Home assignment on MEM tool

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Rules

• Deadline for sending the homework to me is Wednesday, 23:59 5th of October

• I will grade your works by the beginning of the next seminar, 10:15 7th of October

• I will provide you with feedback during the week after the next seminar

• Please, send me your works via email even if you are not confident about your answers

• You can send your works in any format you like, but it must be readable
Why do we need to apply normalisation to the expression data?
Explain in few words why we need to measure global coexpression instead of just local one.
• Go to the MEM page (http://biit.cs.ut.ee/beta_mem/)

• Choose an organism you want (platform name)

• Choose the gene that attracts your attention most

• If you want you can try to change some more settings (if you feel curious enough to read help page)

• Now run the MEM query

• Analyse the received results (what are the most similar to the query genes; what is a biological condition in which they are mostly coexpressed)

• Prepare a short report, don’t forget to mention all the parameters settings you used
Give a short feedback about the MEM tool:

• interface

• usability

• what can be done better

• …