Toets Bioinformatics for Translational Medicin

Aantal vragen: 10
Afnameperiode: 31 mei 2023 08:30 - 11:45
Tijdsduur: 135 minuten

Instructie

Welcome to the exam of the course Bioinformatics for Translational Medicine (X_405092) in June 2022.

The exam consists of 2 parts:
- A theory part consisting of 6 questions. You should only make 4 of these. Two of them you need to leave blank. [60%]
- A workflow part with 4 questions about the workflow. [40%]

The following tools are permitted:
- Papers as PDF via testvision:
  - Beekhof_2019_Mol. Syst. Biol.
  - Bosdriesz_2020_bioRxiv
  - van_den_Broek_et_al_2015
  - Mourragui et al 2021
  - Rentroia Pacheco et al 2022
  - May et al. - 2015 - metaModules identifies key functional subnetworks in microbiome-related disease
  - Kemper et al. - 2016
  - Claireaux_2022
  - Smakaj et al. 2020
  - Wilkinson et al. - 2016

- Max. two sides of A4 paper with personal notes on / summaries of the papers.
- Max. one side of A4 paper with your workflow (see below).
- Scrap paper and pen/pencil; scrap 'paper' will also be provided via testvision
- The calculator is provided via testvision
- A spell check is provided via testvision

After the exam you can contact the teacher for questions about the content of the test.

If you have not signed up for this exam, you will not receive a result. Through VUnet you can object to the fact that you can no longer sign up after the expiry of the registration deadline (and the fact that you will not receive a result for this exam). Submit your appeal online within one week after the exam. More information can be found at www.vu.nl/intekenen.

Block Theory questions (choose 4 out of 6)

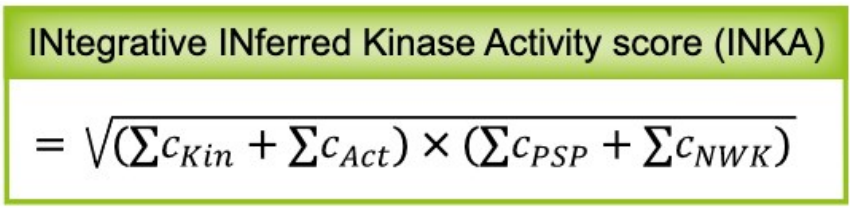
The first part of the exam consists of 6 theory questions. You can choose 4 questions to answer and leave the other one blank. If you answer all 6 questions (i.e. leave none blank), only questions 1-4 will be graded.

Note that the word limits are upper limits. It is no problem if you use less words. If you exceed the word limit, up to 20% of the points for that questions can be deduced. We do not consider the word limits for the sub-questions separately.

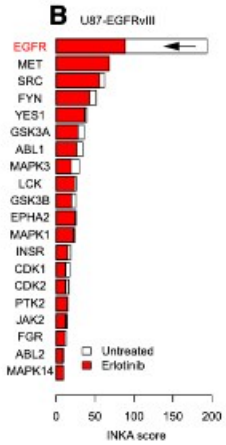
Vraag 1 – Open – ID: 322418 (15 punten)

Q1 Beekhof

Paper: Beekhof_2019_Mol. Syst. Biol.



Q1A. The INKA score is built out of 4 elements (c_{kin}, c_{act}, c_{psp} and c_{nwk}, see part of Figure 1B reproduced above). What does each of these mean, and what is the rationale for using these? [8 pts] (word limit: 75)



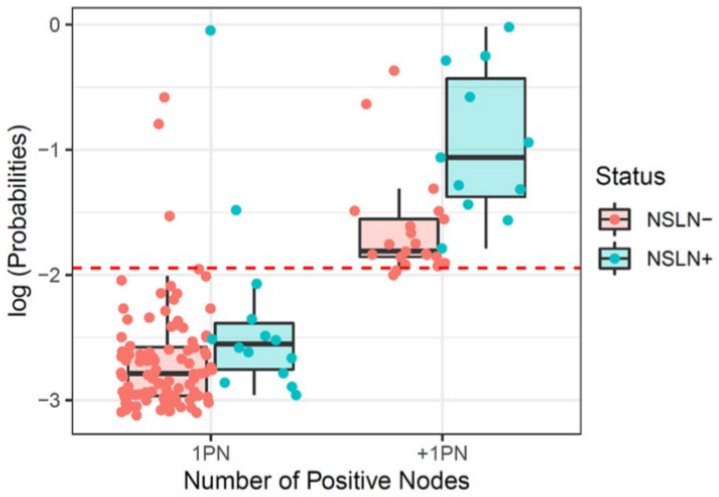
Q1B Consider Figure 5B. What do you conclude from this, and is this what you would expect? Motivate your answer. [7 pts] (word limit: 50)

Vraag 2 – Open – ID: 322419 (15 punten)

Q2 Rentroia-Pacheco

Paper: Rentroia Pacheco et al 2022

Q2A. What is the main research question that this paper aims to answer? Specifically, if the clinicopathologic model prediction is accurate, what clinical decision should be based on it. [6 pts] (word limit: 50)



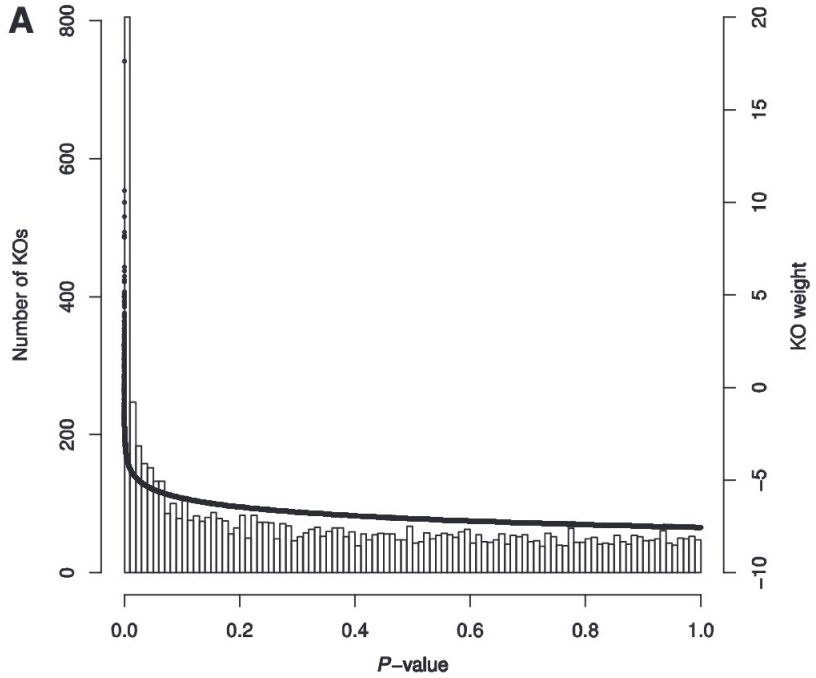
Q2B. Figure 1 (reproduced above) shows the output of the Bertolli model, colour-coded by NSLN status and stratified by number of positive SLNs. What is the main conclusion from this figure about the usefulness of the Bertolli model, and why? Relate your answer to the red dashed line. (Word limit: 100)[9 pts]

Vraag 3 – Open – ID: 322420 (15 punten)

Q3 May 2015

Paper: May et al. - 2015 - metaModules identifies key functional subnetworks in microbiome-related disease

The goal of metaModules is to identify gene-modules that are deregulated in disease. This is done by searching for the highest scoring subnetwork of KOs.



Q3A Consider Figure 1 A from May et al (replicated above). Explain what the *x*-values in the histogram mean, and from what kind of analysis they are derived. Please be precise. [5 pts] (word limit: 50)

Q3B With respect to the differential expression analysis, what is the range of x-values that is of largest interest/contains the signal in the data? Briefly explain why. [2 pts] (word limit: 50)

Q3C Explain what the thick black line indicates, and how it is subsequently used to generate Figure 2 A. [8 pts] (word limit: 100)

Vraag 4 – Open – ID: 322421 (15 punten)

Q4 Mourragui [15 pts]

Paper: Mourragui et al 2021

Consider the methods discussed in this paper (i.e. TRANSACT) and similar methods (e.g. PRECISE, the other method that was discussed during the lecture).

Q4A. List all the inputs and the output of these methods. [4 pts]

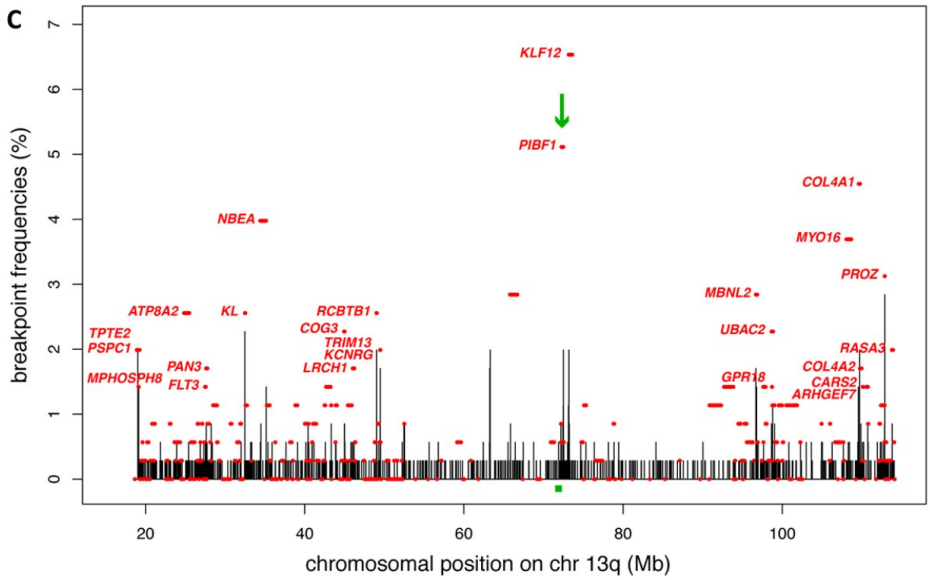
Q4B.What is the main biomedical challenge that these methods aim to solve. Relate it to the inputs and output? (word limit: 75) [5 pts]

Q4C. Do you think TRANSACT is suitable to study cancer immunotherapies? Motivate your answer, relate it to the consensus features. (Word limit: 50) [6 pts]

Vraag 5 – Open – ID: 322422 (15 punten)

Q5: van der Broek 2015 [15 pts]

Paper: van_den_Broek_et_al_2015



Q5A. Consider Figure 1C of van der Broek et al. (reproduced above). What is depicted on the y-axis, and what are the named red bars? In your own words, briefly describe from what data-type they are derived and how. Include how the named red bars are determined. [10 pts] (word limit: 100)

Q5B. To what kind of biological abberation are the red bars related? And how are these abberation related to tumour biology? [5 pts] (word limit: 50)

Vraag 6 – Open – ID: 322454 (15 punten)

Q6 Bosdriesz et al. [15 pts]

Paper: Bosdriesz_2020_bioRxiv

Q6A What is the main goal of the pipeline described in this paper? Relate this to simple drug response prediction and mention at least two ways in which it differs from this? (word limit: 100)[9 pts]

Q6B To what extent was this approach successful? Describe both something that worked and something that did not work. (word limit: 50)[6 pts]

Block Workflow

You were asked to prepare a workflow to adres a research questions within the domain of translational bioinformatics, based on at least two components (A "component" can be an experimental technique, computational method, workflow, experimental- or processed data, biological samples, patient cohorts and general ideas / insights.) from the papers discussed in the guest lectures, and upload a sketch of this to Canvas prior to the exam. In the next questions, you will describe the aim of this workflow and the approach to accomplish this aim.

Vraag 7 – Open – ID: 322413 (10 punten)

Write down the research question that the workflow you have prepared aims to answer in the textbox below.

Vraag 8 – Open – ID: 322414 (4 punten)

List the two components from the guest lecture papers that you used in your workflow, and indicate in which papers these components were used. (If you used more than two components from the guest lecture papers, pick two.) Cite the paper by the last name of the first author, and name or describe the component you use. For instance: May et al.; Optimal scoring subnetwork detection using HEINZ.

Vraag 9 – Open – ID: 322415 (16 punten)

A. Describe the "external" inputs and outputs of your workflow. What raw data does your workflow use? What processed data or reports does it ultimately produce? (50 words)

B. For one of the components you listed above, describe how it fits in the workflow. Indicate which component you pick and:

- if it is a computational method, describe what the input and output of that step is.
- If it is a data-set or experimental technique, describe to what step it serves as an input, and describe the output of that step.

Word limit: 50 words.

Vraag 10 – Open – ID: 322416 (10 punten)

For this question, assume everything works as expected. Either the results of your workflow are directly applicable in the clinic, or more/additional research is required before it can affect clinical practice. If your results are directly applicable, please describe how this will be implemented practically, and how it benefits patients. If your proposal doesn't directly impact clinical practice (which is OK and even likely), please describe which follow-up research (e.g. validations, translation, clinical trial) will be required before it can impact patient treatment.

Please first state explicitly if your workflow is directly applicable (150 words).

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