Naveen Kumar Bansal

GENE EXPRESSION ANALYSIS & QUEUEING THEORY

Detecting Targeted Genes

- Our genes are affected by external or internal sources such as COVID or Age.
- *Numerous data are available on the gene expressions based on biotech such as Microarray or RNASeq*.
- Objective is to determine the affected genes. Statistically this can be done via multiple hypothesis Testing.
- Steps involve normalizing, modeling, and performing multiple hypotheses.

Modeling and Multiple Hypotheses

- Directional Hypothesis

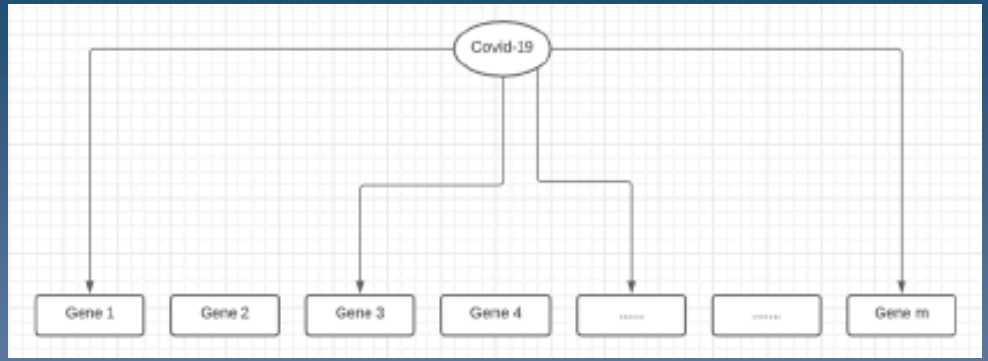
$$H_0^i: \theta_i = 0 \;\; vs. H_-^i: \theta_i > 0 \; or \; H_+^i: \theta_i > 0,$$
$$\mathrm{i} = 1,2, \ldots \mathrm{m}$$

- Introducing Prior with Skewness that allows

$$P\left(H_-^i\right) < P\left(H_+^i\right)$$

- Why Skewness?
- If genes are affected internally or from an outside source, it suppresses or elevates expressions of some genes (Targeted genes)
- It is unreasonable to assume $P(H_-^i) = P(H_+^i)$
- We develop Bayesian decision rules with controlled false discovery rate (DFDR).

Correlation Among Only Targeted Genes



- Only the affected genes are correlated
- There may be different layers of correlations

Statistical Inference on Queueing Models

- Birth and Death process
- Customers' arrivals and service times
- There are many probabilistic models on queue sizes under equilibrium.
- Performance Measures of the Queueing Systems

Hierarchical Bayesian Inference

- Queueing system over the period of the day with traffic intensity (ρ_t) changing over time
- Hierarchical Prior on $\rho_t, t = t_1, t_2, \dots, t_k$
- Predictive Inferences of the future queue sizes