



All homework submissions occur via github

Homework (part 1):

1. Create an account at github.com (Slack —> Mark with your userid)
2. Acquaint yourself with git/github [1]
3. Make sure you know how to check in / out files from command line or app [2]
4. Create a new public repository, add a README.md (using markdown [3]) and add some content
 - Include an image; Include a web link
 - add an Issue to the 'material' repo to give the link of your repo
 - (you can delete the repo after I've closed the issue, if you want)

[1] <https://gist.github.com/andrewpmiller/9668225>

[2] <https://confluence.atlassian.com/stash/basic-git-commands-278071958.html>

[3] <http://markdowntutorial.com/>

Rmarkdown / knitr for executable documents / reproducibility

Homework (part 2):

Acquaint yourself with knitr HTML Rmarkdown documents:

1. Create an HTML document that samples 100 values from a log-normal distribution (say, $\mu=1$, $\sigma=.25$); create a histogram of the sample on both the linear and log scale; report the mean and variance of the sample in line in the text.
 - NB: Do not just dump the R code and plots in the HTML document; add some text and headings and make it readable (i.e., the document should be self-explanatory)



Status update

- 39 students “registered” (35 registered in the University system)
- NB: for those later-to-register, if you need an account to use the Macs in 01-F-50, email tina@ieu.uzh.ch (me in cc) with: name, Uni email address, matriculation number
- 32 have sent me their GitHub usernames; 8 inferred from Issues
- **7 need to send GitHub usernames**
- 32 Issues sent (Part 1)
- 29 private repos created (Part2; *exercise-1-r-markdown-USERNAME*)
- NB: Exercise 1 due 18.00 26 Sep 2018



Exercises

- “Across 14 weeks, the *best 9* exercises are counted towards the 30%”
- After the marking has been done each week, you will receive an automatic email with an update of all exercises
- Solutions (when applicable) will be made available in a private repo
- Feedback on exercises (when applicable) will be given as Issues in the private repos
- Please join the #exercises Slack channel (not added automatically); questions should go there

Other notes

- Next week's 'Technology Day': very important to attend; we will survey a bunch of statistical methods, high-throughput genomic assays and relate them to each other; Github exercise with *pull requests*
- Journal Club: start thinking about a statistical-method-in-genomics paper to present to the class; given the number of students, groups of 2; can use also the #papers channel

Date	Lecturer	Topic	Exercise	JC1	JC2
17.09.2018	Mark + Hubert	admin; mol. bio. basics	R markdown; git(hub)		
24.09.2018	Hubert	NGS intro; exploratory data analysis	EDA in R		
01.10.2018	Mark + Hubert	interactive technology/statistics session	group exercise: technology pull request		
08.10.2018	Hubert	mapping	Rsubread		
15.10.2018	Mark	limma + friends	linear model simulation + design matrices		
22.10.2018	Hubert	RNA-seq quantification	RSEM		
29.10.2018	Charlotte	hands-on session #1: RNA-seq	FASTQC/Salmon/etc.	X	X
05.11.2018	Mark	edgeR+friends 1	basic edgeR/voom		
12.11.2018	Mark	edgeR+friends 2	GLM/DEXSeq		
19.11.2018	Mark	single-cell dim. reduction + clustering; FDR	conquer		
26.11.2018	Lukas	hands-on session #2: cytometry	cytof null comparison	X	X
03.12.2018	Hubert	classification	MLInterfaces		
10.12.2018	Mark	loose ends: HMM, EM, robustness	segmentation, peak finding		
17.12.2018	Mark	hands-on session #3: single-cell RNA-seq	full scRNA-seq pipeline	X	X