

# Computing and Lab information

- C.1 Computing Information
- C.2 Computing Help
- C.3 Software information

## C.1 Computing information:

- We will use a Statistics virtual computer, running a linux operating system: – [statgen.stat.washington.edu](http://statgen.stat.washington.edu).
- All programs will be installed, and instructions on running the programs given.
- All the software we will use is comand-line driven.
- All the software is freely available – some may prefer to download and run their own versions on own machines.
- Software we will use is C, C++, Java. (Also R).

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## C.2 Computing help:

- StatGen software page:  
<https://depts.washington.edu/statgen/Computing/software.html>
- Statgen computing web pages:  
<https://depts.washington.edu/statgen/Computing/intro.html>
- Brief intro to linux for StatGen:  
<https://depts.washington.edu/statgen/Computing/linux-tut.html>
- Useful unix/linux commands  
<https://portal.biostat.washington.edu/computing/education/UsefulUNIXCommands.pdf>

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## C.3 Software to be used:

- PHASE or fastPHASE from Mathew Stephens  
An older program for phasing and imputation of missing alleles  
<http://stephenslab.uchicago.edu/software.html>
- BEAGLE 3.3.2 from the Brownings  
Also phasing, imputation, but also detecting shared genome  
<http://faculty.washington.edu/browning/beagle/beagle.html>
- Pedfiddler: a pedigree drawing program  
<http://www.stat.washington.edu/thompson/Genepi/Pedfiddler.shtml>
- MORGAN 3.2 – includes many programs for analysis of pedigrees and genetic data thereon, and also *ibd\_haplo* a program for inferring shared genome in absence of pedigree information.  
<http://www.stat.washington.edu/thompson/Genepi/MORGAN/Morgan.shtml>
- Also, R ....