

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

Article selection

- 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

Article selection

- 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/gky384*

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

PLOS COMPUTATIONAL BIOLOGY

Bálint Mészáros, Gábor Erdős and Zsuzsan

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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 selection



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

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Article selection

Bioinformatics, 35(15), 2019, 2529–2534

doi: 10.1093/bioinformatics/bty981

Advance Access Publication Date: 10 December 2018

Discovery Note



Genome analysis

Deciphering the complex non-coding promoter-pro

**Sarah N. Mapelli^{1,2,3}, Sara Napoli¹, Giu
Ramon Garcia-Escudero^{1,4}, Giuseppin
Carlo V. Catapano^{1,3,5,*}**

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

BMC Bioinformatics

SOFTWARE

Open Access

NDRindex: a method for the quality assessment of single-cell RNA-Seq preprocessing data



Ruiyu Xiao¹, Guoshan Lu¹, Wanqian Guo² and Shuilin Jin^{2,3*}

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

Article selection

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



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



Gene expression

netAE: semi-supervised clustering for single-cell RNA sequencing

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Associate Editor: Jan Gorodkin

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Gene expression

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

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Article selection

Bioinformatics, 34(11), 2018, 1859–1867

doi: 10.1093/bioinformatics/bty004

Advance Access Publication Date: 12 January 2018

Original Paper

OXFORD

Gene expression

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

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Luciane T. Kagohara¹, Genevieve L. Stein-O'Brien¹, Dylan Kelley²,
Emily Flam², Kristina D. Zambo², Patrick K. Ha⁴, Donald Geman⁵,
Michael F. Ochs⁶, Joseph A. Califano⁷, Daria A. Gaykalova²,
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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?