

File Edit View Favorites Tools Help

globus

Manage Transfers Groups Support jarekp

start transfer | view activity | manage endpoints | dashboard

Transfer Files

Get Globus Connect Personal
Turn your computer into an endpoint.

Endpoint biohpc#cbsulogin Path ~/ Go

select all | none up one folder refresh list

- Buckler-RNASeq Folder
- Desktop Folder
- Documents Folder
- Downloads Folder
- Kerry Folder
- MixMapper Folder
- Music Folder
- Pictures Folder
- Public Folder
- Templates Folder
- TestFiles Folder
- Videos Folder
- ViennaRNA Folder
- VirtualBox VMs Folder
- arabidopsis Folder
- billie Folder
- blast2go Folder
- blastdb Folder
- blastdb20130521 Folder
- blastdb20130521.fasta Folder

Endpoint jarekp#clownfish Path ~/ Go

select all | none up one folder refresh list

- C Folder

Your local computer endpoint name.
Usually account#computer
Globus Connect must be running and local
endpoint registered

See this pdf for details
http://cbsu.tc.cornell.edu/lab/doc/Globus_at_BioHPC_Lab.pdf

100%

Exercise: transfer BLOSUM100 file to your laptop using Globus

Getting started with a new account

- ✖ You need hours: create and fund your own Lab Credit Account or get added to one
- ✖ Get extra storage if needed – all users get free storage allocations, but it may not be enough
 - Verify that your software is available and read instructions
- ✖ Transfer data to your Lab storage
- ✖ Make reservation(s)
- ✖ Connect to reserved workstations
 - *Compute!*

Software

<https://cbsu.tc.cornell.edu/lab/userguide.aspx?a=software>

<https://cbsu.tc.cornell.edu/lab/labsoftware.aspx>

Please read the information provided, and consult author's website if needed.

Some programs require special setup to run, some need to be run with full path, some are installed only on a subset of workstations.

Software

BioHPC Lab: Software

←

→

↺

🔒

cbsu.tc.cornell.edu/lab/labsoftware.aspx

📖

☆

≡

✎

🔔

⋮

☆ CBSU @ Cornell

☆ Dryden Fish and

📍 Freeville, NY 10 Day

☆ Google Maps

☆ Ithaca NY Cloud

☆ Jarek's Amateur

☆ Live Search Maps

☆ WCMC HepC

Please check detailed information before running any program, it may contain important instruction on how to properly use the software in BioHPC Lab.
[Non-tabular Lab Software pagee](#)

Filter by:

Name: go About: go

☒ Show Windows
☒ Show Linux

Order by Name ▾ Ascending ▾

241 Records found. Show 1-200 ▾

Name	Version	OS	About	Installed	Updated	More
454 gsAssembler or gsMapper	2.8	Linux	Assembly and alignment software for 454 or other long reads.	12/13/2011	3/24/2014	detailed information
a5	20140401	Linux	A genome assembly pipeline for bacteria and archaea	10/14/2013	1/21/2015	detailed information
ABYSS	1.5.2	Linux	Illumina short reads assembly tool.	12/13/2011	12/1/2014	detailed information
AdapterRemoval	2.1.1	Linux	Remove adapters from sequences in either single end or paired end experiments	9/16/2015		detailed information
Admixtools	1.1	Linux	The ADMIXTOOLS package implements 5 methods described in Patterson et al (2012) Ancient Admixture in Human History.	11/6/2013	1/22/2015	detailed information
Admixture	1.23	Linux	Software tool for maximum likelihood estimation of individual ancestries from multilocus SNP genotype datasets.	2/19/2014	2/19/2014	detailed information
Alder	1.03	Linux	The ALDER software computes the weighted linkage disequilibrium (LD) statistic for making inference about population admixture.	11/6/2013	11/6/2013	detailed information
AlleleSeq	1.1	Linux	Detects SNVs from ChIP-seq or RNA-seq experiments.	4/2/2014		detailed information
ALLMAPS	20150710	Linux	ALLMAPS is capable of computing a scaffold ordering that maximizes the colinearity to a collection of maps, including genetic, physical or comparative maps into the final chromosome build.	7/10/2015		detailed information
ALLPATHS-LG	49148	Linux	Illumina short reads assembly tool.	12/14/2011	12/5/2014	detailed information
AMOS	3.1.0	Linux	AMOS is a collection of tools and class interfaces for the assembly of DNA reads.	1/12/2013	1/14/2013	detailed information

Software

BioHPC Lab: User Guide

+

← → ↺

🔒 cbsu.tc.cornell.edu/lab/userguide.aspx?a=software

📖 ☆

☰ ✎ 🔔 ⋮

☆ CBSU @ Cornell ☆ Dryden Fish and 🇺🇸 Freeville, NY 10 Day ☆ Google Maps ☆ Ithaca NY Cloud ☆ Jarek's Amateur ☆ Live Search Maps

Overview Quick Start Guide Accounts Access Storage Storage Space Databases **Software** Workflows FAQ

BioHPC Lab Software

There is 241 software titles installed in BioHPC Lab. The software is available on all machines (unless stated otherwise in notes), complete list of programs is below, please click on a title to see details and instructions. Tabular list of software is available [here](#)

Please read details and instructions before running any program, it may contain important information on how to properly use the software in BioHPC Lab.

454 [gsAssembler](#) or [gsMapper](#), [a5](#), [ABYSS](#), [AdapterRemoval](#), [Admixtools](#), [Admixture](#), [Alder](#), [AlleleSeq](#), [ALLMAPS](#), [ALLPATHS-LG](#), [AMOS](#), [analysis](#), [ANGSD](#), [AnnoVar](#), [Atlas-Link](#), [ATLAS_GapFill](#), [ATSAS](#), [Augustus](#), [bamtools](#), [BayeScan](#), [Beagle](#), [Beagle4](#), [bedops](#), [BEDtools](#), [bgc](#), [biobambam](#), [Bioconductor](#), [BioPerl](#), [BioPython](#), [Birdsuite](#), [Bismark](#), [blasr](#), [BLAST](#), [blast2go](#), [BLAT](#), [Boost](#), [Bowtie](#), [Bowtie2](#), [BWA](#), [CAP3](#), [CBSU RNAseq](#), [cd-hit](#), [CEGMA](#), [Circos](#), [Circuitscape](#), [Clustal Omega](#), [CLUSTALW](#), [Cluster](#), [CNVnator](#), [Cufflinks](#), [cutadapt](#), [dadi](#), [delly](#), [diamond](#), [Discover](#), [Discover de novo](#), [dsk](#), [ea-utils](#), [ecopcr](#), [EIGENSOFT](#), [EMBOSS](#), [exonerate](#), [eXpress](#), [FastML](#), [fastq_species_detector](#), [FastQC](#), [FastTree](#), [FASTX](#), [fineSTRUCTURE](#), [flash](#), [Flexible Adapter Remover](#), [freebayes](#), [GATK](#), [GCTA](#), [GEMMA](#), [geneid](#), [GeneMark-ES](#), [GeneMarker](#), [Genome STRiP](#), [GenomeStudio \(SoftGenetics\)](#), [germline](#), [GMAP/GSNAP](#), [GNU parallel](#), [Gubbins](#), [hapflk](#), [HaploMerger](#), [HapSeq2](#), [HMMER](#), [HOTSPOT](#), [HTSeq](#), [HyPhy](#), [iAssembler](#), [IBDL](#), [IDBA-UD](#), [IGV](#), [IMAGE](#), [impute2](#), [InterProScan](#), [java](#), [jellyfish](#), [JoinMap](#), [julia](#), [kallisto](#), [Kent source utilities](#), [khmer](#), [LDAK](#), [leeHom](#), [LocusZoom](#), [LUCY](#), [LUCY2](#), [LUMPY](#), [MACS](#), [MACS2](#), [MAFFT](#), [MAKER](#), [MAQ](#), [MaSuRCA](#), [Mauve](#), [mccortex](#), [megahit](#), [MEGAN](#), [MEME Suite](#), [MetAMOS](#), [MetaPhlAn](#), [MetaVelvet](#), [MetaVelvet-SL](#), [mira](#), [miRDeep2](#), [MISO \(misopy\)](#), [MixMapper](#), [MKTest](#), [MMSEQ](#), [MrBayes](#), [mrsFAST](#), [msld](#), [MSMC](#), [MSR-CA Genome Assembler](#), [msstats](#), [MSTMap](#), [mugsy](#), [MUMmer](#), [muscle](#), [ncftp](#), [Nemo](#), [Netbeans](#), [NEURON](#), [new_fugue](#), [NextGenMap](#), [ngsTools](#), [Novoalign](#), [NovoalignCS](#), [Oases](#), [OBITools](#), [Orthomcl](#), [PAML](#), [pandas](#), [pandaseq](#), [Panseq](#), [PASTEC](#), [PBJelly](#), [PBSuite](#), [PeakSplitter](#), [PEAR](#), [PennCNV](#), [ph5tools](#), [PHAST](#), [PHYLIP](#), [PhyML](#), [Picard](#), [Pindel](#), [PIQ](#), [plink](#), [prinseq](#), [prodigal](#), [progressiveCactus](#), [pyRAD](#), [QIIME](#), [QUAST](#), [R](#), [RACA](#), [RAPTR-SV](#), [RAXML](#), [Ray](#), [RepeatMasker](#), [RFMix](#), [RNAMMER](#), [RSEM](#), [RSeQC](#), [Samtools](#), [Satsuma](#), [scythe](#), [SeqPrep](#), [SHAPEIT](#), [SHRiMP](#), [sickle](#), [SignalP](#), [skewer](#), [SMRT Analysis](#), [snap](#), [SNPhylo](#), [SOAP2](#), [SOAPdenovo](#), [SOAPdenovo-Trans](#), [SOAPdenovo2](#), [SPAdes](#), [SRA Toolkit](#), [stacks](#), [stampy](#), [STAR](#), [StringTie](#), [STRUCTURE](#), [sutta](#), [SVDetect](#), [sweepsims](#), [tabix](#), [Tandem Repeats Finder \(TRF\)](#), [TASSEL 3](#), [TASSEL 4](#), [tcoffee](#), [TEToolkit](#), [TMHMM](#), [TopHat](#), [traitRate](#), [TransDecoder](#), [treemix](#), [trimmomatic](#), [Trinity](#), [Trinotate](#), [UCSC Kent utilities](#), [Variant Effect Predictor](#), [vcf2diploid](#), [vcfCooker](#), [vcflib](#), [vcftools](#), [Velvet](#), [ViennaRNA](#), [VirusFinder 2](#), [vsearch](#), [wgs-assembler \(Celera\)](#), [Wise2 \(Genewise\)](#), [vaha](#)

Software

The screenshot shows a web browser window with two tabs: "BioHPC Lab: Software" and "BioHPC Lab: User Guide". The address bar shows the URL `https://cbsu.tc.cornell.edu/lab/userguide.aspx?a=software&i=22#c`. The page title is "Details for **bamtools** (hide)".

The page displays the following details for **bamtools**:

- Name: bamtools
- Version: 2.3.0
- OS: Linux
- About: BAM file processing and filtering.
- Added: 12/13/2011 2:56:40 PM
- Updated: 3/24/2014 3:26:48 PM
- Link: <http://seqanswers.com/wiki/BamTools>
- Platform: all

Notes:

The latest version of the program is in your PATH, and can be used directly by typing its name at the prompt:

```
bamtools [options]
```

There are 1 previous version(s) available. Any version can be accessed either by typing full path, or by adding it to the PATH and then typing its name at the prompt. NOTE: you need to set PATH only once per login/session.

version	access
2.3.0 (latest)	full path: <code>/programs/bamtools-2.3.0/bin/bamtools [options]</code> add to PATH: <code>export PATH=/programs/bamtools-2.3.0/bin:\$PATH</code>
2.2.3	full path: <code>/programs/bamtools-2.2.3/bin/bamtools [options]</code> add to PATH: <code>export PATH=/programs/bamtools-2.2.3/bin:\$PATH</code>

Details for Trinity (hide)

Name: Trinity

Version: 2.0.4

OS: Linux

About: De novo transcriptome assembly.

Added: 12/13/2011 3:22:56 PM

Updated: 3/9/2015 1:18:17 PM

Link: <http://trinityrnaseq.github.io/>

Notes: You need to use full path to the binaries:

```
/programs/trinityrnaseq-2.0.4/Trinity [options]
```

You can also add the program to your PATH:

```
export PATH=/programs/trinityrnaseq-2.0.4:$PATH
```

and then use it directly by typing program name at the prompt.

It is recommended to run on medium memory nodes (e.g., cbsumm03). A large memory machines (e.g. cbsulm05) may be needed to process larger datasets.

To launch Trinity, use the full path to the executable, like so:

```
/programs/trinityrnaseq-2.0.4/Trinity [options] >& trinity.log &
```

If you need to run TransDecoder that is part of Trinity release, you will need to download the Pfam-A.hmm.gz file to your working directory, and add path to hammer before you run the tool (You will need to run "export ..." command every time before you run TransDecoder).

```
wget ftp://ftp.sanger.ac.uk/pub/databases/Pfam/current_release/Pfam-A.hmm.gz
```

```
export PATH=/programs/hammer/binaries:$PATH
```

If you prefer to run any of the earlier versions of the program (2012-10-05 or earlier), you will need to first modify the environment to use an earlier version of java by executing the following commands:

```
export JAVA_HOME=/usr/lib/jvm/jre-1.6.0-openjdk.x86_64
```

```
export PATH=$JAVA_HOME/bin:$PATH
```

There are 9 previous version(s) available. Any version can be accessed either by typing full path, or by adding it to the PATH and then typing its name at the prompt. NOTE: you need to set PATH only once per login/session.

version	access
2.0.4 (latest)	full path: /programs/trinityrnaseq-2.0.4/Trinity [options]
	add to PATH: export PATH=/programs/trinityrnaseq-2.0.4:\$PATH
20140413p1	full path: /programs/trinityrnaseq_r20140413p1/Trinity [options]
	add to PATH: export PATH=/programs/trinityrnaseq_r20140413p1:\$PATH
r20131110	full path: /programs/trinityrnaseq_r20131110/Trinity [options]
	add to PATH: export PATH=/programs/trinityrnaseq_r20131110:\$PATH

Software

You can “lock in” the program version by using full path or prepending your version to the PATH.

The commands to do it are always listed on the Lab program page.

Getting started with a new account

- ✖ You need hours: create and fund your own Lab Credit Account or get added to one
- ✖ Get extra storage if needed – all users get free storage allocations, but it may not be enough
- ✖ Verify that your software is available and read instructions
- ✖ Transfer data to your Lab storage
- ✖ Make reservation(s)
- ✖ Connect to reserved workstations

- *Compute!*

