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| **Week/Date** | **Activity/Location** | **Assignments & Due Dates** |
| April 5, 2016 | Orientation I:  Logging In and File Management  **ALS 4000** | HW1: Basic Command Line (ungraded)  Due: January 6 at 5 p.m. |
| April 7, 2016 | Orientation II:  More shell commands  **ALS 4000** | HW2: Preparatory Reading Assignment: PLEASE READ BEFORE CLASS BEGINS ON TUESDAY, APRIL 12th.  Davey et al. Genome-wide genetic marker discovery and genotyping using next-generation sequencing.  http://teaching.cgrb.oregonstate.edu/MCB/Rhodes/GBS\_Spring\_2016/Davey\_2011\_NatureGenotypingReview.pdf  Wange, Gerstein and Snyder 2009. RNA-Seq: a revolutionary tool for transcriptomics  <http://teaching.cgrb.oregonstate.edu/MCB/Rhodes/RNA_Seq_Winter_2016/RNA-Seq%20-%20a%20revolutionary%20tool%20for%20transcriptomics%20_%20supplemental.pdf>  Ozsolak and Milos. 2011. RNA sequencing: advances, challenges and opportunities  <http://teaching.cgrb.oregonstate.edu/MCB/Rhodes/RNA_Seq_Winter_2016/RNA%20sequencing%20-%20advances%2C%20challenges%20and%20opportunities.pdf>  Due: January 11 at 5 p.m. |
| January 12, 2016 | Syllabus  Discussion Activity  Lecture  **ALS 3005** | In class discussion activity. (10 pts.)  HW3: FastQC on command line and answering questions. (20 pts.)  Due: January 13 at 5 p.m. (20 pts.) |
| January 14, 2016 | Guest Lecture: Matthew Peterson, CGRB  Tutorial:  FastQC, Trimming and Clipping  **Cordley 3003** | In class completion of tutorial. (10 pts.)  HW4: Quality Control and digital normalization on the command line (20 pts.)  Reading Assignment:  Martin and Wang 2011. Next-generation transcriptome assembly  <http://biology.umd.edu/uploads/2/7/8/0/27804901/martin_and_wang_2012.pdf>  Steijger et al. 2013. Assessment of transcript reconstruction methods for RNA-seq  <http://www.nature.com/nmeth/journal/v10/n12/pdf/nmeth.2714.pdf>  Due: January 18 at 5 p.m. |
| January 19, 2016 | Guest Lecture:  Eli Meyer, IB  **ALS3005** | In class quiz on quality control terms. (10 pts.)  HW5: Evaluating an assembly and answering questions. (20 pts.)  Reading Assignment:  Garber et al. 2011 Computational methods for transcriptome annotation and quantification using RNA-seq  <http://teaching.cgrb.oregonstate.edu/MCB/Rhodes/RNA_Seq_Winter_2016/Computational%20methods%20for%20transcriptome%20annotation%20and%20quantification%20using%20RNA-Seq.pdf>  Li et al. 2014. Evaluation of de novo transcriptome assemblies from RNA-Seq data  <http://www.genomebiology.com/2014/15/12/553>  Due: January 20 at 5 p.m. |
| January 21, 2016 | Tutorial:  Effect of kmer size on assembly metrics.  Choosing an assembly program.  **Cordley 3003** | In class tutorial completion. (10 pts.)  HW6: Running an assembly using two alternative programs and comparing the results. (20 pts.)  Reading Assignment:  Trapnell et al. 2012. Differential gene and transcript expression analysis of RNA-Seq experiments with TopHat and Cufflinks <http://teaching.cgrb.oregonstate.edu/MCB/Rhodes/RNA_Seq_Winter_2016/Differential%20gene%20and%20transcript%20expression%20of%20analysis%20of%20RNA-Seq%20experiments%20with%20TopHat%20and%20Cufflinks.pdf>  Kim et al. 2013. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions  <http://www.genomebiology.com/content/pdf/gb-2013-14-4-r36.pdf>  Quinn et al. 2013. Development of strategies for SNP detection in RNA-Seq Data: application to lymphoblastoid cell lines and evaluation using 1000 Genomes data  <http://www.plosone.org/article/fetchObject.action?uri=info:doi/10.1371/journal.pone.0058815&representation=PDF>  Due January 26 at 5 p.m. |
| January 26, 2016 | Guest Lecture:  Kelly Vining  Touch base on final project.  **ALS3005** | In class quiz on assessing an assembly. (10 pts.)  HW 7: Read alignment programs and choices. (20 pts.)  & Final project topic (10 pts.)  Due January 28 at 5 p.m. |
| January 28, 2016 | Tutorial:  SNP detection in RNA-Seq data  Simple annotation.  **Cordley 3003** | In class tutorial completion. (10 pts.)  HW 8: Pick a recent paper that utilizes RNA-Seq data for *de novo* assembly for RNA-Seq or SNP detection and diagram the pipeline they utilized to construct their transcriptome. Write an analysis of 1.) Two or three items that you agreed with and would not change, 2.) Two or three items you would change to improve the results, and 3.) Describe the research question and whether the method chosen was the most efficient way to answer the question. (40 pts.)  Reading assignment:  Oshlack, Robinson and Young 2010. From RNA-seq reads to differential expression results  <http://www.genomebiology.com/content/pdf/gb-2010-11-12-220.pdf>  Due February 1 at 5 p.m. |
| February 2, 2016 | Lecture  Discussion Activity  **ALS 3005** | In class quiz on putting it all together. (30 pts.)  In class discussion activity based on HW 8 (20 pts.) |
|  |  | Final project write-up due February 3at 5 p.m. (100 pts.) |
| February 4, 2016 | In-class presentations  ALS 3005 | 4 minute lightning talks on your *de novo* transcriptome assembly project. (50 pts.) |
| February 9, 2016 | RNA-Seq orientation for Module II  ALS 3005 | Shawn O’Neil will be getting us ready for Module II by providing a two-day familiarization class on R and R Studio. |
| February 11, 2016 | RNA-Seq orientation for Module II  ALS 3005 |  |
|  |  | Details for Module II will be posted as they become available. |