| **Component** | **Description** | **Rationale** |
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| **General Information** | Unix for Computational Biologists - Part I - 1.5 hr | Usage of Unix in Computational Biology |
| **Learning Objectives** | Give the novice participants a flavor of Unix and give the experience participants ideas on how Unix scripting can be used in computational biology. | The raw output of biological research exists as *in silico* data, usually in the form of large text files. Unix  is particularly suited to working with such files and has several powerful (and flexible) commands that can process such data. I want the participants to appreciate the real strength of learning Unix is that most of these commands can be combined in an almost unlimited fashion. |
| **Resources** | Handouts and lecture | Class will focus on hands on exercises along with the lectures. |
| **Procedures, Content, Activities** | * Introduction to Unix * Commonly used Commands (*ls, cd, man, mkdir, touch, mv, cp, rm, less, vi*) * Creating .profile file and aliases * Changing permission of file * File manipulation with *grep, sed awk* | The participants will be given a cheat sheet for common Unix commands. Novice Unix users will be encouraged to use the commands to manipulate files with Unix commands and create a .profile file. More experienced participants will be encouraged to implement some practices that makes data handling easier. |