

Initial Experimental Design

1. What is an appropriate question?

- a. Background: miRNA
 - i. Small non-coding RNA
 - ii. Complementary to mRNA
 - iii. Regulate gene expression:
 1. Degrade mRNA
 2. Repress translation
 - iv. Potential novel biomarkers for diagnosis, miRNA mimics can be used as therapeutics
- b. Using differentially expressed miRNA data:
 - i. Which miRNAs are up-/down-regulated during certain stages of breast cancer?
 - ii. Use miRNA expression data as a novel way of categorizing breast cancer tumours → look for trends?
 - iii. Just an idea from Wayne: use miRNA expression data to trace back the phylogenetic development of breast cancer tumour to identify tumor subtypes

2. What is my hypothesis?

- a. (i.) Each stage of breast cancer has distinct miRNA expression patterns
 - i. Same patient
- b. (ii.) miRNA expression varies among the different breast cancer tumour subtypes
 - i. There's many subtypes
- c.

3. What are my datasets and tools to work with?

- a. TCGA database
 - i. <https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga>
 - ii. E.g. TCGA-BRCA
 - iii. Contains miRNA expression data for breast cancer tumour samples
- b. ArrayExpress
 - i. <https://www.ebi.ac.uk/arrayexpress/>
- c. METABRIC
 - i. https://www.cbioportal.org/study/summary?id=brca_metabric
- d. Can use these databases to identify the target genes of miRNA:
 - i. miRWalk: <http://mirwalk.umm.uni-heidelberg.de/>

- ii. miRBase database: <http://www.mirbase.org/>
- e. miRNA analysis: <https://tools4mirs.org/>
 - i. Differential expression analysis tool
- f. Matplotlib package for data analysis: <https://matplotlib.org/>
- g. miRGE, analysis of miRNA sequencing data:
 - i. <https://github.com/mhalushka/miRge>
 - ii. <https://www.biorxiv.org/content/10.1101/250779v1.full>

4. What is a method to answer the question?

- a. Obtain breast tumour miRNA data from database(s)
- b. Determine which miRNAs are differentially expressed in breast cancer tumours (this has been studied before)
 - i. New profiling algorithm → different results
 - ii. Some studies use small sample sizes → our research can use more samples from multiple databases

5. How much do I need to learn from scratch?

- a. Learn more about statistical analysis
- b. Python and Object-oriented programming
- c. Matplotlib
- d. Biological background of breast cancer
- e. Bioinformatic concepts

6. What is a likely outcome?

- a. Much of the literature supports differential miRNA expression → hypotheses are likely true
 - i. 4 miRNA signatures predict breast cancer metastasis:
 - <https://pubmed.ncbi.nlm.nih.gov/29555574/>
 - ii. miRNA suppresses ER+ breast cancer:
 - <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6134714/#Sec2title>
 - iii. 5 miRNA signatures are predictive of breast tumor aggressiveness:
 - <https://onlinelibrary.wiley.com/doi/full/10.1002/ijc.28171>

7. What are the visualizations like when presenting results?

- a. Flow chart to give an overview of the methods
- b. Visualize data in graphs
 - i. Bar graphs for miRNA expression levels
 - ii. Clustering plots for the association of different miRNA and breast tumour subtypes
- c. Identify the differentially expressed miRNA and conduct statistical analysis
- d. (or) comparison of different stages of breast cancer instead of analyzing one patient at a time

8. How do I validate what I am doing?

- a. Look for statistical significance (e.g. P-value)
- b. Compare findings from the experiment to literature (i.e. what did we get vs. what was expected?)
- c. ROC curve: used to evaluate machine learning algorithms. (yet to decide whether useful or not)

<https://reader.elsevier.com/reader/sd/pii/S0031320396001422?token=9CABF06B85626DE67AFB4DCD76B0A76E4020C96BAEF6DE873FC203972254209248F5D71F0923C0C5FAD85D4FC46FCC51>

Scratch:

<https://portal.gdc.cancer.gov/files/76fc8f6f-8332-4a64-809a-7f106393a269>

De novo

<https://onlinelibrary.wiley.com/doi/epdf/10.1002/psc.595>