Gene regulatory network drift and speciation occurs rapidly under neutrality

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Abstract

We introduce an analytical theory to study the evolution of biological systems such as gene regulatory networks, applying insight and tools from control engineering, systems identification, and dynamical systems theory. We describe a null model of regulatory network evolution by analytically describing the set of all linear gene networks (of any size) that produce identical phenotypes and the evolutionary paths connecting them. Under constant selection and environmental stasis, neutral evolution proceeds as a random walk through phenotypically identical network-space. Under neutral conditions, this model can describe the rates at which Dobzhansky-Muller incompatibilities arise in reproductively isolated populations. This analysis provides insight into the mechanisms and parameters important for understanding developmental systems drift and speciation.

Additional ideas to consider adding:

- Haldane's rule (easy point in discussion: makes F1s look like F2s)
- add point about F1: quartic and F2: quadratic to results and maybe abstract/discussion
- hybrid vigor (need to do calculation)
- discuss linearity, linearization, and canalization in introduction
- obtain estimates of variation in A from thermodynamic occupancy model

Introduction

Bridging the gulf between an organism's genome and phenotype is a poorly understood and complex molecular machinery. Progress in a suite of biological subdisciplines is stalled by our general lack of understanding of this molecular machinery: with respect to both its function and evolution. There does exist a growing body of experiment and data on the evolutionary histories and molecular characterizations of particular gene regulatory networks [Jaeger, 2011, Davidson and Erwin, 2006, Israel et al., 2016], as well as thoughtful verbal and conceptual models [True and Haag, 2001, Pavlicev and Wagner, 2012, Weiss and Fullerton, 2000, Edelman and Gally, 2001]. However, as Hardy and Weinberg taught us over a century ago, verbal theories are often insufficient, if not downright misleading [Hardy, 1908, Weinberg, 1908, Servedio et al., 2014]. This is especially pertinent given the staggering complexity and scope of contemporary research programs. This outlook necessitates the advancement of conceptual frameworks of such precision, only mathematics will suffice, as models allow the development of concrete numerical predictions. Previously it has been suggested that any idealized study of evolution is incomplete without a mathematically sufficient description of the genotype, phenotype, and transformation from one to the other [Lewontin et al., 1974].

The molecular machinery, interacting with the environment, and bridging genotype to phenotype can be mathematically described as a dynamical system – or a system of differential equations[Jaeger et al., 2015]. Movement in this direction is ongoing, as researchers have begun to study the evolution of both abstract [Wagner, 1994, 1996, Siegal and Bergman, 2002, Bergman and Siegal, 2003, **?**] and empirically inspired computational and mathematical models of gene regulatory networks (GRNs) [Mjolsness et al., 1991, Jaeger et al., 2004, Kozlov et al., 2012, 2015, 2014, Crombach et al., 2016, Wotton et al., 2015, Chertkova et al., 2017]. If we allow the reasonable assumption that the genotype-phenotype map can be represented as a system of differential equations, we can immediately discuss its evolution and function in a much more mechanistic, yet general, manner.

In some fields that seek to fit parametric models to experimental data, such as control theory, chemical engineering, and statistics, it is well known that mathematical models can fundamentally be *unidentifiable* and/or *indistinguishable* – meaning that there can be uncertaintity about an inferred model's parameters or even its claims about causal structure, even with access to complete and perfect data [Bellman and Åström, 1970, Grewal and Glover, 1976, Walter et al., 1984]. Models with different parameter schemes, or even different mechanics can be equally accurate, but still not *actually* agree with what is being modelled. In control theory, where electrical circuits and mechanical systems are often the focus, it is understood that there can be an infinite number of "realizations", or ways to reverse engineer the dynamics of a black box, even if all possible input and output experiments on the black box are performed [Kalman, 1963, Anderson et al., 1966, Zadeh and Deoser, 1976]. In chemical engineering, those who study chemical reaction networks sometimes refer to the fundamental unidentifiability of these networks as "the fundamental dogma of chemical kinetics" [Craciun and Pantea, 2008]. In computer science, this is framed as the relationship among processes that simulate one another [Van der Schaft, 2004]. Although this may frusturate the occasional engineer or scientist, viewed from another angle, the concepts of unidentifiability and indistinguishability can provide a starting point for thinking about externally equivalent systems – systems that evolution can explore, so long as the parameters and structures can be realized biologically. In fact, evolutionary biologists who study convergent versus parallel evolution, homology, and analogy are very familiar with such functional symmetries; macroscopically identical phenotypes in even very closely related species can in fact be divergent at the molecular and sequence level [True and Haag, 2001, Tsong et al., 2006, Hare et al., 2008, Vierstra et al., 2014, Stergachis et al., 2014, Taylor et al., 2016, Matsui et al., 2015].

In this paper we outline a theoretical framework to study the evolution of biological systems. We expect wide applicability to this approach (*i.e.* non-neutral evolution), however presently, we focus solely on neutral evolution, that is where phenotype is conserved over evolutionary time.

We derive an analytical description of the set of all linear biological systems with identical phenotypes – that is we decribe the set of all gene network architectures that yield identical phenotypes, and show that all biological systems can, in principal, can undergo systems drift. In the neutral case, this set desribes a manifold that evolution explores leaving phenotype invariant with respect to mutation, and predicts that if two populations become reproductively isolated, hybrid incompatibility can occur, despite the absence of adaptation, directional selection, or environmental change. Speciation typically occurs on timesclaes approximately on the order of N_e generations, where N_e is the effective population size.

Gene Networks as Linear Dynamical Systems

Here we outline a method to model biological systems, such as gene regulatory networks, as linear dynamical systems. We define an organism's phenotype $\phi(t)$ to be the molecular time-dynamics directly relevant to survival. These dynamics are the result of the interconnections of a gene regulatory network (or some other biological system) A (an $n \times n$ matrix) and an environmental input $u(t)$. Such a system $\mathcal{S}$, is composed of two equaitons,

$$\mathcal{S} := \begin{cases} \dot{\kappa}(t) & = A\kappa(t) + Bu(t) \\ \phi(t) & = C\kappa(t) \end{cases} \tag{1}$$

Where the *kryptotype* $\kappa(t)$, is a list of a system's molecular concentrations at time t – or more generally the systems *internal dynamics*. As some system dynamics may not be visible nor relevant to selection, we distinguish the *kryptotype* (as it is hidden) from the *phenotype* – which is the systems *external dynamics*. The change in internal molecular concentrations as a function of time $\dot{\kappa}(t)$ is simply a function of the systems current state (or kryptotype), the system architecture A – such as a gene regulatory network, the environmental input $u(t)$, and B (an $n \times l$ matrix) – how the system processes its environment. C (an $l \times n$ matrix) filters the dynamics relevant to survival. Thus the phenotype is simply a convolution of the system

organization and the environment,

$$\phi(t) = \int_0^t Ce^{At}Bu(t)dt, \tag{2}$$

where we sometimes refer to $h(t) := Ce^{At}B$ as the *impulse response* of the system. As A specifies gene regulatory network architecture, the i^{th} row of A can be interpreted as the *cis*-regultory element (or promoter) for gene i.

Example 1 (Oscillating Gene Network: Cell Cycle Control) *Cellular division is a complicated phenomena, governed by many different processes, however it is agreed that its rhythm is partially controlled by periodic (oscillating) gene transcription [Orlando et al., 2008]. Consider a simplified model of oscillating gene transcription. In the present framework periodic expression requires at minimum two interacting genes.*

Suppose gene-2 up-regulates the transcription of gene-1 and that gene-1 down-regulates the transcription of gene-2 with equal magnitude (of 1) and relative to each of their concentrations, denoted by κ_1 and κ_2. Furthermore, suppose that only the dynamics of gene-1 are consequential to the cell cycle (perhaps the amount of gene-1 activates another downstream gene network). Lastly suppose that the production of both genes is stimulated by an impulse of a molecule present immediately after division.

If the rate each of these genes is expressed is a linear function of their concentrations, the dynamics of the system are given by

$$\dot{\kappa_1}(t) = \kappa_2(t) + u(t)$$
$$\dot{\kappa_2}(t) = -\kappa_1(t) + u(t)$$

where $\dot{\kappa}$ denotes the time derivative. The initial conditions $\kappa_1(0)$ and $\kappa_2(0)$, and the input $u(t)$ then determiine the concentrations through time. If we record the regulatory coefficients in the matrix

$$A = \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix},$$

and define the column vector $B = \begin{bmatrix} 1 & 1 \end{bmatrix}^T$, then in matrix notation the dynamics are

$$\dot{\kappa} = A\kappa(t) + Bu(t).$$

Since only the dynamics of gene-1 are directly relevant to biological function, the dynamics of interest are given by

$$\phi(t) = C\kappa(t)$$

where the row vector C is defined as $C = \begin{bmatrix} 1 & 0 \end{bmatrix}$. (Note: if the dynamics of both genes were physiologically relevant to the cell cycle, we would set C to be the identity matrix).

Since the input is simply an impulse, its phenotype is equivlanet to its impulse response

$$\phi(t) = h(t) = \sin(t) + \cos(t).$$

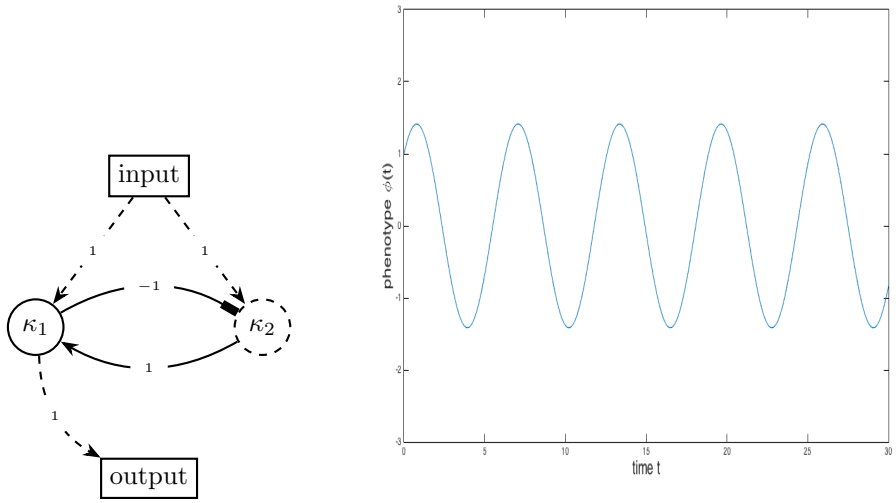

Figure 1: (Left) Graphical representation of the cell cycle control gene network, and (right) plot of the phenotype $\phi(t)$ against time t.

We return to the evolution of such a system below.

Linear Evolutionary Systems

The literature is filled with detailed observations of molecular systems and their diversity. There are examples of significant diversity in the networks underlying processes such as circadian rhythm [Sancar, 2008], cell cycle control [Cross et al., 2011, Kearsey and Cotterill, 2003], pattern formation, and metabolism [Lavoie et al., 2009, Martchenko et al., 2007, Dalal et al., 2016, Christensen et al., 2011, Hartl et al., 2007, Alam and Kaminskyj, 2013]. Despite a symmetry in functionality or phenotype these systems often differ, sometimes substationaly, at the molecular level. How many different mechanisms have the same function? We urge the reader to consider the metaphorical black box.

Gene regulatory networks with identical phenotypes (external dynamics) do not necessarily have identical kryptotypes (internal dynamics). Any linear and minimal system (a gene network) – minimal, informally meaning that the system's phenotype is achieved with the fewest possible number of genes – has an identical phenotype up to a change of coordinates.

$$h(t) = Ce^{At}B \tag{3}$$
$$= CV^{-1}Ve^{At}V^{-1}VB \tag{4}$$
$$= CV^{-1}e^{VAV^{-1}t}VB \tag{5}$$
$$= \bar{C}e^{\bar{A}t}\bar{B} \tag{6}$$

Two biological systems, $\mathcal{S} = \{A, B, C\}$, and $\bar{\mathcal{S}} = \{\bar{A} = VAV^{-1}, \bar{B} = VB, \bar{C} = CV^{-1}\}$, have the same phenotype if they are related by a change of coordinates.

Although systems may not be identifiable beyond a change of coordinates, at present we are primarily interested in a subset of these systems. That is, systems that not only have equivalent external dynamics, but also equivalent input and output relationships. Formally, this means systems related by a change of coordinates (any invertible matrix V) that leaves B and C invariant:

$$VB = B \implies \bar{B} = B \tag{7}$$
$$CV = C \implies \bar{C} = C \tag{8}$$

In other words systems with varying gene regulatory network architectures yet identical selection pressures, environment, and phenotype.

Define $V(\tau)$ as the parameterized change of coordinates matrix that preserves B and C, with τ a vector of free parameters. The set of *all* phenotypically invariant (minimal) gene networks is,

$$A(\tau) = V(\tau)A(0)V^{-1}(\tau), \tag{9}$$

and a *Linear Evolutionary System* is,

$$\mathcal{S}(\tau) := \begin{cases} \dot{\kappa}(t) & = A(\tau)\kappa(t) + Bu(t) \\ \phi(t) & = C\kappa(t) \end{cases} \tag{10}$$

That is, all (linear and minimal) mechanisms capable of producing the same phenotype can be realized by a unique choice of τ in $\mathcal{S}(\tau)$.

More generally, *introduce Kalman*, we denote by $\mathcal{A}_n(A_0)$ the set of all n-dimensional systems equivalent to A_0:

$$\begin{aligned} \mathcal{A}_n(A_0) &= \left\{A : Ce^{At}B = Ce^{A_0 t}B \text{ for } t \geq 0\right\} \\ &= \left\{A : CA^kB = CA_0^kB \text{ for } 1 \leq k \leq n-1\right\}. \end{aligned} \tag{11}$$

Equivalence of the two characterizations follows from the Cayley-Hamilton theorem. Usually, the dimension n and the reference system A_0 is implicit and we write only $\mathcal{A}$.

Regardless of minimality, two systems, even in different dimensions, can have identical external dynamics if they are in $\mathcal{A}$. This set can be completely parameterized using the *Kalman Decomposition*; the set of all linear gene regulatory networks with equivalent phenotypes can be precisely defined. Note that this implies that there is always more than one possible gene regulatory network architecture per phenotype, however we can analytically describe the complete set.

Example 2 (All Phenotypically Equivalent Cell Cycle Control Networks) *Let*

$$A(0) = \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix}, \qquad B = \begin{bmatrix} 1 & 1 \end{bmatrix}^T, \qquad C = \begin{bmatrix} 1 & 0 \end{bmatrix},$$

with $V(\tau)$ preserving both B and C, then the set of all two-gene regulatory networks phenotypically equivalent to the cell cycle control network in Example 1 are given by

$$A(\tau) = \begin{bmatrix} 1 & 0 \\ \tau & 1-\tau \end{bmatrix} \begin{bmatrix} 0 & 1 \\ -1 & 0 \end{bmatrix} \begin{bmatrix} 1 & 0 \\ \frac{\tau}{\tau-1} & \frac{-1}{\tau-1} \end{bmatrix} \qquad \forall\ \tau \neq 1$$

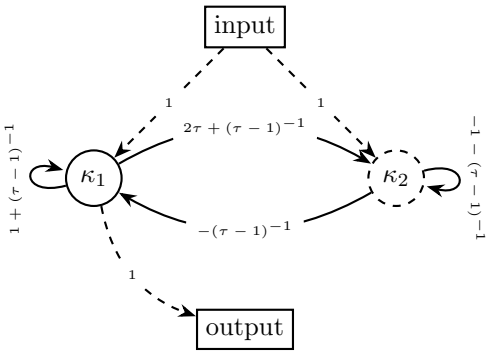

Figure 2: A graphical depiction of the set of all externally equivalent cell cycle control networks, $A(\tau)$. τ can take any valye

Despite the phenotypic equivalence of all instantiations of $A(\tau)$, the internal dynamics, or kryptotypes, vary as a function of τ. Gene-1 dynamics (blue) are equivalent for network architectures $A(0)$ and $A(2)$, however the dynamics of gene-2 (orange) differ with τ.

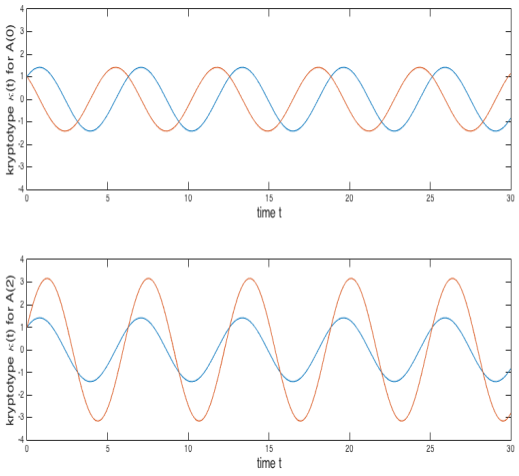

Figure 3: Gene-1 (blue) and gene-2 (orange) dynamics for $A(0)$ (top) and $A(2)$ (bottom). Both (top and bottom) gene-1 dynamics are given by $\kappa_1 = \sin(t) + \cos(t)$, and gene-2 by $\kappa_2 = \cos(t) - \sin(t)$ (top) and $\kappa_2' = \cos(t) + 3\sin(t)$ (bottom).

Intraspecific variation and genetic drift

At any given time, there will be a range of network coefficients present in the population due to segregating genetic polymorphism. Over many generations, even if selective pressures do not change, this range of networks will shift as recombination, mutation, and demographic noise create new alleles and shift allele frequencies. How much variation do we expect to find within a population? Is this range limited by available variation or kept in check by selection? How fast will a population explore the space of equivalent networks? To answer these questions, we need to know two things known at best only roughly [**?**] – the strength of stabilizing selection on the phenotype, and the amount (and structure) of heritable variation in the genotype. We aim to get order-of-magnitude estimates.

amount of heritable variation We quantify (roughly) the amount of heritable variation by σ^2, the genetic variance present in a population in a typical entry of A. The coefficient A_{ij} measures how much the rate of net production of i changes per change in concentration of j. It is generally thought that regulatory sequence change contributes much more to inter- and intraspecific variation than does coding sequence change affecting molecular structure [**?**]. In the context of transcription factor networks this may be affected not only by the binding strength of j to the promoter region of i but also the effects of other transcription factors (e.g., cooperativity) and local chromatin accessibliity [**?**]. For this reason, the mutational target size for variation in A_{ij} may be much larger than the dozens of base pairs typically implicated in the handful of binding sites for transcription factor j of a typical promoter region. (Recall that although these are best modeled through nonlinear terms, by linearizing we essentially consider first-order effects.) On the other hand, a diverse set of buffering mechanisms are thought to contribute to phenotypic stability in the presence of substantial molecular noise [**??**], suggesting that substantial variation in the micro-scale dynamics we consider here may be necessary to produce relevant phenotypic effects downstream. *replace "micro-scale" with sthg else or discuss earlier* Differences in A_{ij} due to a sequence change are hard to measure – the closest available data we could find either related to variation in transcription factor binding site occupancy or in expression

levels (e.g., cis-eQTL). The former may be an overestimate, since it does not capture buffering effects (if for instance only one site of many needs be occupied for transcription to begin) and the latter probably measures changes in steady-state concentration (our x_i) rather than the rate of change. **?** found differential occupancy in 7.5% of binding sites of a transcription factor (p65) between human individuals. **?** showed that cis-regulatory variation accounts for around 2–6% of expression variation in human blood-derived primary cells, while [**?**] found that human population variation explained about 3% of expression variation. *Get some data from at least one other species in here!* Taken together, this suggests that variation in the entries of A may be on the scale of 1% between individuals of a population – doubtless varying substantially between species and between genes.

merge this above The amount and structure of this standing variation is established over long time scales by many factors, including mutation-selection balance, shifts in the phenotypic optimum, and/or spatial variation in the optimum [**?**]. Quantitative genetics models of mutation-selection balance predict precise levels and structure of standing variation [**???**], but it is unclear how well these predictions match reality [**?**] and how much they are expected to change over time [**?**]. However, empirical work allows us to estimate at least the rough magnitude of variation.

strength of selection It seems certain that selection is not so strong that intrapopulation variation is strongly deleterious, so that if u is the typical scale on which selection acts – e.g., a phenotype that differs from the optimum by x has fitness of $\exp(-x^2/2u^2)$ – then $u > \sigma$. However, a range of studies *find them* have found evidence for weak stabilizing selection on regulatory SNPs and cis-eQTL. For instance, **?** (others?) found evidence that large-effect regulatory mutations are weakly selected against in Drosophila. This suggests that the strength of selection on phenotype is sufficient to weakly constrain regulatory variation, so that perhaps σ and u are relatively close. This is as would be expected if available variation is held in check by mutation–selection balance rather than genetic drift. A conservative estimate would be that $u = 5\sigma$; taking $\sigma = .01$ as above, this suggests that changes in phenotype of 5% are sufficient to effect a noticable drop in fitness. *BUT σ IS VARIATION IN A NOT PHENOTYPE*

We have guessed that within a population the entries of A vary by a factor of $\sigma = 0.01$, at least for networks whose function is strongly constrained. Subsequent generations for the most part resample from this diversity, so in a population of effective size N_e, simply by the variance of the mean of a random sample, the population mean binding strengths will move a few multiples of $\sigma/\sqrt{N_e}\%$ per generation [**?**]. (This could be taken as a definition of N_e.) Selection will tend to push this mean towards the optimal set of networks [**?**], but mean movement parallel to the optimal set (that leaves the phenotype invariant) is unconstrained unless recombination load is substantial [**?**]. The action of genetic drift is also strongly determined by covariance between standing genetic variation in different regulatory coefficients – known as the G matrix [**?**], covariance which may arise due to functional constraints and/or statistical linkage. There may well be functional constraints – but these are not sufficiently well-known to say anything general about. Linkage will almost certainly lead to covariance if the variation is due to *cis*-regulatory variants, in which case the genetic basis of each *row* of A likely lies within a few kilobases of tightly linked sequence, across which a population may carry only a few common haplotypes. However, covariance due to transiently assembled haplotypes is not expected to be stable over long periods of time – a common *cis*-regulatory haplotype of transcription factor k with particularly strong binding to both i and j (leading to positive covariance between A_{ik} and A_{jk}) is no more likely to appear than one with strong binding to i but particularly weak binding to j (negative covariance). (Such transient covariances may well increase the variance of the per-generation change in network mean, however [**?**].) In principle, there may be substantially less variation away from the set of optimal coefficients than there is along the set, due to the action of selection. If so, this might require substantial epistatic load – mortality or reduced fitness of a large proportion of new offspring due to recombination between somewhat incompatible alleles. However, it is unclear if this is likely to occur and XXX we revisit this below.

It therefore seems reasonable to coarsely model the time evolution of population variation in network coefficents as (a) a "cloud" of width X about the population mean, which (b) moves as an unbiased Brownian motion through the set of network coefficients that give the optimal phenotype. In fact, the population mean will not produce exactly the optimal phenotype, but it will be convenient to refer to this closest point on

the optimal set as "the population mean".

Brownian motion on the set of equivalent networks: The set $\mathcal{A}$ is characterized as the solutions to the equations (11), and is hence an algebraic variety. In fact, the Kalman decomposition *XXX above* provides us with an explicit characterization of the set. Above we argued that the population mean set of coefficients A was subject to genetic drift, with each entry A_{ij} changing with mean square displacement $\sigma^2/\sqrt{N_e}$ per generation. Since selection constrains the population mean to stay near to the set of optimal networks $\mathcal{A}$, to a good approximation, the population mean moves as Brownian motion in the space of matrices $\mathbb{R}^{n\times n}$ but conditioned to stay on the optimal set. This Brownian motion on $\mathcal{A}$ is a stochastic process driven by the Laplace-Beltrami operator on $\mathcal{A}$ where this makes sense, with special behavior at the singular points (if any *XXX*). Unlike Brownian motion in flat space, this stochastic process can have *bias* – for instance, it is pushed away from regions of negative intrinsic curvature (because there is "less space" in such regions).

NOT TRUE?: However, the process always has the property that changes in A accumulate at constant (mean squared) rate: if $\mathcal{A}$ is locally isomorphic to $\mathbb{R}^m$ around A_0 (there are m degrees of freedom in the solutions to (11)) then

$$\mathbb{E}\left[\|A_t - A_0\|^2\right] = m\sigma^2 T + O(T^2). \tag{12}$$

add Kalman decomposition stuff here

Speciation via Reproductive Incompatibility

An F1's genetic regulation is a consequence of both of its genomes, where genes and regulatory sequences from both parents are equally present. Thus we say that a diploid organism's gene network is simply the average of both of its gene network copies; one from each parent. Further, each haploid parental gene network copy is formed via meiosis – by swapping independent genes (specifically their *cis*-regulatory modules) randomly. Assuming two distinct but genetically homogeneous populations evolving in allopatry meet and form hybrids, the first generation hybrids (F1s) gene network dynamics will be determined by the average of the parental haplotypes. The second generation hybrids (F2s), however, will be the product of a meiosis between parental haplotypes followed by an averaging of gametes.

Specifically, F_1 is the first generation hybrid gene network architecture formed by mating (averaging) $A(\tau)$ and $A(\hat{\tau})$,

$$F_1(\tau, \hat{\tau}) = \frac{A(\tau) + A(\hat{\tau})}{2}. \tag{13}$$

and F_2 is the second generation hybrid gene network architecture formed by gametes $G(i)$ and $G(j)$. Where each G is formed by randomly swapping rows between $A(\tau)$ and $A(\hat{\tau})$, such that the ith gene comes from $A(\tau)$ (i and j are orthogonal vectors, each element 0 or 1, and $i \neq j$).

$$F_2(i, j) = \frac{G(i) + G(j)}{2} \tag{14}$$

The fitness of an organism can be computed by comparing its impulse response with the optimal response, *this is either zero or infinite. apply a weighting function (see appendix)?*

$$\mathcal{F}\left(\widehat{\phi}(t)\right) = \exp\left\{-\frac{1}{\sigma}\int_0^\infty \left\|\phi(t) - \widehat{\phi}(t)\right\|^2 dt\right\}. \tag{15}$$

Therefore a hybrid's fitness can be computed by comparing its impulse response with that of its parents.

Definition 1 (Reproductive Incompatibility) *According to Mayr's* Biological Species Concept*, two populations can be considered different species if they are reproductively isolated, meaning crosses between them produce low fitness offspring.*

We quantitatively describe the degree of incompatibility between two populations P_1 and P_2 as

$$\mathcal{I} = \frac{2\langle \mathcal{F}(\phi_{F_1})\rangle}{\langle \mathcal{F}(\phi_{P_1})\rangle + \langle \mathcal{F}(\phi_{P_2})\rangle},$$

where angled brackets imply averaging.

F1s created by crossing phenotypically equivalent oscillators $A(0)$ and $A(2)$ have an $\phi_{F_1}(t) = e^t$, in contrast to both parents with $\phi_{P_1}(t) = \phi_{P_2}(t) = \sin(t) + \cos(t)$. The hybrid phenotype is significantly different (it does not oscillate and increases infinitely) despite the phenotypic equivalence of the parents.

$$\begin{aligned} \mathcal{F}(\phi_{P_1}) = \mathcal{F}(\phi_{P_2}) &= 1 \\ \mathcal{F}(\phi_{F_1}) &= 0 \\ \mathcal{I} &= 0 \end{aligned}$$

Thus if populations 1 and 2 are homogenous $A(0)$ and $A(2)$, respectively, we say that they are completely incompatible as $\mathcal{I} = 0$.

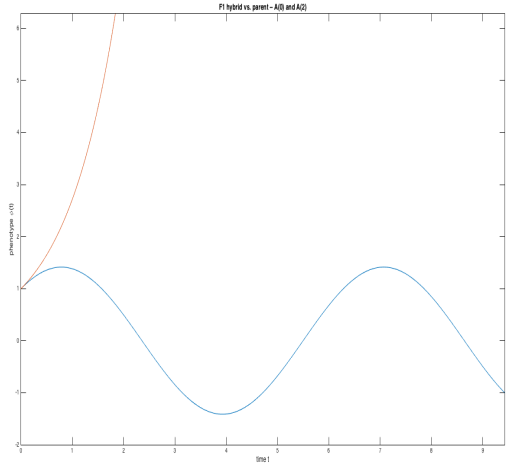

Figure 4: F1 hybrid (orange) and parental (blue) phenotypic oscillator dynamics for an $A(0)$ by $A(2)$ cross. The hybrid fails to oscillate and exhibits qualitatively different dynamics.

Example 3 (Hybrid Incompatibility in an Oscillating Gene Network) *Here we compare the phenotypes for F2 hybrids formed by crossing oscillators $A(2)$ with $A(2.01)$, $A(2.1)$, and $A(2.5)$ (B and C are the same as above). Each A has is phenotypically identical ($\phi(t) = \sin(t) + \cos(t)$), however some of the hybrids exhibit markedly different dynamics. These differences tend to increase with time, quadratically (x^2) in F2s, and quartically (x^4) in F1s.*

$$A(2) = \begin{bmatrix} 2 & -1 \\ 5 & -2 \end{bmatrix} \qquad A(2.01) = \begin{bmatrix} 2 - \frac{1}{101} & -1 + \frac{1}{101} \\ 5 + \frac{1}{99} & -2 + \frac{1}{101} \end{bmatrix}$$

$$A(2.1) = \begin{bmatrix} 2 - \frac{1}{11} & -1 + \frac{1}{11} \\ 5 + \frac{6}{55} & -2 + \frac{1}{11} \end{bmatrix} \qquad A(2.5) = \begin{bmatrix} 2 - \frac{1}{3} & -1 + \frac{1}{3} \\ 5 + \frac{2}{3} & -2 + \frac{1}{3} \end{bmatrix}$$

F1 gene regulatory networks are formed by averaging the two parental $A(\tau)$ matrices; F2s are formed by first recombining parental matrices followed by an averaging.

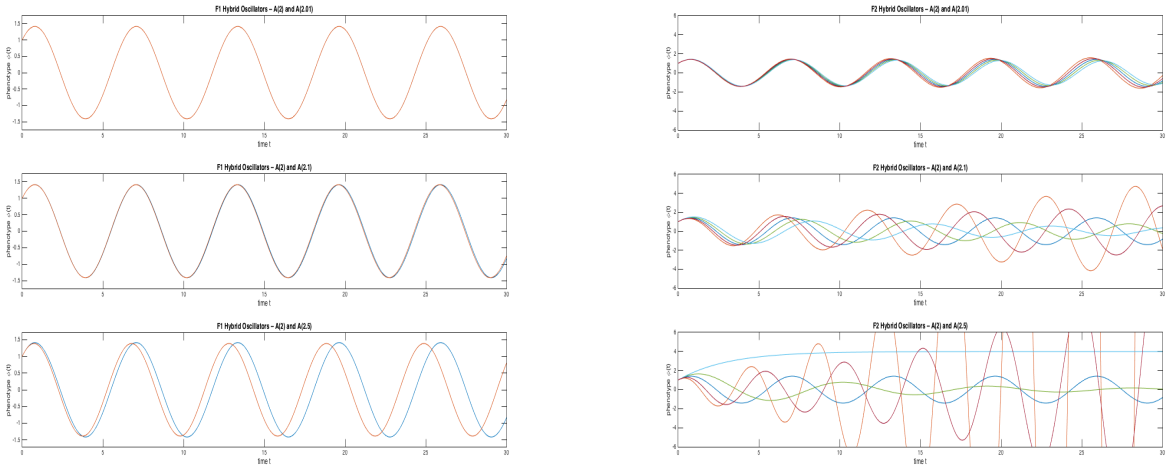

Figure 5: F1 (left) and F2 (right) hybrids crossing $A(2)$ with $A(2.01)$ (top), $A(2.1)$ (middle), and $A(2.5)$ (bottom). Note the difference in scale on the y-axis. F2 hybrids display more phenotypic divergence than F1s, on average. Further, some F2s completely fail to oscillate, as seen in an $A(2.5)$ F2 (light blue).

$A(2)$ and $A(2.1)$ differ in regulatory interaction strengths by 5.09%. If intrapopulation regulatory variation is approximately 5%, then this level of divergence is expected after $\sqrt{\frac{t}{N_e}} = 1$ generations.

The rate of speciation under neutrality in allopatric populations

In general terms, if fitness $\mathcal{F}$ is some function g of phenotypic divergence from an optimal scaled by the strength of selection β,

$$\mathcal{F} = g\left(\frac{\phi - \phi_0}{\beta}\right)$$

And a population P is normally distributed around a mean gene network architecture $A(\tau)$ and σ^2 is the intrapopulation regulatory variance,

$$P_T \sim \mathcal{N}\left(A(\tau), T\frac{\sigma^2}{N_e}\right)$$

the population mean architecture will move at rate

$$\Delta\tau = \sigma\sqrt{\frac{T}{N_e}}$$

where T is time measured in generations. USING GENERAL MATH FROM MULTIVARIATE TAYLOR SERIES.... we know that the phenotype of a first generation F_1 hybrid diverges from that of its parents (assuming both parents are at an optimum and phenotypically equivalent) quartically as a function of $\Delta\tau$. Thus the squared difference of it's phenotype will be,

$$\Delta\Phi_1^2 = c_1^2\sigma^4\left(\frac{T}{N_e}\right)^2$$

and F_1 fitness will decline linearly with respect to $\frac{T}{N_e}$. ARGUMENT FOR WHY $\sigma^2 c_1 \sim \beta$ HERE.

$$\Delta\mathcal{F}_1 = \left(\frac{\Delta\Phi_1}{\beta} = \frac{c_1 \sigma^2 \frac{T}{N_e}}{\beta} \approx \frac{T}{N_e} \right)$$

It follows FROM THE SAME MATH ABOUT THE MULTIVAR TAYLOR that the phenotypes of second generation F_2 hybrid crosses diverges quadratically as a function of $\Delta\tau$,

$$\Delta\Phi_2^2 = c_2^2 \left(\sigma \sqrt{\frac{T}{N_e}} \right)^2 = c_2^2 \frac{T}{N_e}$$

$$\Delta\mathcal{F}_2 = \left(\frac{\Delta\Phi_2}{\beta} = \frac{c_2 \sigma \sqrt{\frac{T}{N_e}}}{\beta} \approx \sqrt{\frac{T}{N_e}} \right)$$

and that F_2 fitness drops rapidly – at approximately rate $\sqrt{\frac{T}{N_e}}$. ARGUMENT FOR WHY $c_2\sigma \sim \beta$ HERE.

This suggests that reproductively isolated populations can speciate rapidly – on timescales much less than N_e generations, depending on the specifics of the fitness function.

Additional Examples

Discussion

mention B part of genetic architecture

Discussion guidelines:

- *Why is this important/useful?*
- *What are the assumptions and shortcomings of the research?*
- *Compare to other studies in the literature.*
- *Future directions.*
- *Wild speculations?*
- *Conclusion and overall impact.*

The complexity of biological systems has limited our understanding of their function and evolution. Above we outline an approach, a first step, towards untangling this complexity in reference to function and evolution. This methodology borrows successfully applied tools from engineering and aims to synthesize these with the concepts and tools of molecular and evolutionary biology.

Theoretical models in evolution and population genetics often lack the molecular details of physiology or of the genotype-phenotype map. Here, we offer a tractable and simple model which includes these missing features. Further, we provide, in clear mathematical language, an analytical description of phenomena hitherto only discussed verbally and conceptualy (phenogenetic drift [Weiss and Fullerton, 2000], developmental systems drift [True and Haag, 2001], biological degeneracy [Edelman and Gally, 2001], *etc.*). The tractability and relative simplicity of this exposition enables the interested biologist to work out by hand, if desired, the dynamics of a genetic system, as well as perturbations to the system – an attribute not likely to be found in less tractable models and simulations.

We have suggested an interpretation of system identification: to see it as an evolutionarily neutral manifold, and not simply a computational nuissance. We have demonstrated a method to analytically determine the set of all phenotypically invarint gene networks; by a simple change of coordinates in the

minimal configuration, or more generally by applying the Kalman decomposition in higher dimensions. Further, we emphasize that evolution proceeds through this high dimensional space as stochastic coordinate transformation, constrained by sexual reproduction and selection. This set is explored over evolutionary time when phenotype is conserved, and can lead to a diverse set of consequences, including the accumulation of Dobzhansky-Muller incompatibilities. We emphasize that these incompatibilities are a consequence of recombining different, yet functionally equivalent, mechanisms.

Furthermore, using a quantitative genetic approach, we estimated that a genetically variable population will drift in neutral system space at a rate determined by its intrapopulation variation and its effective population size. Because mechanistically distinct yet phenotypically equivalent biological systems can fail to produce viable hybrids, we predict allopatric populations to speciate at a rate on the order of N_e under reasonable population genetic parameter estimates. Additionally we see second-generation hybrid fitness plummet much faster than that of first-generation hybrids. This insight is a consequence of combinding our mechanistic model with a quantitative genetic one: we observe that F_1 phenotypes diverge quartically, and F_2 phenotypess quadratically, with evolutionary time. This result is also consistent with Haldane's rule; that if only one hybrid sex is inviable or sterile it is likely the heterogametic sex. The consistency comes from gene networks localized to the sex chromosomes functioning as an F_2 hybrid cross within a diploid F_1 heterogamete as there is only one sex chromosome.

We also suggest that gene networks may not always use their components parsimoniously as network size tends to ratchet up in the absence of strong selection against extra parts. Although unexplored presently, this phenomena may lead to insights on evolvability and developmental innovation. Lastly, we show that hybrid gene networks break down as function of genetic distance, and may, in part, explain broad patterns of reproductive isolation among diverse phyla [Roux et al., 2016].

As Richard Levins opined, models in population biology face a tradeoff among precision, realism, and generality [Levins, 1966]. As Levins expects, any tractable and general model, such as the present one under discussion, will have limitations. Most notable is linearity. It is often stated that life is not linear. This is often true, however, many of the ideas developed here should be generalizable to nonlinear cases (multilinear systems, say). Futher, we see this as a necessary first step in the direction of more life-like nonlinear evolutionary systems theory. Depending on an actual biological system's particularities, its (potential) nonlinearity, may buffer or exacerbate effects elucidated in this paper, such as the aquisition of Dobzansky-Muller incompatibilities.

This theoretical framework can easily be applied to other interesting questions in evolutionary biology not tackled presently: such as the evolution of linkage, the necessity of network complexity (does evolution tend towards Rube Goldberg or parsimonious network organization?), evolvability, structure/function inference, and intrapopulation context dependency of mutational effects, as well as many others.

literature comparison:

Over the last several years, several different computational approaches have been applied to study reproductive incompatibility and speciation. **?** simulated the evolution of a transcription factor and its binding site using a thermodynamic model. Their simulations suggest that the language by which a transcription factor recognizes its binding site can change, and potentially lead to hybird incomaptibility when allopatric populations employ divergent readout languages. This study, despite looking at gene regulation, does not analyze overall gene network architecture – as we do here – it only looks at the expression level of a single gene. Furthermore, they report reproducitve isolation primarily following direcitonal selection for a change in expression levels in each allopatric population; the evidecne for reproductive isolation following balancing selection is much weaker. Johnson and Porter 2000 did not observe any hybrid fitness declines under stabilizing selection – only under directional selection. Khatari et al, Tulchinsky et al, and Porter et al, all study hybrid incompatibility from a transcription factor/binding site interaction perspective, not from an overal network architecture perspective. Palmer and Feldman only see hybrid incompatibility in constant environments if the parental populations are relatively poorly adapted initially. Otherwise hybrids between two allopatric populations have fairly high fitnesses.

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A Kalman Decomposition

Definition 2 (Phenotypic equivalence of systems) *Let $(\kappa(t), \phi(t))$ and $(\bar{\kappa}(t), \bar{\phi}(t))$ be the solutions to (??) with coefficient matrices (A, B, C) and $(\bar{A}, \bar{B}, \bar{C})$ respectively, and both $\kappa(0)$ and $\bar{\kappa}(0)$ are zero. The systems defined by (A, B, C) and $(\bar{A}, \bar{B}, \bar{C})$ are* ***phenotypically equivalent*** *if*

$$\phi(t) = \bar{\phi}(t) \qquad \text{for all } t \geq 0.$$

Equivalently, this occurs if and only if

$$h(t) = \bar{h}(t) \qquad \text{for all } t \geq 0,$$

where h and $\bar{h}$ are the impulse responses of the two systems.

One way to find other systems equvalent to a given one is by change of coordinates ("algebraic equivalance"): if V is an invertible matrix, then the systems (A, B, C) and (VAV^{-1}, VB, CV^{-1}) have the same dyanamics because their transfer functions are equal:

$$CV^{-1}(zI - VAV^{-1})^{-1}VB = CV^{-1}V(zI - A)^{-1}V^{-1}VB = C(zI - A)^{-1}B.$$

However, the converse is not necessarily true: systems can have identical transfer functions without being changes of coordinates of each other. In fact, systems with identical transfer functions can involve interactions between different numbers of molecular species.

The set of all systems phenotypically equivalent to a given system (A, B, C) is elegantly described using the Kalman decomposition, which also clarifies the system dynamics? tells us a lot about how it works? *or something* To motivate this, first note that the the input $u(t)$ only directly pushes the system in directions lying in the span of the columns of B. As a result, different combinations of input can move the system in any direction that lies in the *reachable subspace*, which we denote by $\mathcal{R}$, and is defined to be the closure of $\text{span}(B)$ under applying A (or equivalently, the span of $B, AB, A^2B, \ldots A^{n-1}B$). Analogously to this, we define the *observable subspace*, $\mathcal{O}$, to be the closure of $\text{span}(C^T)$ under applying A. (Or: $\bar{\mathcal{O}}$ is the largest A-invariant subspace contained in the null space of C; and $\mathcal{R}$ is the largest A-invariant subspace contained in the image of B.)

If we define

1. The columns of $P_{r\bar{o}}$ are an orthonormal basis for $\mathcal{R} \cap \bar{\mathcal{O}}$.
2. The columns of P_{ro} are an orthonormal basis of the complement of $\mathcal{R} \cap \bar{\mathcal{O}}$ in $\mathcal{R}$.
3. The columns of $P_{\bar{r}o}$ are an orthonormal basis of the complement of $\mathcal{R} \cap \bar{\mathcal{O}}$ in $\bar{\mathcal{O}}$.
4. The columns of $P_{\bar{r}\bar{o}}$ are an orthonormal basis of the the remainder of $\mathbb{R}^n$.

If we then define

$$P = \left[\begin{array}{c|c|c|c} P_{r\bar{o}} & P_{ro} & P_{\bar{r}o} & P_{\bar{r}\bar{o}} \end{array} \right],$$

then

$$P^T P = \left[\begin{array}{c|c|c|c} I & 0 & 0 & 0 \\ \hline 0 & I & U & 0 \\ \hline 0 & V & I & 0 \\ \hline 0 & 0 & 0 & I \end{array} \right].$$

Check this. Can we get $U = V = 0$?

The following theorem can be found in SOME REFERENCE.

Theorem 1 (Kalman decomposition) *For any system (A, B, C) with corresponding Kalman basis matrix P, the transformed system (PAP^{-1}, PB, CP^{-1}) has the following form:*

$$\widehat{A} = PAP^{-1} = \begin{bmatrix} A_{r\bar{o}} & A_{r\bar{o},ro} & A_{r\bar{o},\bar{r}\bar{o}} & A_{r\bar{o},\bar{r}o} \\ 0 & A_{ro} & 0 & A_{ro,\bar{r}o} \\ 0 & 0 & A_{\bar{r}\bar{o}} & A_{\bar{r}\bar{o},\bar{r}o} \\ 0 & 0 & 0 & A_{\bar{r}o} \end{bmatrix},$$

and

$$\widehat{B} = PB = \begin{bmatrix} B_{r\bar{o}} \\ B_{ro} \\ 0 \\ 0 \end{bmatrix},$$

and

$$\widehat{C} = CP^{-1} = \begin{bmatrix} 0 & C_{ro} & C_{\bar{r}\bar{o}} & 0 \end{bmatrix}.$$

The transfer function of both systems is given by

$$H(z) = C_{ro}(zI - A_{ro})^{-1}B_{ro}.$$

In the latter case, we say that the system is *minimal* – there is no equivalent system with a smaller number of species. Note that this says that any two equivalent minimal systems are changes of basis of each other.

Since any system can be put into this form, and once in this form, its transfer function is determined only by C_{ro}, A_{ro}, and B_{ro}, therefore, the set of all equivalent systems are parameterized by the dimension n, the choice of basis (P), the remaining submatrices in $\widehat{A}$, $\widehat{B}$, and $\widehat{C}$ (which are unconstrained), and a invertible transformation of span(P_{ro}), which we call T_{ro}.

Theorem 2 (Parameterization of equivalent systems) *Let (A, B, C) be a minimal system.*

(a) Every equivalent system is of the form given in Theorem 1, i.e., can be specified by choosing a dimension, n; submatrices in $\widehat{A}$, $\widehat{B}$, and $\widehat{C}$ except for $A_{ro} = A$, $B_{ro} = B$, and $C_{ro} = C$; and choosing an invertible matrix P.

(b) conjecture: The parameterization is unique if P is futhermore chosen so that each P_x other than P_{ro} is a projection matrix, and that

$$0 = P_x^T P_y$$

for all (x, y) except $(ro, \bar{r}\bar{o})$.

Another way of saying it: pick the $\mathcal{R}$ and $\bar{\mathcal{O}}$ subspaces, that must intersect in something of the minimal dimension; then let P be the appropriate basis?

In some situations we may be interested in only "network rewiring", where A changes while B and C do not. For instance, if all non-regulatory functions of each molecule are strongly constrained, then C cannot change. Likewise, if responses of each molecule to the external inputs are not changed by evolution, then B does not change.

B Genetic drift with a multivariate trait

For completeness, we provide a brief argument of how the population mean moves under genetic drift with a quantitative genetics model, as in **?** or **?**. These ignore details of the underlying genetic basis, but developing a more accurate model is beyond the scope of this paper.

Completing the square First note that

$$(x-y)^T A(x-y) = x^T A\,(x-2y) + y^T Ay,$$

and so

$$\begin{aligned}(x-y)^T A(x-y) + x^T Bx &= x^T (A+B)\left(x - 2(A+B)^{-1}Ay\right) + y^T Ay \\ &= \left(x-(A+B)^{-1}Ay\right)^T (A+B)\left(x-(A+B)^{-1}Ay\right) + (\text{terms that don't depend on } x).\end{aligned}$$

Therefore, if $f(x;\Sigma,y)$ is the density of a Gaussian with mean y and covariance matrix Σ then substituting $A=\Sigma^{-1}$ and $B=U^{-1}$ above,

$$\frac{f(x;\Sigma,y)f(x;U,0)}{\int_x f(z;\Sigma,y)f(z;U,0)dz} = f(x;(\Sigma^{-1}+U^{-1})^{-1}, (\Sigma^{-1}+U^{-1})^{-1}\Sigma^{-1}y).$$

Now suppose that the population is distributed in genotype space as a Gaussian with covariance matrix Σ and mean y. Selection has the effect of multiplying this density by the fitness function and renormalizing, so that if expected fitness of x is proportional to $f(x;U,z)$ then the above argument shows that the next generation will be sampled from a Gaussian distribution with covariance matrix $(\Sigma^{-1}+U^{-1})^{-1}$ and mean $z+(\Sigma^{-1}+U^{-1})^{-1}\Sigma^{-1}(y-z)$ Taking a sample of size N to construct the next generation will produce something close to this but with a slightly (stochastically) deviating mean. The next generation's mean is drawn from a Gaussian distribution with mean with covariance matrix $(\Sigma^{-1}+U^{-1})^{-1}/N$ and mean $z+(\Sigma^{-1}+U^{-1})^{-1}\Sigma^{-1}(y-z)$.

Roughly, what is this doing? Suppose that the population mean differs from the optimum by ϵ, that $\Sigma=\sigma^2 I$ and $U=sI$. Then the population mean gets closer to the optimum on average, moving to $\epsilon/(1+\sigma^2/s)$ and adds noise of size $\sqrt{s}\sigma/\sqrt{N\sigma^2+Ns}$. At equilibrium, these two movements will be of the same order, so that ϵ is of order $(\sigma/\sqrt{N})\sqrt{1+\sigma^2/s}$.

C Differentiating the fitness function

Suppose that $\rho(t)\geq 0$ is a weighting function on $[0,\infty)$ so that fitness is a function of $L^2(\rho)$ distance of the impulse response from optimal. With A_0 a representative of the optimal set:

$$\begin{aligned}D(A) &:= \int_0^\infty \rho(t)\left|h_A(t)-h_{A_0}(t)\right|^2 dt \\ &:= \int_0^\infty \rho(t)\left|Ce^{At}B - Ce^{A_0 t}B\right|^2 dt \\ &= \int_0^\infty \rho(t)\left|C\left(e^{At}-e^{A_0 t}\right)B\right|^2 dt \\ &= \int_0^\infty \rho(t) C\left(e^{At}-e^{A_0 t}\right)BB^T\left(e^{At}-e^{A_0 t}\right)^T C^T dt\end{aligned} \tag{16}$$

How does this change with A? Since

$$\frac{d}{du}e^{(A+uZ)t}|_{u=0} = \int_0^t e^{As}Ze^{A(t-s)}ds, \tag{17}$$

we have that

$$\begin{aligned}\frac{d}{du}D(A+uZ)|_{u=0} &= 2\int_0^\infty \rho(t)C\left(\int_0^t e^{As}Ze^{A(t-s)}ds\right)BB^T\left(e^{At}-e^{A_0 t}\right)^T C^T dt \\ &= 2\int_0^\infty \rho(t)C\left(\int_0^t e^{As}Ze^{A(t-s)}ds\right)B\left(h_A(t)-h_{A_0}(t)\right)^T dt\end{aligned} \tag{18}$$

and, by differentiating this and supposing that A is on the optimal set, i.e., $h_A(t) = h_{A_0}(t)$, (so wolog $A = A_0$):

$$\begin{aligned}\mathcal{H}(Y,Z) &:= \frac{1}{2}\frac{d}{du}\frac{d}{dv}D(A_0 + uY + vZ)|_{u=v=0} \\ &= \int_0^\infty \rho(t)C\left(\int_0^t e^{A_0 s}Ye^{A_0(t-s)}ds\right)BB^T\left(\int_0^t e^{A_0 s}Ze^{A_0(t-s)}ds\right)^T C^T dt.\end{aligned} \tag{19}$$

Here $\mathcal{H}$ is the quadratic form underlying the Hamiltonian. By defining Δ_{ij} to be the matrix with a 1 in the (i,j)th slot and 0 elsewhere, the coefficients of the quadratic form is

$$H_{ij,k\ell}(A) := \mathcal{H}(\Delta_{ij}, \Delta_{k\ell}). \tag{20}$$

We could use this to compute the gradient of D, or to get the quadratic approximation to D near the optimal set. To do so, it'd be nice to have a way to compute the inner integral above. Suppose that we can diagonalize $A = U\Lambda U^{-1}$. Then

$$\int_0^t e^{As}Ze^{A(t-s)}ds = \int_0^t Ue^{\Lambda s}U^{-1}ZUe^{\Lambda(t-s)}U^{-1}ds \tag{21}$$

Now, notice that

$$\int_0^t e^{s\lambda_i}e^{(t-s)\lambda_j}ds = \frac{e^{t\lambda_i} - e^{t\lambda_j}}{\lambda_i - \lambda_j}. \tag{22}$$

Therefore, defining

$$X_{ij}(t,Z) = \left(U^{-1}ZU\right)_{ij}\frac{e^{t\lambda_i} - e^{t\lambda_j}}{\lambda_i - \lambda_j} \tag{23}$$

moving the U and U^{-1} outside the integral and integrating we get that

$$\int_0^t e^{As}Ze^{A(t-s)}ds = UX(t,Z)U^{-1}. \tag{24}$$

Following on from above, we see that if $Z = \Delta_{k\ell}$, then

$$X_{ij}^{k\ell}(t) = \frac{e^{t\lambda_i} - e^{t\lambda_j}}{\lambda_i - \lambda_j}(U^{-1})_{\cdot k}U_{\ell\cdot}, \tag{25}$$

where $U_{k\cdot}$ is the kth row of U, and so

$$H_{ij,k\ell}(A) = \int_0^\infty \rho(t)CUX^{ij}(t)U^{-1}BB^T(U^{-1})^T X^{k\ell}(t)^T U^T C^T dt. \tag{26}$$

This implies that

$$D(A_0 + \epsilon Z) \approx \epsilon^2 \sum_{ijk\ell} H^{ij,k\ell}Z_{ij}Z_{k\ell} \tag{27}$$

and so

$$D(A_0 + \epsilon Z) \approx \epsilon^2 \sum_{ijk\ell} H^{ij,k\ell}Z_{ij}Z_{k\ell} \tag{28}$$

By section B, if we set $\Sigma = \sigma^2 I$ and $U = H$, then a population at $A_0 + Z$ experiences a restoring force of strength $(I + \sigma^2 H^{-1})^{-1}Z$ (treating Z as a vector and H as an operator on these). If σ^2 is small compared to H^{-1} then this is approximately $-\sigma^2 H^{-1}Z$. This suggests that the population mean follows an Ornstein-Uhlenbeck process, as described (in different terms) in **?**.