Supporting docs & instructions

- Lecture 1_ HW Organization
    - At the end of the year, each group should have selected minimally 1 Genetics Literature Style homework and minimally 1 Bioinformatics Literature Style homework. Depending on HW1 choices, you may have limited choice for HW2 (X)

Group	Assignment	Genetics		Bioinformatics	
		Q&A	Literature	Q&A	Literature
1	1	X		X	
	2		X		X
2	1	X			X
	2		X	X	
3	1		X		X
	2	X		X	
4	1		X	X	
	2	X			X

- Literature Style Homework:
    - Lecture 1_ Critical Evaluation of a Paper
    - Duration of group presentations will depend on the number of groups who selected "Literature Style"
- Communicate your selection for Genetics and for Bioinformatics to kristel.vansteen@uliege.be before 24th of October 2020
- Send your completed homework assignments for Genetics to fdequiedt@uliege.be and for Bioinformatics to kristel.vansteen@uliege.be

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Homework Assignment Bioinformatics

- **Bioinformatics Q&A style**

Q1. (2 pts)

Select the correct statement:

(a) Pleiotropic genes exhibit single phenotype

(b) Pleiotropy is caused by a gene that has multiple phenotypic effect

(c) Lethal genes causes the appearance of ancestral characters

(d) Sickle cell anemia is an example of multifactorial inheritance

Q2. (2pts)

A population has structure when there are large-scale systematic differences in ancestry. What is false?

(a) Population structure (PS) is a primary consideration in studies of the genetic determinants of human traits.

(b) Failure to control for PS may lead to confounded GWAS hits

(c) Population structure is often closely aligned with geography

(d) Mixing populations typically do not contribute to population structure.

Q3. (2pts)

The proteome

(a) can only usefully be studied in conjunction with the phenome

(b) refers to the entire complement of proteins

(c) is what functional genomics is primarily interested in understanding

(d) is now most commonly studied using RNA microarrays

Q4. (2pts)

With respect to personality, the decreasing order of effect/control on a trait is

(a) genes, unique environment, shared environment

(b) unique environment, genes, shared environment

(c) genes, shared environment, unique environment

(d) unique environment, shared environment, genes

Q5. (2pts)

RNA microarrays

(a) make use of SNPs

(b) utilize microsatellites

(c) monitor 1000s of genes simultaneously

(d) monitor 100s of genes simultaneously

Q6. (5pts) [linked to class 24 Nov 2020]

Which normalization method(s) is/are recommended when performing differential expression analyses between samples ?

(a) FPKM (Fragments Per Kilobase Million)

(b) CPM (Counts Per Million)

(c) DESeq2 (Median of ratios)

(d) TMM (trimmed mean of M values)

Which normalization method(s) is/are recommended when performing gene count comparisons

between genes within a sample ?

(a) FPKM (Fragments Per Kilobase Million)

(b) CPM (Counts Per Million)

(c) DESeq2 (Median of ratios)

(d) TMM (trimmed mean of M values)

- **Bioinformatics Literature style**

Select one of the following papers. Topics are complementary to the classes.

- **GWAS bridging paper including interactions:**
  Platt A, Vilhjálmsson BJ, Nordborg M. Conditions under which genome-wide association studies will be positively misleading. *Genetics*. 2010;186(3):1045-1052. doi:10.1534/genetics.110.121665

- **Epistasis**
  Cowper-Sal lari R, Cole MD, Karagas MR et al (2011) Layers of epistasis: genome-wide regulatory networks and network approaches to genome-wide association studies. Wiley Interdiscip Rev Syst Biol Med 3:513–526

- **Translation:**
  Maren E. Cannon, Karen L. Mohlke. Deciphering the Emerging Complexities of Molecular Mechanisms at GWAS Loci, The American Journal of Human Genetics, Volume 103, Issue 5, 2018.

- **Connectivity in cancer co-expression networks:**
  Anglani R, Creanza TM, Liuzzi VC, Piepoli A, Panza A, Andriulli A, et al. (2014) Loss of Connectivity in Cancer Co-Expression Networks. PLoS ONE 9(1): e87075.

- **Omics integration:**
  Rappoport N, Safra R, Shamir R (2020) MONET: Multi-omic module discovery by omic selection. PLoS Comput Biol 16(9): e1008182. https://doi.org/10.1371/journal.pcbi.1008182

- **Systems and Personalized Medicine**
  Kidd BA, Readhead BP, Eden C, Parekh S, Dudley JT. Integrative network modeling approaches to personalized cancer medicine. *Per Med*. 2015;12(3):245-257. doi:10.2217/pme.14.87

Homework assignment Genetics

- **Genetics Q&A style**

Q1: With regards to transcriptome profiling, compare the following approaches: Microarray and RNA-sequencing.

Q2: Compare eukaryotic and prokaryotic gene regulation mechanisms.

Q3: You are studying a new enzyme called TKT-ALZ. To identify the potential substrate, you decide to go for an affinity approach an express a TAP-tagged version of TKT-ALZ in mammalian cells. You find that find that 75% of TKT-ALZ in the cell extract does not bind to your affinity column. Give all the reasons you can think of that could explain this results. Your colleague suggests that this may be due to a sub-population of the TKT-ALZ that is resistant to affinity purification. Describe an experiment to test this hypothesis and tell how you will interpret the data. If the hypothesis is proved false, suggest an alternative most likely reason for why the 75% of TKT-ALZ was not recovered in your original experiment and an experiment to test this hypothesis.

- **Genetics Literature style**

Select one of the following papers.

- Yadi Zhou, Yuan Hou, Jiayu Shen, Yin Huang, William Martin & Feixiong Cheng. Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2. Cell Discovery 2020 volume 6, Article number: 14

- Zhu X, Gerstein M, Snyder M. Getting connected: analysis and principles of biological networks. Genes Dev. 2007 May 1;21(9):1010– 24.

- Wolf JBW. Principles of transcriptome analysis and gene expression quantification: an RNA-seq tutorial. Mol Ecol Resour. 2013 Jul 1;13(4):559– 72.

- Choi SG, Olivet J. Maximizing binary interactome mapping with a minimal number of assays. Nat Commun. 2019 Aug 29;10(1):3907.