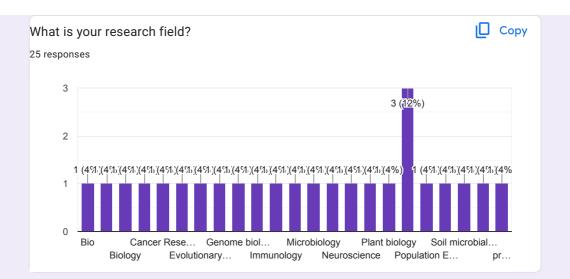


Why did you attend this course? 25 responses NGS is popular interest Improving my skills To learn basics of Linux and use it for my data analysis Good to refresh my knowledge of Bash before BIO610 To learn the coding for data analysis to get basics of Linux Because I will work with the presented technologies - and have no previous knowledge. To learn data analysis I'll need to do bioinformatics of NGS data Get basic knowledge about Bash To have a proper introduction to bash scripting Learning about Bash scripting and sequencing data analysis I need a last ECTS from a method course, and thought it would be a good occasions to learn something different, even if I don't need it for my research To learn necessary skills for genomic data processing and analysis for my PhD project To learn how to analyse data for my PhD project to use Linux for computational modelling To learn very basics To get a refresher in linux need basics of linux Need some Bash Scripting for my master thesis I want to get an insight about the use of Linux for sequenced dada I will start analyzing genomic data and I thought it would be useful to get an introduction to Linux.

To get some basic knowledge.





Would you recommend this course to others? Why? 25 responses Yes yes, helpful To learn coding Yes, because it was mostly hands on and even if it was very fast it's still better than listening to someone reading through slides the whole time Yes, I found it clear and very informative yes, it is useful and informative for new beginners Yes, nice entry point, even if it was fast. Good to get a first idea and lernen autonomously from then on. Yes, though since it's so fast, it would be beneficial to prepare a bit from home Yes. Very useful Yes, well done and nice instructors yes, useful if you need to learn basics of bash Yes; this is very helpful to get a clear idea + some essential basic knowledge to be able to perform data-related tasks using bash scripting Yes, it's a good course for starting at bioinformatics I would recommend this course to people who have already some experiences. For begginers would be better go threw it slowly and maybe devide the course to more days. Yes, if you have prior knowledge or experience with code Not really, the problems involves some contents which are not introduced in the course Yes, was a good introduction for someone who has never worked with Bash Yes, because its always to learn something new Yes, because it was very easy to follow and it covered the most important topics to get started with bash. Yes, very helpful for beginners.

Additional comments or suggestions about this course. 25 responses No None nο Nothing Installing the docker was a nightmare and costed many hours. It would be great if there could be a simpler alternative like a server to log into. It would help if can put the issue and solution which people met when installing docker and git in advance no, everythings good With fast I mean: instructor should dwell longer on slides/his terminal instead of jumping around that fast Nice to have genomics example, maybe ask people who could not set up the system to be earlier at the course so we don't waste time with this at the beginning Sometimes the course was too fast, especially when we were trying to type and getting the meaning of what was explained the last exercise was too complicated for a beginner course Could talk a bit about the prerequisites / related concepts that we might encounter, e.g. What are WSLs, Ubuntu, etc. Overall the course was very good. Questions were answered clearly. I very appreciate presence of more experts who were able to give advices during the whole course. The speech was very nice, there was appropriate amount of theory for introduction. The beggining of the course was very nice with exercises after learning small amount of commands. But the end of the morning and the afternoon part was very quick for begginers. Also would be much more better to have the slides to follow the commands because it is not easy to remember everything in just one day. So from the afternoon part I did not took much, because I did not keep up the speaker. I see the point with not distributing the slides beforehand, BUT it makes it super stressfull to note everything down as one simply cannot remember every command immediately. Especially for the end exercise I was confused on wether to do the exercise myself or just wait and follow

his explantions (but impossible to do both simultaniously..!).

Also, typing down urls is very 2010, just provide a gr code. Unnecessary source of errors and waste of time if you have to check every character if your code doesn't work due to a typo.

please prepare good problems for students who has no basement in this field. The difficult problem will only make students depressed and lose their interest of keep learning

I was not happy with the fact that I was not in the participant list and therefore could not prepare the Docker-Linux for practical. I wasted my time to find out how it works instead of focusing on the course.



It would have been useful to get an email with all the links so that we did not have the need to copy them from the screen.

Reduce the difficulty of practice questions.

General Comments about the PSC Graduate Program / the URPP Evolution in Action / the PhD Program in Evolutionary Biology

he PhD Program in Evolutionary Biology
25 responses
Good
No comment
None
No
no
-
Nothing
NA
Great program
This is the first course within the PSC that I'm attending
Nice Programm, very diverse, just as the attendees of the course.
I am not from these programs
Would be nice to have more courses about evolution or population genetics
Courses like this are really great. It would be great to have more frequency
I am not part of any of these
N.A.
Good program so far
No comments
none
I am not in this program
I'm not part of the PSC Graduate Program
Nice



Other topics you would like to see offered.
25 responses
None
none
No
no
-
Other programing systems
Data plotting in python/ R
More bioinformatics and more soil science
don't know now
Nothing I have in mind right now.
introduce awk command
I currently can't tell
WGBS data analysis
Population genetics
I don't know
N.A.
About seed development and germination
Compiling Source Codes in Linux
Simmilar course focused more on beginners
more knowledge about codes
How to create a library, do sequencing
It would also be useful to have a lecture on how to use the cluster and it thinks it aligns well with the content of this course.
It is good for me.

If you would like to contribute to further improve the course, please leave your email.
3 responses
mona.sauder@gmail.com
-
robin.weber@uzh.ch

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