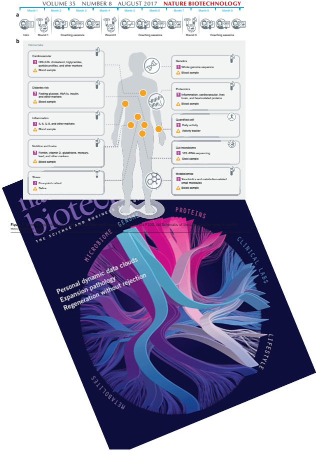
Statistical Genomics: Master of Science in Bioinformatics and Master of Science in Statistical Data Analysis

Lieven Clement
Ghent University, Belgium

Scientific Integrity and Reproducible Research

Bio-informatics research is based on empirical data



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Mass spectrometrists should search only for peptides they care about

William Stafford Noble

WEBINAR
Proteogenomic strategies to advance drug development and precision medicine
Recorded live on September 6, 2017
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TECHNOLOGY FEATURE

Big biological impacts from big data

By Mike May | Jun. 13, 2014 , 5:45 PM

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Mass spectrometrists should search for all peptides, but assess only the ones they care about

NATURE METHODS | VOL.14 NO.7 | JULY 2017 | 643

Adriaan Sticker1–4, Lennart Martens2–5 & Lieven Clement1,4,5

COMMENT

A tragedy of errors

Mistakes in peer-reviewed papers are easy to find but hard to fix, report David B. Allison and colleagues.

Personal dynamic data clouds
Expansion pathology
Regeneration without rejection

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→ Number of observations <<< number of features

→ Need for statistics to distinguish real patterns from random patterns in high dimensional data

Topics

Module I: Quantitative Proteomics

1. Identification and quantification of peptides and proteins
2. Data exploration and quality control using plots
3. Preprocessing: log-transformation, Filtering, Normalization, Summarization
4. Dealing with batch effects and other confounders
5. Statistical Concepts
    1. Linear models/Linear mixed models
    2. Trade-off between biological relevance/effect size vs statistical significance
    3. Empirical Bayes Methods
    4. Multiple testing

Module II: Next generation sequencing (NGS, Transcriptomics)

1. NGS Data exploration
2. Preprocessing/normalization
3. Additional Statistical Concepts
    1. Generalized linear models (GLM) for binary data
    2. GLM for count data
    3. Overdispersion

Organisation

1. Theory and Tutorials are blended
   - Module I: week 1-5
   - Module II: week 6-10
   - Project: week 1-10 via small assignments + week 11-12

2. Communication and submission of projects via Ufora
3. All tutorials from week 2 onwards are based on R/Bioconductor
   - via R-studio
   - Scripts are made in R/markdown: a file format to combine text, R code and R output.

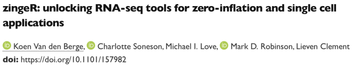
   → This makes it very easy to document your analysis and to distribute them in a way which is reproducible.

Organisation

4. Project
   - Projects: 10/20
   - Written Exam: 10/20.
     - Open book
     - Deep insight expected
     - Critical assessment of R-output,

Projects + Master thesis

- Project 201415, Master thesis 201516:

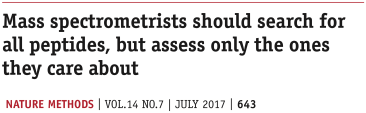


zingeR: unlocking RNA-seq tools for zero-inflation and single cell applications

Koen Van den Berge, Charlotte Soneson, Michael I. Love, Mark D. Robinson, Lieven Clement

doi: https://doi.org/10.1101/157982

- Project 201516: Neurogenomic profiling reveals distinct gene expression profiles between brain parts that are consistent across cichlid species of the genus Ophthalmotilapia. Derycke et al. 2018.
- Project 201516: Manuscript in preparation. A leap of the hurdle in mass spectrometry based proteomics. (Presentation at HUPO conference 2017).



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NATURE METHODS | VOL.14 NO.7 | JULY 2017 | **643**

- Master thesis 201516:

Adriaan Sticker[1–4], Lennart Martens[2–5] & Lieven Clement[1,4,5]

- Design Project 201718: paper in preparation.
- Continuing on statistical genomics project for thesis is possible.