- Do gene networks drift into uneccesarily complex configurations? If the optimal dynamics of a system can be realized by g genes and/or started in a state with only g genes, during evolution, will the system be composed of $> g$ genes. How many more genes than necessary?
- Are there forces constraining gene network size other than a fitness cost associated with the expense of uncessary energy? For instance, will genes in a non-minimal gene network contribute less overall to the system's output, diminising the cost of their removal (on average)?
- as the population explores neutral network space, how often will the population be on or near a point on the manifold where a gene becomes unccessary? Does this probability go up significantly as unneccsary dimensionality goes up?
- Does the unncessary complexity of some gene networks confer evolvability advantages?

Let,

$$\mathcal{F}_n = \left\{A : C_n(zI - A)^{-1}B_n = H(z)\right\} \subseteq \mathbb{R}^{n\times n}$$

be an n dimensional manifold, where A is gene network (not necessarily minimal), and $H(z)$ is a description of the phenotype in the Laplace domain. In the non-minimal case, C_k and B_k are augmented with zeroes.

$$\begin{aligned} C_n &= \left[\begin{array}{c} C_k \\ \hline 0 \end{array}\right], C_i \neq 0 \\ B_n &= \left[\begin{array}{c|c} B_k & 0 \end{array}\right], B_i \neq 0 \end{aligned}$$

Let,

$$P_i : \mathcal{F}_n \to \Omega_{n-1}$$

be a projection from an $n \times n$ network to an $(n-1)\times(n-1)$ network. Biologically, this is a gene deletion or removal from the system.

Let $G_{n,i}$ be the set of networks with identical phenotypes following a deletion.

$$\begin{aligned} G_{n,i} = \{f \in \mathcal{F}_n : P_i f \in \mathcal{F}_{n-1}\} \\ G_n = \cup_i G_{n,i} \\ d(f) = \#\{i : P_i f \in \mathcal{F}_{n-1}\} \end{aligned}$$

$d(f)$ is the number of different genes that can potentially be deleted to end up in a phenotypically identical space.

Gene duplication or recruitment is defined by,

$$\begin{aligned} U_i(x)\mathcal{F}_{n-1} \to \mathcal{F}_n \\ \{U_i(x) : x \in \mathbb{R}^n\} \subseteq G_{n,i} \end{aligned}$$

where, x is in the ith row and 0 in the ith column, except along the diagonal.

How much of a d_n-dimensional manifold is near one of $(n-k)(d_{n-1}+n)$-dimenional submanifolds?

$$(n-k)\varepsilon^{d_n - d_{n-1} - n}$$

Alternatively, what is the hitting time of $U(x)$?