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Project Allocation and Discussion

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Learning with projects

- What bioinformatics can do for biology: the projects
- The importance of knowing your data in the context of what you are studying
- What are the project that will be allocated to you for the final assignment
- Critical discussion of the module material

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BMS353 assessment

The exam for this module will be split in two parts:

Part A – A Multiple Choice Question test for the duration of 1hr, that will count 30% of the final grade

Part B – A notebook with the implementation of allocated projects that will count for 70% of the final grade.

The project will be a collection of all the tools experienced in the practical labs implemented on a set of real data. It will be developed in groups of three students, but notebook will have to be handed individually.

MCQ assessment:

Each question will have 4 possible responses A, B, C or D. **ONLY ONE RESPONSE IS CORRECT IN EACH CASE.** Each question is worth one mark, correct answer will count as 1, an incorrect answer will count as 0. **Not answered questions will count as 0**.

Assessment criteria

The grading for each sub-session follows the scale below:

1. Fail
2. Pass
3. Lower Second
4. Upper Second
5. First

1. **Pipelines and experimental design (20 points)**

   Structure of the pipeline (5 point)
   Overall clarity (5 points)
   Use of details (5 points)
   Exhaustive cover of required analysis (5 points)

2. **Use of methods (20 points)**

   Use of data visualization methods (5 points)
   Use of analysis methods (5 points)
   Use of annotation (5 points)
   Use of functional annotation tools (5 points)

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Assessment criteria (cont…)

3. Use of programming tools (20 points)

Clarity of algorithm (5points)
Correctness of the code (5points)
Efficient programming, speed of code (5 points)
Use of innovative tools/code (5 points)

4. Use of basic statistics (20 points)

Appropriateness of the statistics (5points)
Correct implementation of the methods (5 points)
Novel statistics used (5 points)
Interpretation of the results (5 points)

5. Overall impression and interpretation of the results (20 points)

Overall clarity of the notebook (5 points)
Clarity of the code documentation (5 points)
Innovation (5points)
Biological interpretation of the results (5 points)

Feedback

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Some examples of projects

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Project A

This study is to explain the effect of the transcription factor SP1 in colon cells. To elucidate this effect a colon cell line was used and a silencing of the transcription factor SP1 was obtained using RNAi techniques *in vitro*. A gene expression profile of the cells with SP1 silencing and without silencing was done after 48hrs in culture.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:

* M48-1.CEL control at 48hrs in culture - sample 1
* M48-2.CEL control at 48hrs in culture - sample 2
* S48-1.CEL SP1 silenced at 48hrs in culture - sample 1
* S48-2.CEL SP1 silenced at 48hrs in culture - sample 2

After estimating gene expression, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the silencing of SP1 might have altered.

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Project B

This study is to explain the effect of the transcription factor SP1 in colon cells. To elucidate this effect a colon cell line was used and a silencing of the transcription factor SP1 was obtained using RNAi techniques in *vitro*. A gene expression profile of the cells with SP1 silencing and without silencing was done after 72hrs in culture.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:

* M72-1.CEL control at 72hrs in culture - sample 1
* M72-2.CEL control at 72hrs in culture - sample 2
* S72-1.CEL SP1 silenced at 72hrs in culture - sample 1
* S72-2.CEL SP1 silenced at 72hrs in culture - sample 2

After estimating gene expression, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the silencing of SP1 might have altered.

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Project C

This study is to explain the effect of Hypoxia on human Neutrophils to identify possible involvement of inflammatory response in adverse prognosis of hypoxia-related disease, i.e. pulmonary hypertension, myocardial infarction. To elucidate this effect primary cultures of human neutrophils were studied at normal condition and in a hypoxia condition. A gene expression profile of the neutrophil in normal and hypoxia condition was done after certain amount of hrs in culture.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:

* LPGMa.CEL neutrophils at normal condition in culture - sample 1
* LPGMb.CEL neutrophils at normal condition in culture - sample 2
* LPHa.CEL neutrophils with hypoxia induced in culture - sample 1
* LPHb.CEL neutrophils with hypoxia induced in culture - sample 2

After estimating gene expression levels, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the hypoxia might have altered in neutrophils.

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Project D

This study is to explain how Stem cells use their potential to generate different lineages, particularly on how they can provide a solution for replacing damaged or lost cells within the inner ear. It is known that human embryonic stem cells can be induced to differentiate into otic progenitors and then into hair cell-like cells and neurons that display expected electrophysiological properties. Once these otic progenitors are transplanted into animals with induced hearing loss, they differentiate and elicit a significant recovery of auditory function. The generation of otic progenitors is triggered by FGF signalling and this data aims to analyse the global gene expression profile of undifferentiated hESCs and compared with cultures that have been treated with FGF3 and 10.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:

H14_hES.CEL H14 embryonic cell line at normal condition in culture - sample 1
Shef1_hES.CEL Shef1 embryonic cell line at normal condition in culture - sample 2
H14_FGF.CEL H14 embryonic cell line cultured with FGF3 and 10 growth factors - sample 1
Shef1_FGF.CEL Shef1 embryonic cell line cultured with FGF3 and 10 growth factors - sample 2

After estimating gene expression levels, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that FGF3 and 10 might have altered in human Embryonic Stem Cells.

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Project E

This study is to explain how Stem cells use their potential to generate different lineages, particularly on how they can provide a solution for replacing damaged or lost cells within the inner ear. It is known that human embryonic stem cells can be induced to differentiate into otic progenitors and then into hair cell-like cells and neurons that display expected electrophysiological properties. Once these otic progenitors are transplanted into animals with induced hearing loss, they differentiate and elicit a significant recovery of auditory function. The generation of otic progenitors is triggered by FGF signalling and this data aims to analyse the global gene expression profile of undifferentiated hESCs and compared with cultures that are only culture in DFNB reach medium and not treated with FGF3 and 10.

The expression profiles were quantified using Affymetrix GeneChip HGU133 PLUS 2. The files containing the data are as follow:

H14_hES.CEL H14 embryonic cell line at normal condition in culture - sample 1
Shef3_hES.CEL Shef1 embryonic cell line at normal condition in culture - sample 2
H14_DFBN.CEL H14 embryonic cell line cultured in DFNB - sample 1
Shef3_DFBB.CEL Shef1 embryonic cell line cultured in DFNB - sample 2

After estimating gene expression levels, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the DFNB medium alter in human Embryonic Stem Cells.

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Project F

This study investigates the effect of silencing of the SNF4 activator subunit od SnRK1 in Arabidopsis Thaliana. Arabidopsis SnRK1 is activated in response to carbon/glucose limitation and stress conditions causing an imbalance of energy homeostasis increasing the AMP/ATP ratio.

The Silencing of SNF4 (amiR-SNF4) is used to examine how inhibition of SnRK1 affects transcriptional regulation of different cellular pathways seedlings grown for 5 days in light conditions. This is to shows what are the trnscriptional activation following amiR-SNF4 silencing of SnRK1 that induce changes in essential hormonal and metabolic pathways in Arabidopsis.

The expression profiles were quantified using Affymetrix GeneChip ATH1-121501. The files conatining the data are as follow:

File Name	Description	sample
* wtL01.CEL	wild type seedlings grown for 5 days in light conditions	sample 1
* wtL02.CEL	wild type seedlings grown for 5 days in light conditions	sample 2
*wtL03.CEL	wild type seedlings grown for 5 days in light conditions	sample 3
* amiRL01.CEL	SNF4 silenced seedlings after 5 days growing in light conditions	sample 1
* amiRL02.CEL	SNF4 silenced seedlings after 5 days growing in light conditions	sample 2
* amiRL03.CEL	SNF4 silenced seedlings after 5 days growing in light conditions	sample 3

After estimating gene expression, visualise the data and describe the findings. Identify which genes are changing between conditions and define any potential pathway that the silencing of SNF4 might have altered.