

CAPOD Funding Report

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Event /Course Title	Introduction to Linux and Workflows for Biologists
Date of event	Scheduled: 11-15 December 2017. Course was cancelled after two days because instructor was sick. Re-scheduled for 14-18 May 2018.

1. Brief description of Event (50-100 words):

An introduction to the Linux Command line, the language that most high-throughput bioinformatics work is done. This course teaches students to make the most of the tools available within this environment to achieve a higher level of productivity.

2. What were the benefits of attending and what did you gain from the experience in terms of transferable skills and knowledge.

Before this course I had almost no experience using a command line computer environment, which is required for the large datasets and analyses I will be undertaking in my Phd. In today's scientific world, we are able to generate so much more data than ever before and being able to process and analyse giga- or terabytes of data, requires the use of specific software and a skill set that includes confident command line coding. This course is being taught by experts in this field including Dr Martin Jones, the founder of "Python for Biologists" and Edinburgh Genomics. Regardless of what work I end up doing in the future, as a scientist I will need to have the most cutting-edge skills when it comes to processing huge amounts of data, a skill this course has now provided.

3. What actions will you be taking as a result of attending or by making new networking contacts.

My new-found competence and confidence using Linux will allow me to take the first steps in analysing the data I have generated for my PhD. Linux is a massively customizable environment and my new skills will allow me to take advantage of all the resources available when one is able to use a command line environment.

4. Can you share any additional resources produced in connection with the event (e.g. feedback from participants, training resources, website links, and additional materials.

I was provided with all of the course materials so that I may go through each lesson again and continue practicing with the tutorials and practicals. Additionally, further courses are offered both with Martin and Edinburgh Genomics, which I would now be eligible to take since having completed the introductory course first.

5. Tips/experience learned from the event

Apart from beginning to learn a whole new language to incorporate into my analyses using Linux, the most beneficial aspect of this course was the repetition of constantly using Linux and thus becoming immensely more comfortable to conduct my analysis steps in this environment. I have also obtained enough of a background in this subject to be able to efficiently utilise the resources available online to further my skillset.

6. Any additional comments or information regarding the event

This course was massively beneficial for me as an up and coming scientist. Whether the field is genomics or not, understanding and being comfortable in a command line environment will allow me explore vast amounts of data and begin to compile the resources available to conduct whatever analysis I see best fit for the data.