# Lecture 9: Cluster computing

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BIOST 561: Computational Skills For Biostatistics I

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In Lecture 8, you learned how to compute without `R`.

Today, you'll learn how to transfer those skills to computing on a cluster.

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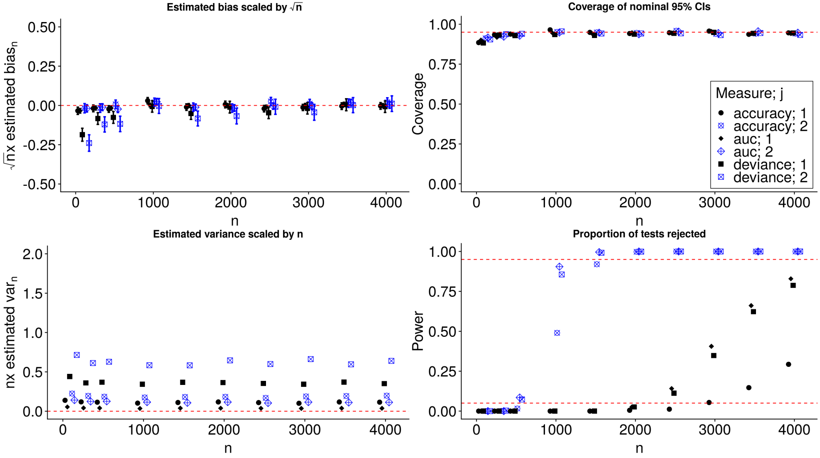

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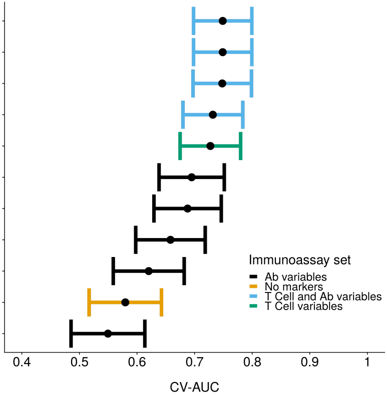
- memory-intensive computations?

| Assay combination | CV-AUC [95% CI] |
|---|---|
| IgG + IgA + IgG3 + T Cells | 0.749 [0.698, 0.799] |
| IgG + IgA + T Cells | 0.749 [0.698, 0.799] |
| All markers | 0.748 [0.697, 0.799] |
| T Cells + Fx Ab | 0.732 [0.680, 0.784] |
| T Cells | 0.727 [0.675, 0.780] |
| IgG3 | 0.695 [0.638, 0.751] |
| IgG + IgA + IgG3 | 0.688 [0.629, 0.746] |
| IgG + IgA + IgG3 + Fx Ab | 0.658 [0.598, 0.718] |
| IgG + IgA | 0.620 [0.559, 0.682] |
| No markers | 0.580 [0.517, 0.643] |
| Fx Ab | 0.550 [0.485, 0.614] |



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[*]: we will discuss this further!

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Consider a sample of $n$ observations generated iid according to

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We will use the cluster to do this!

# Part I: coding for the cluster

# Coding for the cluster

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# Coding for the cluster: modular code

# Coding for the cluster: setting the seed

# Coding for the cluster: saving output

# Coding for the cluster: debugging

# Coding for the cluster: compiling output

# Part II: using the cluster

# Using the cluster

Department resources for HPC*:

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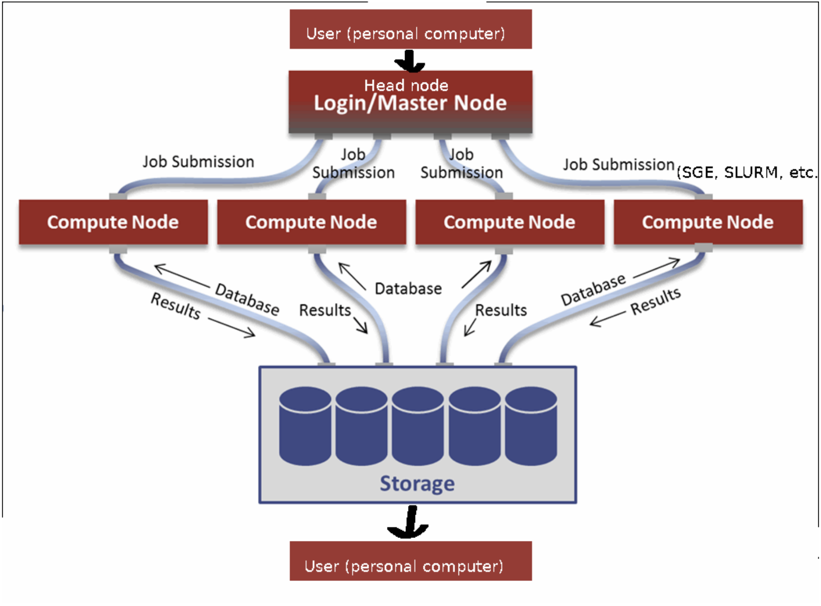
*other groups have similar resources, e.g.,

- `hyak` (managed by UW-IT)
- `pearson` (statistical genetics group only)
- `gizmo` (Fred Hutchinson Cancer Research Center only)
- Microsoft Azure, Amazon Web Services (AWS)

# Using the cluster



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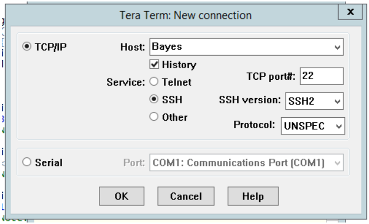
We'll practice good habits for being nice as we go along.

# Using the cluster: logging in (Windows, incl. box)

1. Open TeraTerm [or your favorite secure shell (SSH) client]
2. Enter the address of your favorite cluster, e.g., `bayes.biostat.washington.edu`
3. Make sure that the "New connection" window is filled out as in the figure, except for "Host" (screenshot from `box`)
4. Click `OK`, enter your UW BIOST username and password when prompted (user and pass you use for `box`)



Tera Term: New connection

● TCP/IP — Host: Bayes

☑ History

Service: ○ Telnet — TCP port#: 22

● SSH — SSH version: SSH2

○ Other — Protocol: UNSPEC

○ Serial — Port: COM1: Communications Port (COM1)

# Using the cluster: logging in (Mac/Linux)

1. Open a Terminal window

2. Type `ssh mynetid@cluster.washington.edu`
   - replace `mynetid` with Your UW NetID, and
   - replace `cluster` with Your cluster, e.g., `bayes`

3. Enter password (same password as `box`) when prompted (the field will remain blank but your password will be received)

# Using the cluster: logging in

Your turn!

1. Log into the cluster
2. What is the name of the directory that you are when you log in?
3. Create a directory called `robust_ses` in your `home` directory
4. Create a directory called `robust_ses` on **your** computer, under `biost561/lecture9`

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- navigation,
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- commands, and
- shell scripts

are all used in exactly the same way!

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Example job:

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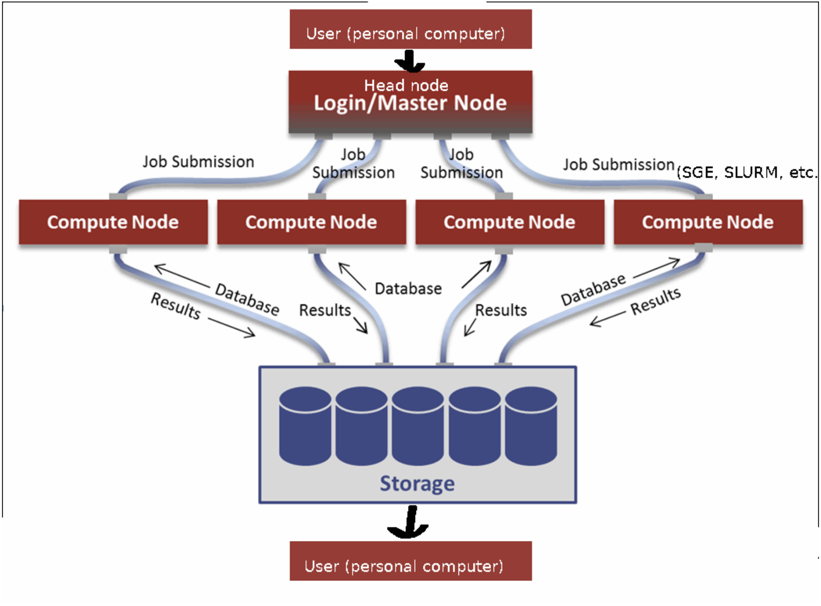

# Using the cluster: submitting jobs

Workhorse command on SGE: qsub

Many options, including:

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Options are specified with a single –, as you saw in Lecture 8.

# Using the cluster: checking jobs

# Using the cluster: other helpful SGE commands

# Appendix: other useful cluster things

# Useful things: Windows file compatability