STA 426: Statistical Analysis of High-Throughput Genomic and Transcriptomic Data

- We've received 4/6 pull requests from last week's technology day. The rest are due: 18.00 Wed 12th Oct

- If you were away on 3th Oct, your assignment is the same: a pull request for one of the technologies from https://liorpachter.wordpress.com/seq/ (not one of the ones already taken)

- The **17 Oct** class is a hands-on RNA-seq session (we will see some of the statistical theory in a few weeks), run by Charlotte Soneson. The whole session will take place in **Y11-J-05**. If you want to use your own computer for it, please: i) install the list of software that Charlotte will post; ii) download the raw data (~300MB) to your computer. More details will be given on Slack this week.

Mark D. Robinson, Statistical Genomics, IMLS

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- Projects: can be done in groups (size 2-3). Or, it can be done solo. (See the slides from the first lecture for more description.)

- Projects: someone contacted me last week about a project involving *differential expression of long non-coding RNAs*, 48 samples paired end. This collaboration would be a reasonable project for the course.

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- Journal club: please start thinking about a journal club paper. There was a question in lecture a couple of weeks ago, and, **YES**, it would be fine if a group of up to 3 work together to prepare the journal club presentation.

- See schedule on next slide. Some pressure will be applied soon (doodle or similar) to sign up for the journal club slot.

Mark D. Robinson, Statistical Genomics, IMLS

Note the schedule for journal clubs

Tentative Schedule

Date	Lecturer	Topic	JC1	JC2
19.09.2016	Mark; Hubert	admin, mol. biology basics, R markdown		
26.09.2016	Hubert	exploratory data analysis		
03.10.2016	Mark; Hubert	interactive technology session		
10.10.2016	Hubert	NGS intro; mapping		
17.10.2016	Charlotte	hands-on RNA-seq session		
24.10.2016	Mark	limma 1		
31.10.2016	Mark	limma 2	x	x
07.11.2016	Hubert	RNA-seq quantification	x	x
14.11.2016	Mark	edgeR+friends 1	x	x
21.11.2016	Mark	edgeR+friends 2	x	x
28.11.2016	Hubert	classification	x	x
5.12.2016	Mark	epigenomics, DNA methylation	x	x
12.12.2016	Mark	gene set analysis	x	x
19.12.2016	Mark	single-cell	x	x