What this course is about incremental: true The goal of this course is to introduce you to the *tools* and *thinking* required for bioinformatics analysis. Introduction to Linux command line Introduction to R Hands-on experience analyzing genomics data Principles of good analysis This is a computer-based class. No bench work. Why R and linux? incremental:true * Both R and Linux have command-line interfaces * Antiquated? * NO! Writen code provides flexibility, creativity, and power not available in any other way * Linux (or Unix / Mac) * Outstanding built-in tools for data crunching * Provides access to hundreds of bioinformatics programs * R * Powerful statistical, data processing, and graphical capabilities * Many bioinformatics packages are developed in R And coding is cool "Every student deserves the opportunity to learn computer programming. Coding can unlock creativity and open doors for an entire generation of American students. We need more coders — not just in the tech industry, but in every industry." - Mark Pincus, CEO and Founder, Zynga "Coding is engaging and empowering. It's a necessary 21st Century skill." - Jan Cuny, Program Officer, National Science Foundation "Code has become the 4th literacy. Everyone needs to know how our digital world works, not just engineers." - Mark Surman, Executive Director, The Mozilla Foundation "If you can program a computer, you can achieve your dreams. A computer doesn't care about your family background, your gender, just that you know how to code. But we're only teaching it in a small handful of schools, why?" - Dick Costolo, CEO, Twitter **Course Schedule** Tuesdays, Thursdays Lecture 1:10 - 2:00 • Lab 2:10 - 5:00 Often lecture will be shorter than 1 hour. We will start lab work as soon as lecture is over. Fridays TA Office hours 12:10 - 1:00 (in this room) Discussion 1:10 - 2:00 Varied use Q&A Student presentations Keep on working **Course History** Third year of the course Previous two years team taught This year it is all me... Some flexibility required... (Tentative) Course Outline incremental: true * Week 1-2: * Linux fundamentals * Markdown, git repositories * Sequence analysis and BLAST * Week 3: * R fundamentals * Weeks 4-5: * Illumina short reads * Calling SNPs * GWAS Weeks 6–7: RNAseq ChIPseq Week 8: Genetic Networks Week 9: Metagenomics Week 10 TBD **Course Grading** 45% Lab assignments 25% Take home midterm (Available May 1, Due May 5, 1:10 PM) • 25% Take home final (Available June 2, **Due June 8, 9:00 AM**) Do your own work incremental: true Developing code is an interactive process. Both your friends and the web can be excellent resources. **However** Any direct copying of text or code **from any source** is considered plagiarism in the context of this course. If you receive inspiration or ideas from an external source give attribution **Course Website** Main website: http://jnmaloof.github.io/BIS180L_web/ Lab instructions Course Schedule Helpful Links (coming soon!) Reading assignments (coming soon!) Smartsite Gradebook Chatroom Why are we here? incremental: true And what is bioinformatics? * OK so it is a requirement, but what else? Three principles of bioinformatics transition: rotate 1. Clear documentation 2. Reproducible results 3. Documents/Data in open (non-proprietary) formats 4. This is essential for achieving 1 and 2 Today's Lab type: section transition: rotate 1. Get a virtual linux machine running 2. Learn a little markdown 3. Learn about linux Virtual linux machine incremental: true The computer lab machines run Windows Bioinformatics on a Windows machine is painful or worse (R is OK) Solution: virtual machine! Use VirtualBox to run a virtual linux machine Your virtual machine is pre-loaded on a flash drive You can download virtualbox to your personal computer and run the machine at home Other virtual machine notes incremental:true As detailed in the lab notes for today: Use the USB 3 (Right hand) USB ports It is imperative that you properly shutdown the virtual machine before removing the flash drive Data will be backed up in the cloud using MEGA If you are already running linux, or want to try installing the relevant software on your Mac, I can give you installation notes. But we will not be able to help you troubleshoot installation problems Markdown Markdown is a text-based formatting system for quickly and easily generating nicely formatted output. It helps achieve all three guiding principles: 1. Clear documentations 2. Reproducibility 3. Open formats Markdown vs docx What is we want to produce this: A markdown example bulleted list point 1 point 2 point 3 some **bolded** or *italicized* text code chunk #simple code x <- 1:10 y <- 1:10 x + yformat # A markdown example ## bulleted list * point 1 * point 2 * point 3 some <u>__bolded__</u> or <u>_italicized_</u> text ## code chunk #simple code x <- 1:10 y <- 1:10 x + yThe markdown file that generates it is Markdown vs docx What is we want to produce this: A markdown example bulleted list point 1 point 2 point 3 some **bolded** or *italicized* text code chunk #simple code x <- 1:10 y <- 1:10 x + yformat The word file that generates it is erald:BIS180L jmaloof\$ cat word\ example.docx 6001111 : CENVHONO COOK, OIC, COOK OCCUPATO COOCO **♦66-6 ♦**KLXAT**©** XX 🐽 | **個≪>α������ �! �**(J宂 �����]� **4**8 q **960** fR**¢i.¢**t&y7**¢00t.d¢g",¢00**Ek**¢*¢00-¢0**\pZki**.¢0**\J**¢~¢0**5I{**¢00000?**)-kbT**¢0000 ¢0>¢6**E@**¢**n{-(**¢0000000?¢00&**(💔 🌖 УЙЙ /�ph3"������^A ~NA�£4-+E?0•x�����Y+**_����**y�**E���**N Z**484666 4-466t94s46n46654** x **366**66

Welcome to BIS180L

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Course Personnel

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Assignments to turn in for this lab

We will provide a system for turning in assignments later this week or next week.

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In the meantime, keep:

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The file from the markdown tutorial

Lets go have fun!

The notes (in Markdown!) from the linux tutorial The answer to "Excercise 1" from the linux tutorial