Brainstorm: Statistics

Distributions

Chi-squared (Inverse)
Normal (Gaussian); Standard Normal
Poisson
Uniform
Bernoulli; Binomial
Beta
Gamma (Inverse Gamma)
Laplace
Weibull
F-distribution
Student's t
Geometric
Exponential
Negative Binomial
Multinomial
Hypergeometric

Statistical Models

Linear model (regression)
Non-linears models
Generalized Linear Models (GLMs)
Mixed effects models
Clustering: k-means, hierarchical clustering, ..
Principal components analysis
Regression trees; Multiple imputation
Logistic model
Times series: ARIMA, ..
Survival models: Kaplan-Meier, Cox regression, proportional hazards
Bayesian models
Generalized additive models (GAMs)
Lasso (L1), ridge regression (L2) $\rightarrow$ combined ridge and lasso
Deep learning network architectures

Methods of estimation

Method of moments
Maximum likelihood estimation (MLE)
Least squares estimation
Iteratively reweighted least squares (IRLS); weighted least squares
Bayesian: Maximum a posteriori (MAP)
(minimum variance)

Hypothesis testing

Student's t-test
Chi-squared test (of independence)
ANOVA (analysis of variance); MANOVA, analysis of covariance
F-test
Wilcoxon rank sum test
Permutation testing
Neyman-Pearson test
Pearson's r test
Kruskall-Wallis test (robust ANOVA using ranks)
Fisher's exact test
Hypergeometric test
White's test
Likelihood ratio test
Score test
Wald test
(Wilson test - confidence interval for proportions)
Difference-in-proportions test
Bartlett's test
Z-test

Technologies (in molecular biology)

DNA and RNA sequencing (RNA-seq)
Nanopore (3rd generation)
Sanger (1st generation)
Illumina (2nd generation)
Proteomics - NMR, mass spectrometry, crystallography
Microscopy - light sheet, etc.
Flow cytometry (antibody-based)
CyTOF (mass cytometry)
Sequence-based cytometry (DNA barcode)
CITE-seq (REAP-seq)
ChIP-seq (protein-DNA interactions)
FISH - fluorescent in situ hybridization
DNA microarrays
Blots - northern, southern, western
qPCR
FRET
Yeast two-hybrid
ATAC-seq

Applications

Gene expression profiling

GWAS - genome-wide association studies - linking genotype to phenotype

Identify new drug targets

Protein (expression) profiling

Protein-protein interactions

Sorting, identifying, classifying, quantifying cell types

Phylogenetics - evolutionary histories

Metagenomics - microbiome (diversity of microbes); metatranscriptomics ..

Synthetic biology

RNA(-RNA) interactions

Gene regulation / gene regulatory networks

Characterizing chromatin states/interactions (histone variants / ATAC)

Gene essentiality (disrupt)

Linking technology -> applications -> statistics

Technology	Applications	Statistics
RNA sequencing	Gene expression profiling	Negative Binomial regression