## Article choice and exam

### Key steps

- Create pairs (VUB/ULB?), but can do alone
- Select the article (by 18/3)
- Reimplement the method (is it reproducible?)
- Write up article
  - Method description, visualise/interpret results, discuss method itself in relation to others
- Submit the article (by 1/6)
- Evaluate other student's article (before exam)
- Exam presentation with question time (students + profs)
  - Dates to be determined when your exam schedules known

- Needs to be an original method, not meta-approach
- All key data to develop the method has to be publicly available
- Choose your own
  - Look in Bioinformatics, PLOS computational biology
  - You can choose others but need to be relevant
  - Is the method itself well described?
    - If models, are the formulas available?
    - If machine learning, is the approach not too complex?
  - Are the results reproducible?
    - If they run their method on many different datasets, this complicates things

- Pick from our list
  - In project\_article\_suggestions directory

Published online 1 June 2018

Nucleic Acids Research, 2018, Vol. 46, Web Server issue W329-W337 doi: 10.1093/nar/gkv384

# IUPred2A: context-dependent prediction of protein disorder as a function of redox state and protein binding PLOS COMPUTATIONAL BIOLOGY

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Received February 26, 2018; Revised April 17, 2018; Editorial Decision

RESEARCH ARTICLE

RNA structure prediction using positive and negative evolutionary information

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Article

## PRIP: A Protein-RNA Interface Predictor Based on Semantics of Sequences

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PLOS COMPUTATIONAL BIOLOGY

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**RESEARCH ARTICLE** 

## Deciphering the RRM-RNA recognition code: A computational analysis

Joel Roca-Martínez 1,2, Hrishikesh Dhondge 3, Michael Sattler 4,5, Wim F. Vranken 1,2 \*\*

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Bioinformatics, 35(15), 2019, 2529–2534 doi: 10.1093/bioinformatics/bty981 Advance Access Publication Date: 10 December 2018 Discovery Note



Genome analysis

Xiao et al. BMC Bioinformatics 2020, **21**(Suppl 16):540 https://doi.org/10.1186/s12859-020-03883-x

#### **BMC** Bioinformatics

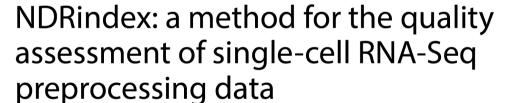
## Deciphering the complex non-coding promoter-pro

Sarah N. Mapelli<sup>1,2,3</sup>, Sara Napoli<sup>1</sup>, Giu Ramon Garcia-Escudero<sup>1,4</sup>, Giuseppin Carlo V. Catapano<sup>1,3,5,\*</sup>

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#### SOFTWARE

Open Access





Ruiyu Xiao<sup>1</sup>, Guoshan Lu<sup>1</sup>, Wanqian Guo<sup>2</sup> and Shuilin Jin<sup>2,3\*</sup>

*From* Biological Ontologies and Knowledge bases workshop 2019 San Diego, CA, USA. 18-21 November 2019

Bioinformatics, 37(1), 2021, 43–49 doi: 10.1093/bioinformatics/btaa669 Advance Access Publication Date: 29 July 2020 Original Paper



Gene expression

## netAE: semi-supervised of single-cell RNA sequenci

#### Zhengyang Dong (1) 1 and Gil Alterovi

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Bioinformatics, 36(4), 2020, 1159–1166
doi: 10.1093/bioinformatics/btz704
Advance Access Publication Date: 10 September 2019
Original Paper



#### Gene expression

## Spectrum: fast density-aware spectral clustering for single and multi-omic data

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OXFORD

Gene expression

# Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer

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### What to do after you select the article?

- Get the raw data for the method reimplementation
  - Can you physically download it?
  - Is it readable, not too large, ...
- Re-implement the method
  - Preferably in Jupyter/Python, is easier to evaluate, but anything is fine
- Mitigation
  - If you have problems, let us know, and discuss it with us
  - It might be possible that you cannot re-implement everything, but we need to know in advance why and what
- Write this up in article form
  - We will have question sessions in case you have problems (see schedule)
  - Submission date 01/06, 23:59, with project code etc. (git rep also OK)

## Matchmaking?

- Can do a quick matchmaking session now?
- Set up a chat channel for this?