

Sufficient Conditions for Coarse-Graining Evolutionary Dynamics

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Genetic Algorithms and the Building Block Hypothesis

- ▶ In 1975 Holland published his seminal work on GAs
 - ▶ Description of the Genetic Algorithm
 - ▶ A theory of adaptation for GAs
 - ▶ which later came to be known as BBH
- ▶ GAs useful for adapting solutions to difficult real world problems
- ▶ However BBH has drawn considerable skepticism amongst many researchers (e.g. Vose, Wright, Rowe)
- ▶ Despite criticism of BBH, no alternate full-fledged theories of adaptation have been proposed

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No Alternate Theories of Adaptation for GAs — Why?

- ▶ For genomes of non-trivial length, current theoretical results do not permit the formulation of *principled* theories of adaptation
 - ▶ Schema theories only permit a tractable analysis of evolutionary dynamics over a single generation
 - ▶ Markov Chain approaches only yield a qualitative description of evolutionary dynamics in the asymptote of time

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- ▶ Even with this assumption there are currently no theoretical results which permit a *principled* analysis of any aspect of GA behavior over the “short-term”
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The Promise of Coarse-Graining

- ▶ Coarse-graining a very useful technique from theoretical Physics
- ▶ If successfully applied to an IPGA it permits a *principled* analysis of certain aspects of the IPGA's dynamics over multiple generations
- ▶ Therefore coarse-graining is a promising approach to the formulation of principled theories of evolutionary adaptation

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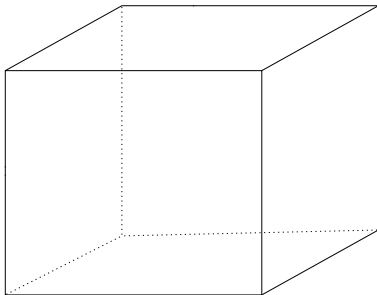
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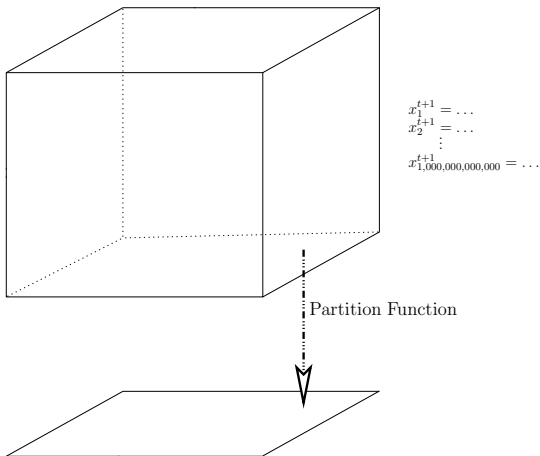
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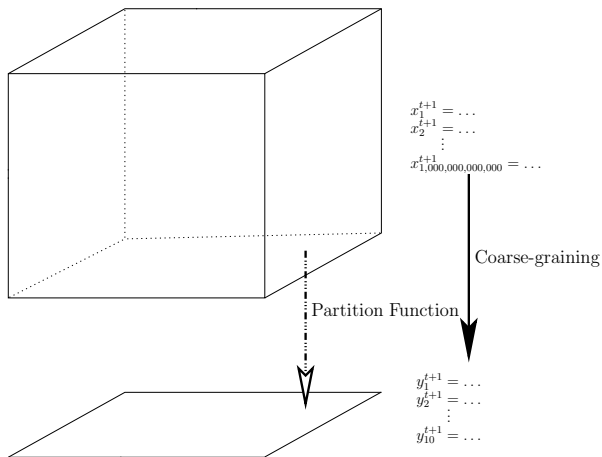


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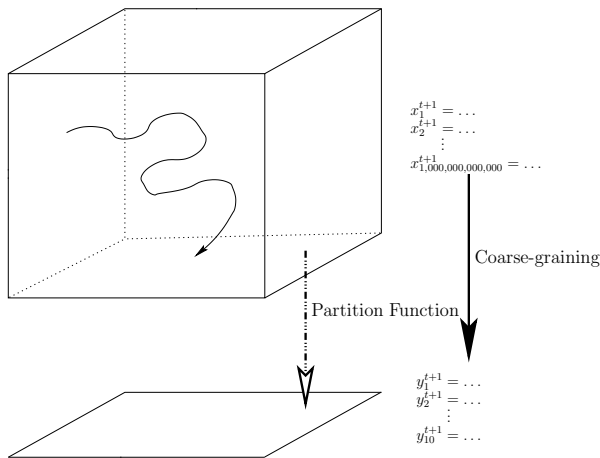
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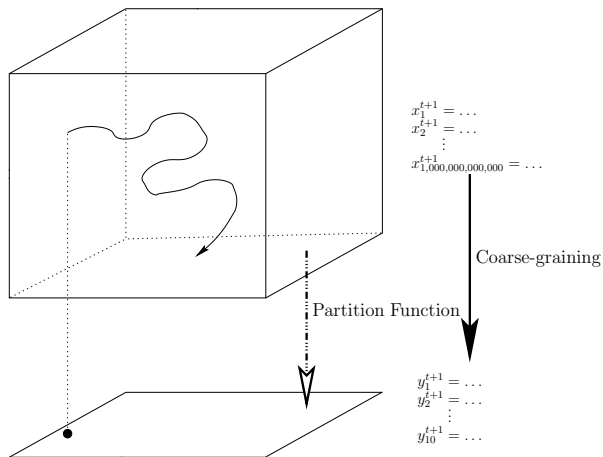
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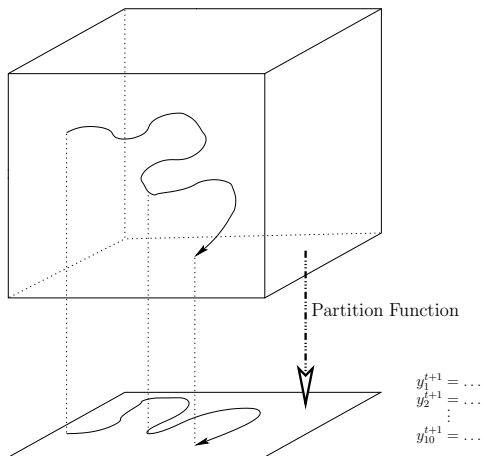
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Previous Coarse-Graining Results

- ▶ Wright, Vose, and Rowe (Wright et al. 2003) show that any mask based recombination operation of an IPGA can be coarse-grained.
- ▶ However they argue that the selecto-recombinative dynamics of an IPGA **with an arbitrary initial population** cannot be coarse-grained unless the fitness function satisfies a **very strong** constraint
- ▶ I call this constraint *schematic fitness invariance*
 - ▶ for some schema partition, and for any schema in the partition, all the genomes in the schema have exactly the same fitness
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Comparison between Coarse-Graining Results

- ▶ I show that if the class of initial populations is appropriately constrained then it is possible to coarse-grain the selecto-recombinative dynamics of an IPGA for a much weaker constraint on the fitness function
- ▶ The constraint on the class of initial populations is not onerous
 - ▶ A uniformly distributed population satisfies this constraint
- ▶ The constraint on the fitness function is weak enough that it makes the coarse-graining result potentially useful in a theory of adaptation

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Wright et al. 2003	None	Severe
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Structure of this Talk

1. Describe an abstract framework for analyzing the dynamics of a selecto-recombinative infinite population EA (IPEA)
2. Describe the theoretical technique used to Coarse-Grain the dynamics of an IPEA
3. Present results that show that these dynamics can be coarse-grained provided that the IPEA satisfies certain **abstract conditions**
4. Describe how the coarse-graining results can be used to coarse-grain the dynamics of an IPGA with long genomes and a non-trivial fitness functions
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Modeling Populations and Operations on Populations

- ▶ Modeling scheme based on the one used in (Toussaint 2003)
- ▶ Populations modeled as distributions over the genome set
 - ▶ Distribution values sum to 1
- ▶ Population-level effect of evolutionary operations modeled as the application of *parameterized* mathematical operators to genomic distributions
 - ▶ Parameter objects used by the operators (fitness function, transmission function) give individual-level information about the genomes

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- ▶ Use transmission functions (Altenberg 1994) to represent the variational information at the individual-level
 - ▶ Example: $T(g|g_1, \dots, g_n)$ is the probability that parents g_1, \dots, g_n will yield a child g when recombined

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Modeling the Effect of Variation on Populations

- ▶ Given some transmission function T , the effect of variation at the population-level is modeled by the variation operator \mathcal{V}_T
- ▶ For some population p , if $p' = \mathcal{V}_T(p)$, then, p' is as follows:

$$p'(g) = \sum_{\substack{(g_1, \dots, g_m) \\ \in \prod_1^m G}} T(g|g_1, \dots, g_m) \prod_{i=1}^m p(g_i)$$

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Modeling the Effect of Selection on Populations

- ▶ Given some fitness function $f : G \rightarrow \mathbb{R}^+$, the effect of fitness proportional selection is modeled by the selection operator S_f
- ▶ For some population p , if $p' = S_f(p)$, then p' is as follows: For any genotype g ,

$$p'(g) = \frac{f(g)p(g)}{\mathcal{E}_f(p)}$$

where \mathcal{E}_f is the weighted average fitness of p

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Some Terminology and Notation

- ▶ $\beta : G \rightarrow K$ a surjective function
 - ▶ Call β a partitioning
 - ▶ Call co-domain K the theme set
 - ▶ Call the elements of K themes
- ▶ $\langle k \rangle_\beta$ denotes the set of all $g \in G$ such that $\beta(g) = k$
- ▶ Call $\langle k \rangle_\beta$ the theme class of k under β

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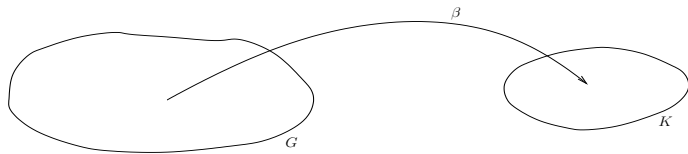
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Projection Operator

- ▶ Let $\beta : G \rightarrow K$ be a partitioning
- ▶ A projection operator Ξ_β 'projects' a distribution p_G over G 'through' β to create a distribution $p_K = \Xi_\beta(p_G)$ over the theme set

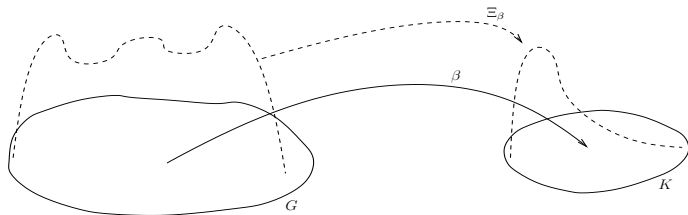


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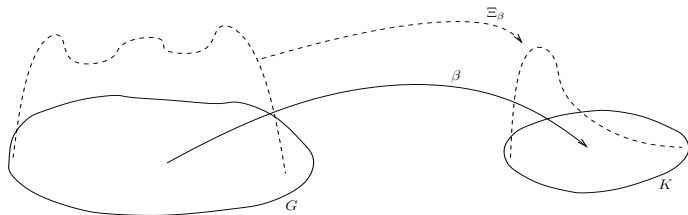


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Semi-Concordance, Concordance, Global Concordance

- ▶ $\beta : G \rightarrow K$ some partitioning (i.e. surjective function)
- ▶ $\mathcal{W} : \Lambda^G \rightarrow \Lambda^G$ some operator
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- ▶ Let $\mathcal{G} = \mathcal{V}_T \circ \mathcal{S}_f$
- ▶ I give sufficient conditions on T and f under which a concordance result can be proved for \mathcal{G}
- ▶ One of these conditions is called Ambivalence.
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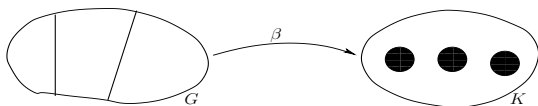
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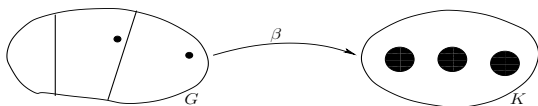
An Ambivalent 2-parent transmission function T



Say that T is *ambivalent under β*

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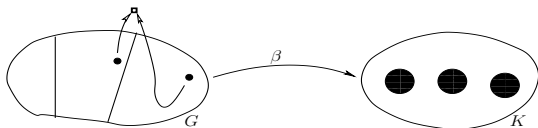
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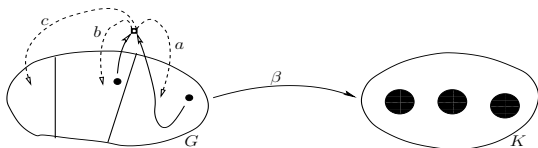
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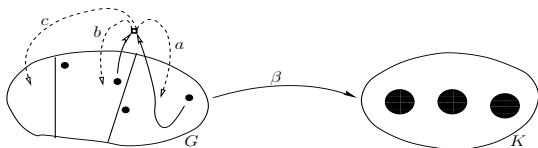
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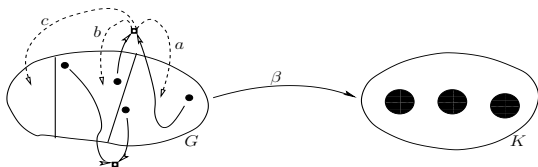
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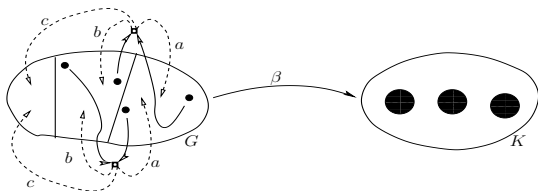
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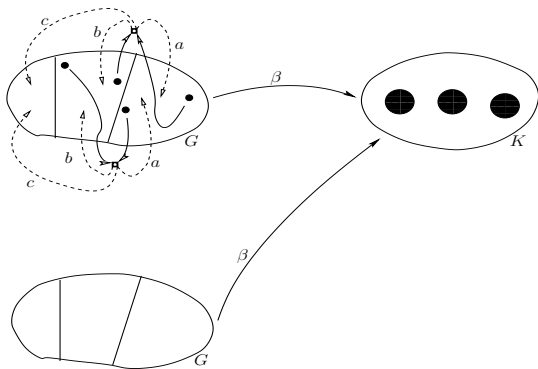
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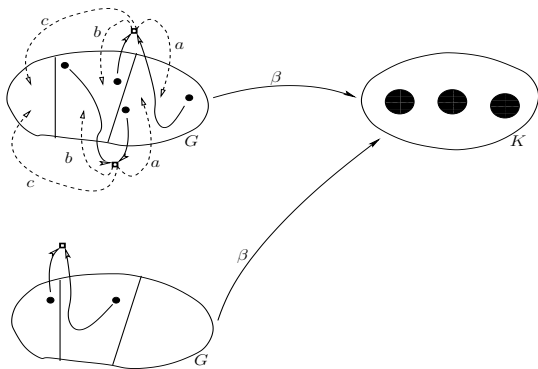
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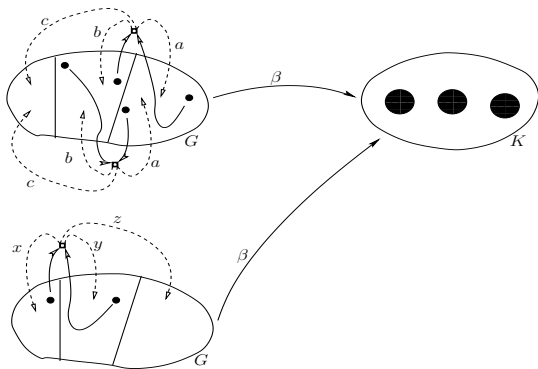
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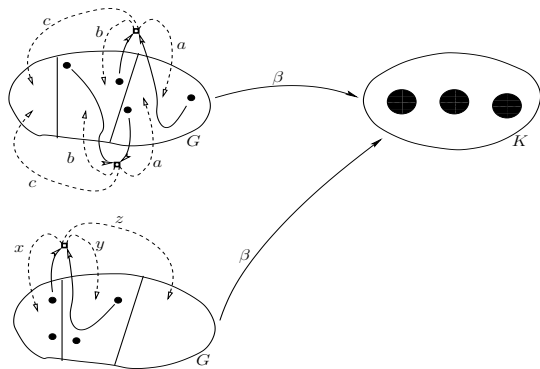
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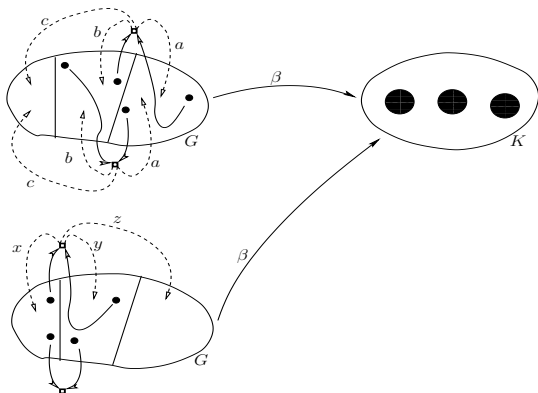
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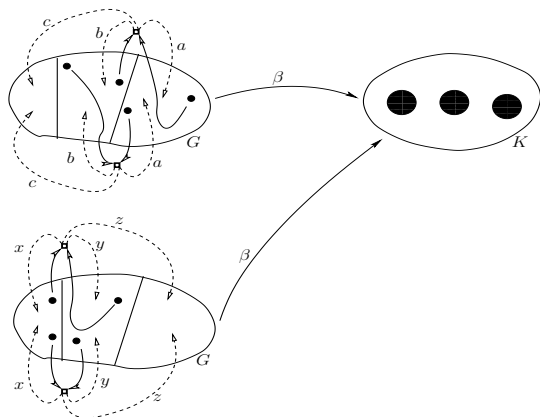
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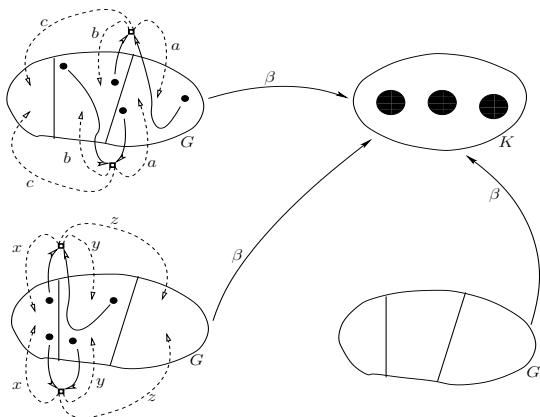
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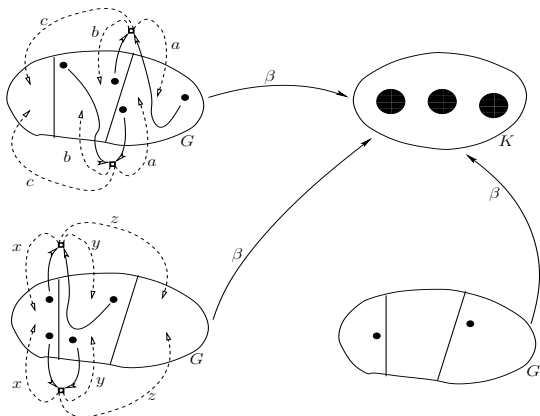
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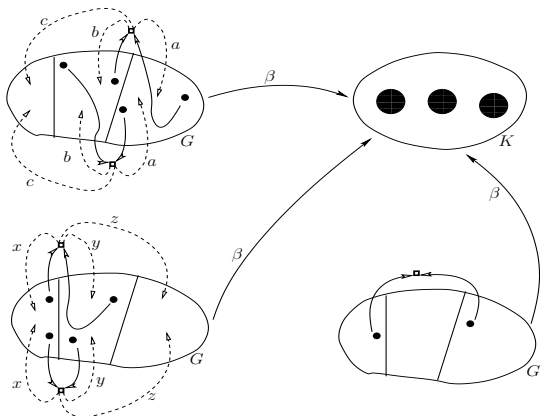
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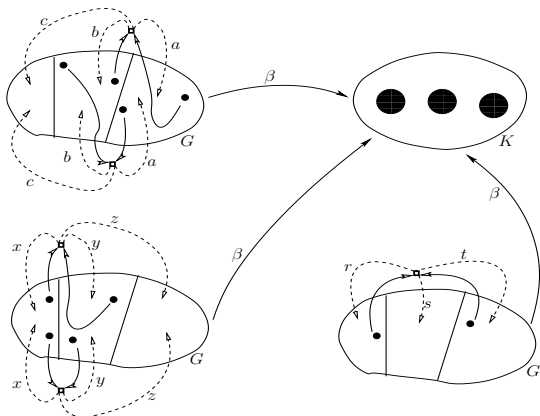
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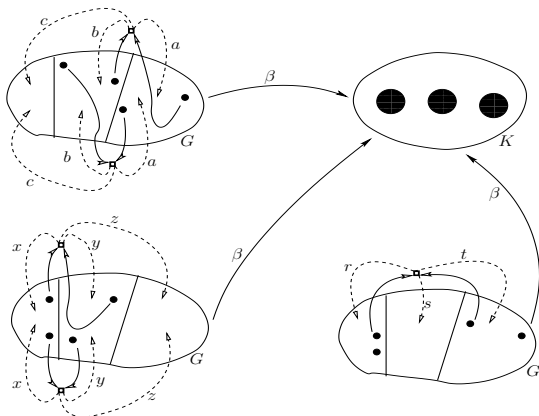
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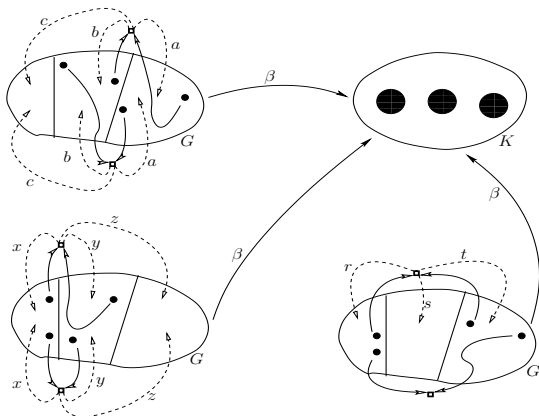
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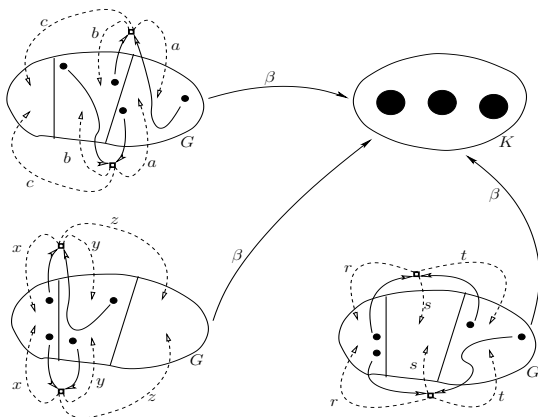
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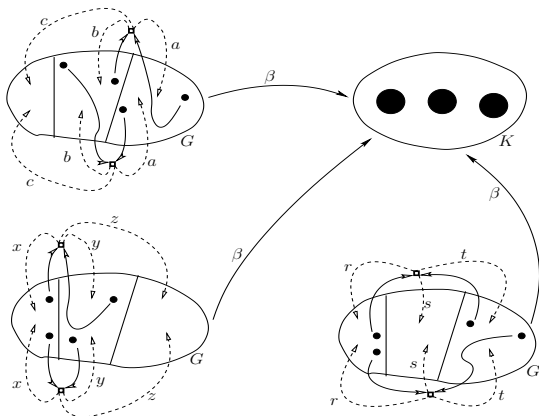
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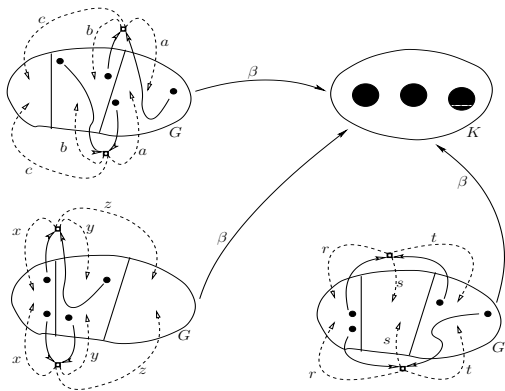
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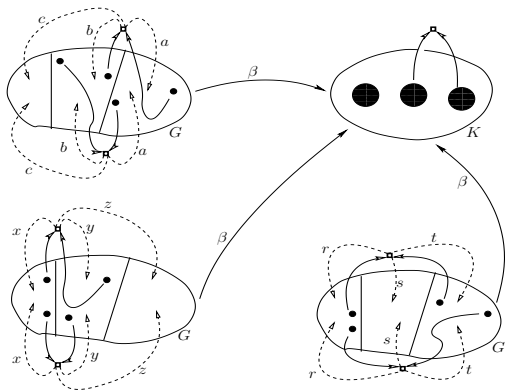
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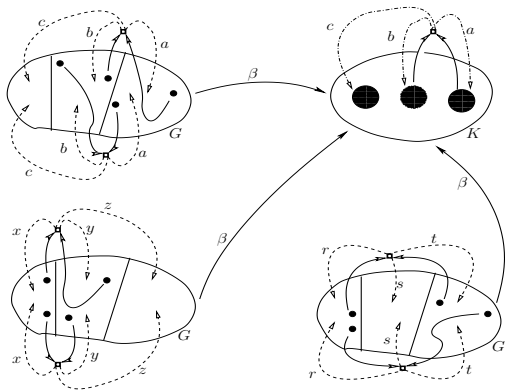
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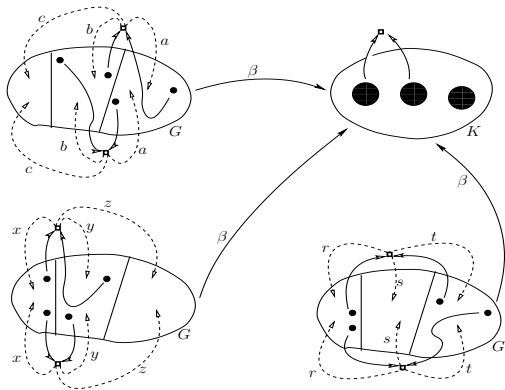
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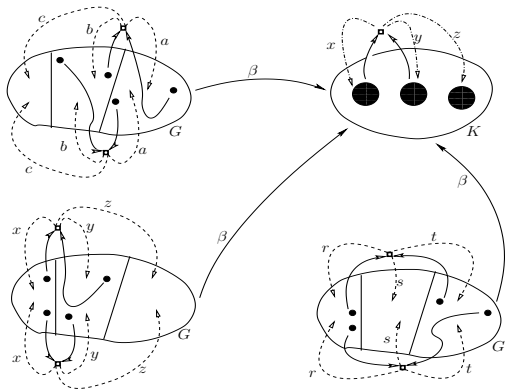
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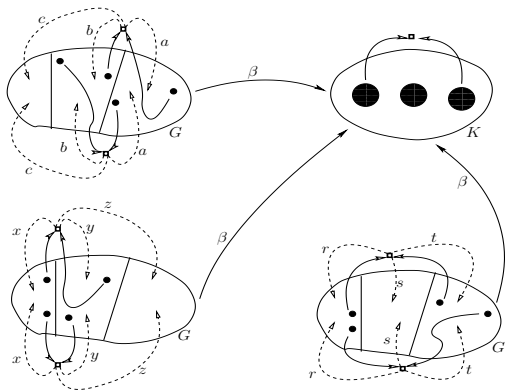
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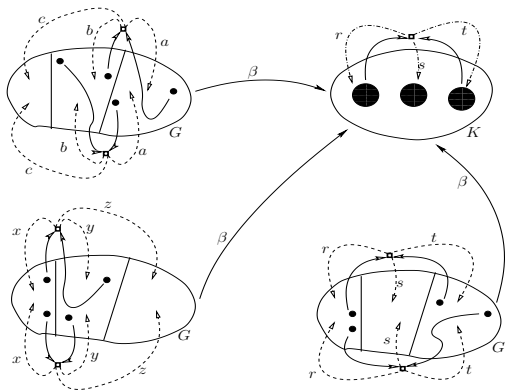
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Theorem: Global Concordance of Variation

- ▶ G, K countable sets
 - ▶ $\beta : G \rightarrow K$ some partitioning over G
 - ▶ T a transmission function over G
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- then, \mathcal{V}_T is globally concordant with β

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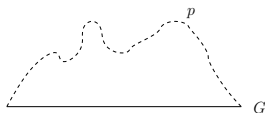
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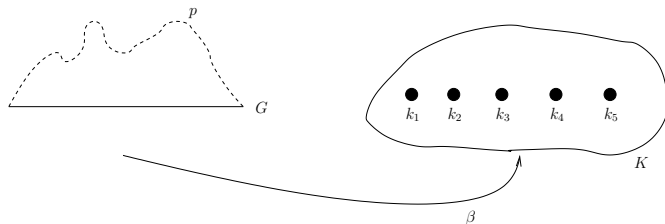
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Theme Conditional Operator (By Example)



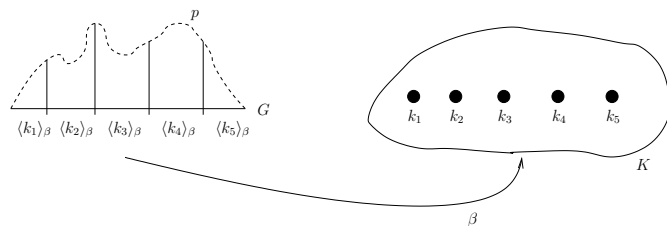
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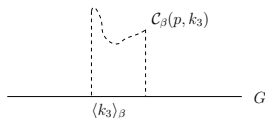
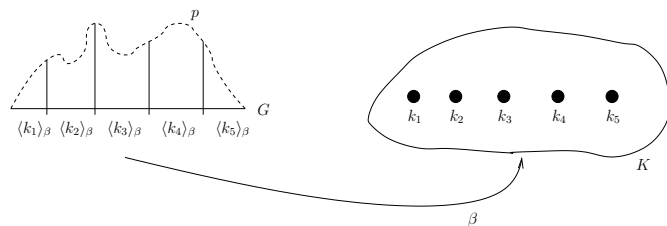
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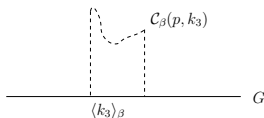
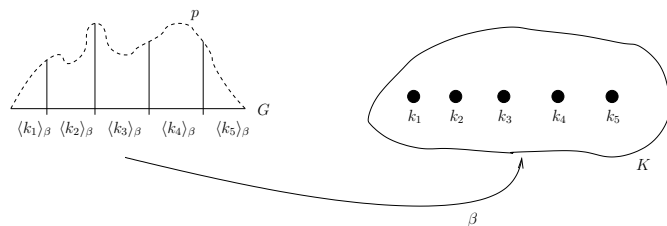
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Bounded Thematic Mean Divergence (By Example)

- ▶ G a finite Set
- ▶ $\beta : G \rightarrow K$ a partitioning
- ▶ $f^* : K \rightarrow \mathbb{R}^+$ some function
- ▶ $\delta \geq 0$
- ▶ $f : G \rightarrow \mathbb{R}^+$
- ▶ $U \subseteq \Lambda^G$

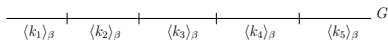
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Thematic mean Divergence of f w.r.t f^* on U under β is bounded by δ if for any $p \in U$ and any $k \in K$,

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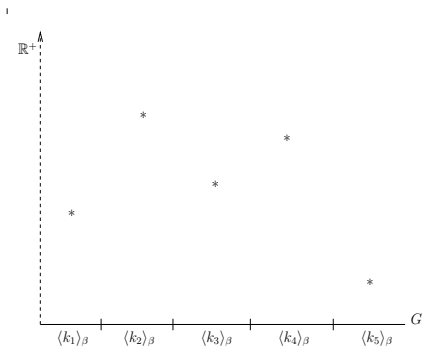


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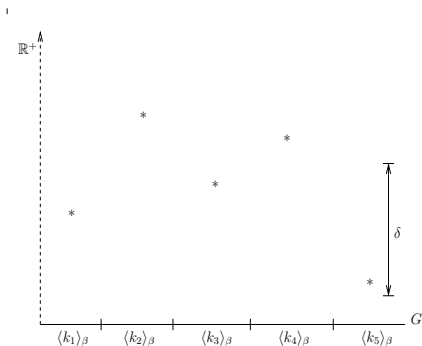


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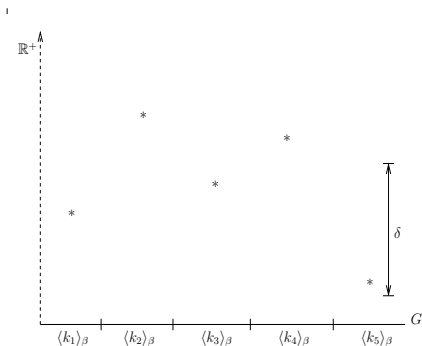


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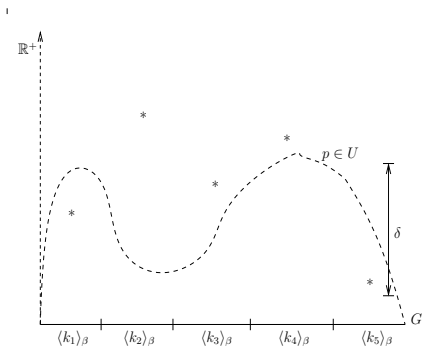


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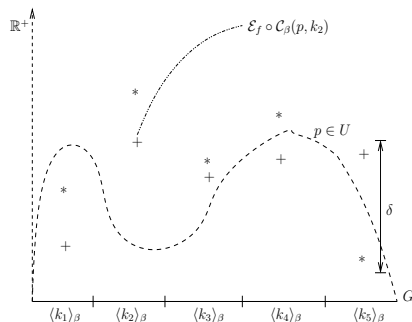


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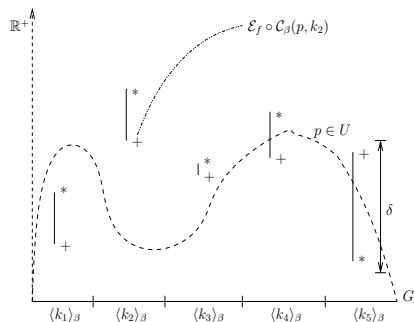


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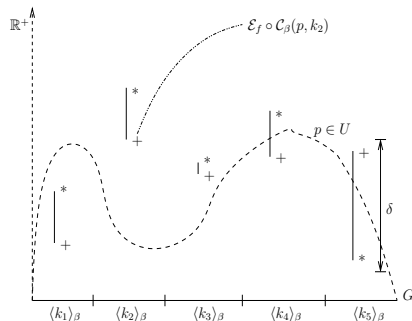


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2. T is ambivalent under β
3. E is non-departing over U

Let $E^* = (K, T^{\vec{\beta}}, f^*)$, then for any $t \in \mathbb{Z}^+$,

$$\begin{array}{ccc}
 U & \xrightarrow{G_E^t} & U \\
 \Xi_\beta \downarrow & \lim_{\delta \rightarrow 0} & \downarrow \Xi_\beta \\
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Theorem: Limitwise Concordance of Evolution

- ▶ $E = (G, T, f)$ an Evolution Machine
- ▶ $\beta: G \rightarrow K$ a partitioning of G
- ▶ $U \subseteq \Lambda^G$ (such that $\Xi_\beta(U) = \Lambda^K$)
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Implications for Coarse-Graining an IPGA

- ▶ Given an IPGA with
 - ▶ long genomes
 - ▶ uniform cross-over
- ▶ And some relatively coarse schema partitioning
- ▶ The IPGA will satisfy the 3 abstract conditions if it satisfies the following 2 concrete conditions:
 1. The initial population is *approximately schematically uniform*
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Approximate Schematic Uniformity (By Example)

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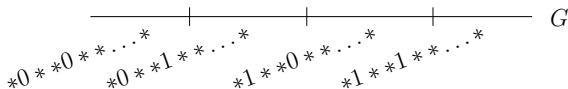
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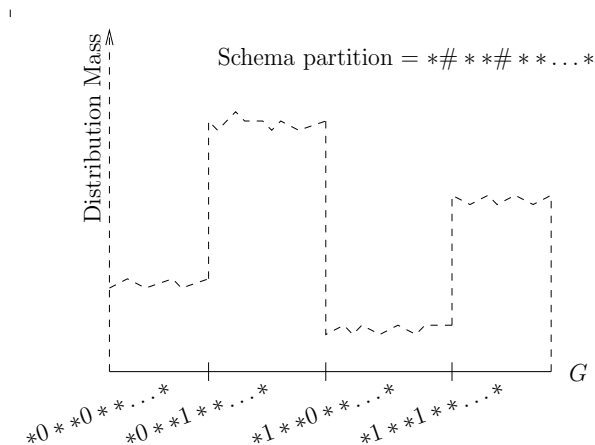
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Schema partition = $*\#**\#**\dots*$



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Low-Variance Schematic Fitness Distribution

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- ▶ Suppose that for each schema,
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- ▶ An ideal validation of these results involves
 - ▶ Constructing an IPGA with large genomes
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 - ▶ Simulating the IPGA and projecting its dynamics onto the schema partition
 - ▶ Seeing if the coarse-grained dynamics of the IPGA approximates the projected dynamics
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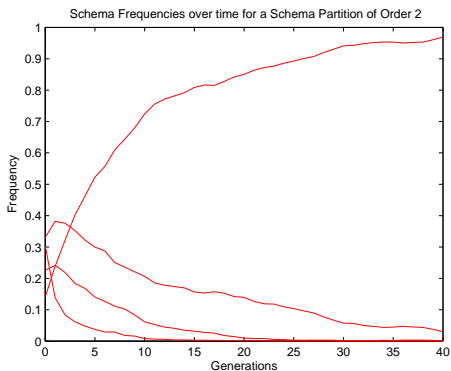
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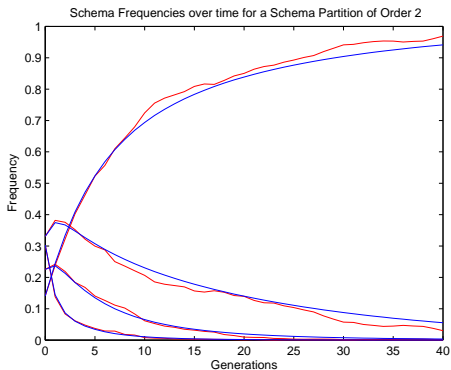
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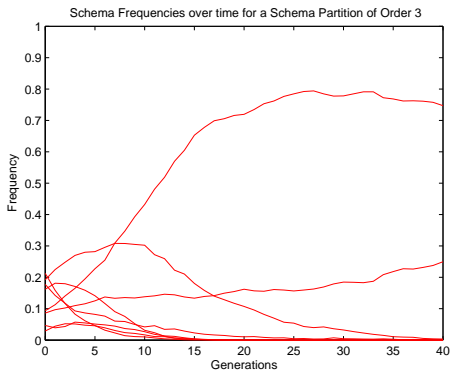
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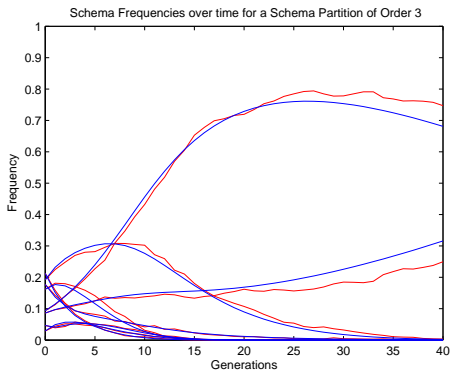
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