Genomics, Computing, Economics & Society

> 10 AM Thu 27-Oct 2005 week 6 of 14

MIT-OCW Health Sciences & Technology 508/510

Harvard Biophysics 101

Economics, Public Policy, Business, Health Policy

Class outline

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(1) Topic priorities for homework since last class

(2) Quantitative exercises: psycho-statistics,

combinatorials, random/compression,

exponential/logistic, bits, association & multi-

- hypotheses, linear programming optimization
- (3) Project level presentation & discussion
- (4) Sub-project reports & discussion:

Personalized Medicine & Energy Metabolism

(5) Discuss communication/presentation tools

(6) Topic priorities for homework for next class



Binomial, Poisson, Normal





Binomial frequency distribution as a function of $X \in \{int \ 0 \dots n\}$

p and q $0 \le p \le q \le 1$ q = 1 - p two types of object or event. Factorials 0! = 1 n! = n(n-1)!

Combinatorics (C = # subsets of size X are possible from a set of total size of n)

$$\frac{n!}{X!(n-X)!} = C(n,X)$$

$$B(X) = C(n, X) p^{X} q^{n-X} \qquad \mu = np \quad \sigma^{2} = npq$$

$$(p+q)^{n} = \sum B(X) = 1$$

B(X: 350, n: 700, p: 0.1) = 1.53148×10^{-157} =PDF[BinomialDistribution[700, 0.1], 350] Mathematica ~= 0.00 =BINOMDIST(350,700,0.1,0) Excel

Poisson frequency distribution as a function of $X \in {int 0 ...\infty}$

 $P(X) = P(X-1) \mu/X = \mu^{x} e^{-\mu}/X! \sigma^{2} = \mu$

n large & p small $\rightarrow P(X) \cong B(X)$ $\mu = np$

For example, estimating the expected number of positives in a given sized library of cDNAs, genomic clones, combinatorial chemistry, etc. X = # of hits.

Zero hit term = $e^{-\mu}$

Normal frequency distribution as a function of $X \in \{-\infty ... \infty\}$

 $Z=(X\text{-}\mu)/\sigma$

Normalized (standardized) variables

 $N(X) = \exp(-Z^2/2) / (2\pi\sigma)^{1/2}$ probability density function

npq large $\rightarrow N(X) \cong B(X)$

Mean, variance, & linear correlation coefficient

Expectation E (rth moment) of random variables X for any distribution f(X)

First moment= Mean μ ; variance σ^2 and standard deviation σ $E(X^r) = \sum X^r f(X)$ $\mu = E(X)$ $\sigma^2 = E[(X-\mu)^2]$

Pearson correlation coefficient $C = cov(X,Y) = E[(X-\mu_X)(Y-\mu_Y)]/(\sigma_X \sigma_Y)$ Independent X,Y implies C = 0, but C =0 does not imply independent X,Y. (e.g. Y=X²)

 $P = TDIST(C*sqrt((N-2)/(1-C^2)))$ with dof= N-2 and two tails.

where N is the sample size.

www.stat.unipg.it/IASC/Misc-stat-soft.html

Under-Determined System

- All real metabolic systems fall into this category, **so far**.
- Systems are moved into the other categories by measurement of fluxes and additional assumptions.
- Infinite feasible flux distributions, however, they fall into a solution space defined by the **convex polyhedral cone**.
- The actual flux distribution is determined by the cell's regulatory mechanisms.
- It absence of kinetic information, we can estimate the metabolic flux distribution by postulating **objective functions**(**Z**) that underlie the cell's behavior.
- Within this framework, one can address questions related to the capabilities of metabolic networks to perform functions while constrained by stoichiometry, limited thermodynamic information (reversibility), and physicochemical constraints (ie. uptake rates)

FBA - Linear Program

• For growth, define a growth flux where a linear combination of monomer (M) fluxes reflects the known ratios (d) of the monomers in the final cell polymers.

$$\sum_{allM} d_M \cdot M \xrightarrow{v_{growth}} biomass$$

• A linear programming finds a solution to the equations below, while minimizing an objective function (Z).

Typically $Z = V_{growth}$ (or production of a key compound).

• *i* reactions

$$\mathbf{S} \cdot \mathbf{v} = \mathbf{b}$$
$$v_i \ge 0$$
$$\alpha_i \le v_i \le \beta_i$$
$$v_i = X_i$$

Steady-state flux optima



Applicability of LP & FBA

- Stoichiometry is well-known
- Limited thermodynamic information is required
 - reversibility vs. irreversibility
- Experimental knowledge can be incorporated in to the problem formulation
- Linear optimization allows the identification of the reaction pathways used to fulfil the goals of the cell if it is operating in an optimal manner.
- The relative value of the metabolites can be determined
- Flux distribution for the production of a commercial metabolite can be identified. Genetic Engineering candidates

Precursors to cell growth

- How to define the growth function.
 - The biomass composition has been determined for several cells, *E. coli* and *B. subtilis*.
 - This can be included in a complete metabolic network
 - When only the catabolic network is modeled, the biomass composition can be described as the 12 biosynthetic precursors and the energy and redox cofactors

in silico cells

	E. coli	H. influenzae	H. pylori
Genes	695	362	268
Reactions	720	488	444
Metabolites	s 436	343	340

(of total genes 4300 1700 1800)

Edwards, et al 2002. Genome-scale metabolic model of Helicobacter pylori 26695. J Bacteriol. 184(16):4582-93.

Segre, et al, 2002 Analysis of optimality in natural and perturbed metabolic networks. PNAS 99: 15112-7. (Minimization Of Metabolic Adjustment) http://arep.med.harvard.edu/moma/

Where do the Stochiometric matrices (& kinetic parameters) come from?

Figures removed due to copyright reasons.

> EMP <u>RBC</u>, <u>E.coli</u> KEGG, Ecocyc

Biomass Composition



Flux ratios at each branch point yields optimal polymer composition for replication



x,y are two of the 100s of flux dimensions

Figure by MIT OCW.

Minimization of Metabolic Adjustment (MoMA)

Figure by MIT OCW.

Figure removed due to copyright reasons.

Figure removed due to copyright reasons.

Flux Data

Predicted Fluxes

200

Competitive growth data: reproducibility

Badarinarayana, et al. Nature Biotech.19: 1060

Competitive growth data

On minimal media

Hypothesis: next optima are achieved by regulation of activities.

Non-optimal evolves to optimal

Figures removed due to copyright reasons.

Ibarra et al. Nature. 2002 Nov 14;420(6912):186-9. Escherichia coli K-12 undergoes adaptive evolution to achieve in silico predicted optimal growth.

Non-linear constraints

Desai RP, Nielsen LK, Papoutsakis ET. Stoichiometric modeling of Clostridium acetobutylicum fermentations with non-linear constraints. J Biotechnol. 1999 May 28;71(1-3):191-205.

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