| **Component** | **Description** | **Rationale** |
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| **General Information** | Unix for Computational Biologists - Part II - 1.5 hr | Usage of bash script in Computational Biology |
| **Learning Objectives** | Give the novice participants a flavor of scripting with bash and give the experience participants example of some advanced scripting practices. | The raw output of biological research exists as *in silico* data. Bash scripting can be useful in standardizing initial analysis of these files and create formatted output which can be easily manipulated by other software packages. I want the participants to appreciate the usage of bash scripting in computational biology. |
| **Resources** | Handouts and lecture | Class will focus on hands on exercises along with the lectures. |
| **Procedures, Content, Activities** | * Introduction to bash scripting * Logic and loops in bash scritping * Math in bash scripting * File manipulation with *grep, sed awk* using bash scripting * Creating pipeline using bash scripting. | The participants will be given a cheat sheet for common Unix commands. Novice Unix users will be encouraged to use the commands and create bash scripts to manipulate some of the data files they are given. More experienced participants will be encouraged to create more advanced pipelines. |

| **Component** | **Description** | **Rationale** |
| --- | --- | --- |
| **General Information** | Sequence Analysis and Function Prediction – 1.5 hr | Predicting protein function from sequence similarities. |
| **Learning Objectives** | Introduce different aspects of computational function annotation. Discuss in more in details of functional annotation from sequence data. Introduce difference computational functional annotation servers and software tools. | Computational function annotation, or computational proteomics, plays a crucial role not only in the annotation process of newly sequenced genomes, but also in the interpretation of high-throughput experimental data such as gene expression patterns by microarray or protein–protein interaction data. I want the participants to know about different aspects of computational function annotation particularly annotation of function from sequence data. |
| **Resources** | Handouts and lecture | Class will focus on hands on exercises along with the lectures. |
| **Procedures, Content, Activities** | * Introduction to computational functional annotation. * Introduction to Sequence similarities. * Functional annotation from seqeunce, genomic, proteomic and structural data. * Discussion about PFP - protein function prediction webserver from GO term. | The participants will know the logic behind the computational function prediction and will be using the PFP and ESG server to predict fucntion from sequences. |