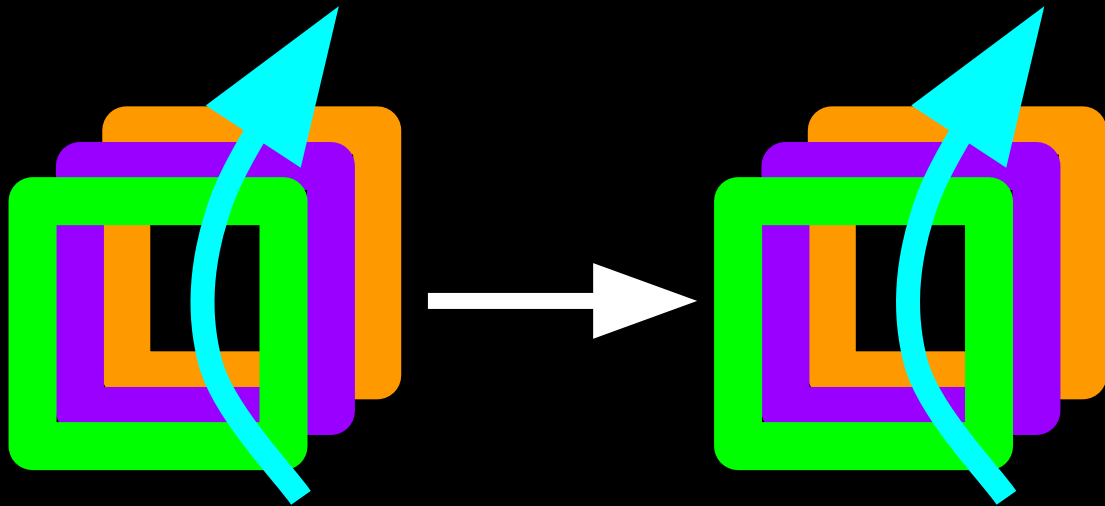


MVEE:

*A Framework for
Evolutionary Studies.*



Daniel Ari
Friedman

2018

Research Question:

How can we formalize the evolution of heredity, environment, and phenotype through time and across biological levels?

Research Question:

How can we formalize the evolution of heredity, environment, and phenotype through time and across biological levels

.....accounting for.....

plasticity & meta-plasticity,

interactions within and among scales,

scientific knowledge/measurement/modeling constraints,

ecological variability over behavioral/developmental/evolutionary time,

diversity & open-endedness of evolving systems (bio/social/computational)



Research Question:

How can we formalize the evolution of heredity, environment, and phenotype through time and across biological levels?

Goal:

- Extend Variational Neuroethology (Ramstead et al. 2017) to specify a tractable general framework for all Evolutionary studies, Biological and Otherwise.
- This would allow us to integrate current data across systems and suggest new measurements/experiments/systems.

This Talk:

- Background theory...Part 1
 - **Claim 1: EcoEvoDevo** is trapped in a locally-optimizing regime because it is trapped in an incoherent **G-P-E** & **F** phrasing.

This Talk:

- Background theory...Part 1
 - **Claim 1:** EcoEvoDevo is trapped in a locally-optimizing regime because it is trapped in an incoherent G-P-E & F phrasing.
- Background theory...Part 2
 - **Claim 2:** The data, theory, math, and philosophy already exist to synthesize a tractable generalized model of evolution.

This Talk:

- Background theory...Part 1

- **Claim 1:** EcoEvoDevo is trapped in a locally-optimizing regime because it is trapped in an incoherent G-P-E & F phrasing.

- Background theory...Part 2

- **Claim 2:** The data, theory, math, and philosophy already exist to synthesize a tractable generalized model of evolution.

MVEE - A Way Forward....

- MVEE sits between VNE and EcoEvoDevo.
- MVEE is a Synergetic framework for Evolutionary studies.
- MVEE == Variational Neuroethology + EcoEvoDevo + Collective Behavior + ML

Theoretical Background

Part 1

“Fitness”?

Theoretical Background

Part 2

Toward a mechanistic explanation of phenotypic evolution: The need for a theory of theory integration

2018

Manfred D. Laubichler^{1,2,3} | Sonja J. Prohaska^{3,4,5} | Peter F. Stadler^{3,5,6,7,8,9,10} 


The challenges and scope of theoretical biology

David C. Krakauer^{a,*}, James P. Collins^b, Douglas Erwin^{a,c}, Jessica C. Flack^a, Walter Fontana^{a,d},
Manfred D. Laubichler^b, Sonja J. Prohaska^e, Geoffrey B. West^a, Peter F. Stadler^{a,f,g}^a Santa Fe Institute, Santa Fe, NM, United States^b School of Life Sciences, Arizona State University, Tempe, AZ, United States^c Smithsonian Museum of Natural History, Washington, DC, United States^d Harvard Medical School, Boston, MA, United States^e Bioinformatics Group, Department of Computer Science, University of Leipzig, Germany^f Fraunhofer Institute IZI, Leipzig, Germany^g Max-Planck Institute for Mathematics in the Sciences, Leipzig, Germany

2011

We need a way to integrate sub-theories.

Toward a mechanistic explanation of phenotypic evolution: The need for a theory of theory integration

Manfred D. Laubichler^{1,2,3} | Sonja J. Prohaska^{3,4,5} | Peter F. Stadler^{3,5,6,7,8,9,10} 

Here, we argue that this philosophical conception of methodological and explanatory pluralism is no longer adequate for several areas of biology because of (1) the data revolution and (2) the computational revolution within the life sciences that have brought the goal of theory integration within reach again. Taken together these two trends, in addition with progress in our understanding of complex systems, enables us to develop appropriately coarse grained explanations of complex phenomena based on the systematic integration of local theories describing specific domains.

In the emerging age of big data, many of these “local” theories are accompanied by large amounts of empirical data that are stored, indexed, and organized according to the theoretical framework in which they were produced. The integration of such “local” theories into a more global one with a wider scope is desirable not only for both theoretical reasons but also pragmatically, as we increasingly rely on the (re)use of a potentially much larger body of data that were produced for and in specific experimental contexts.

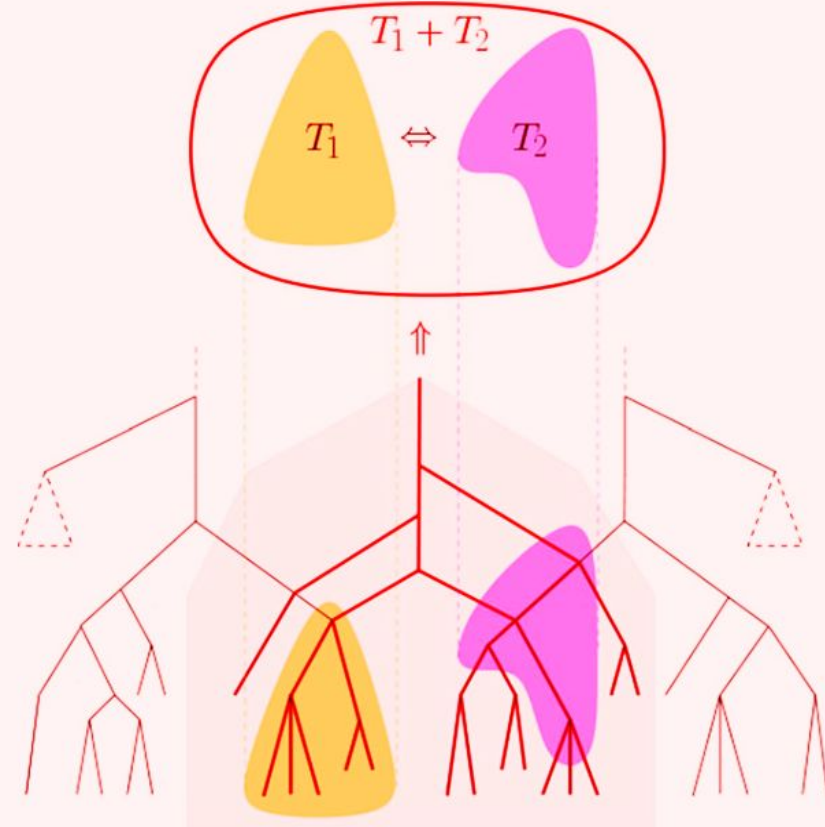
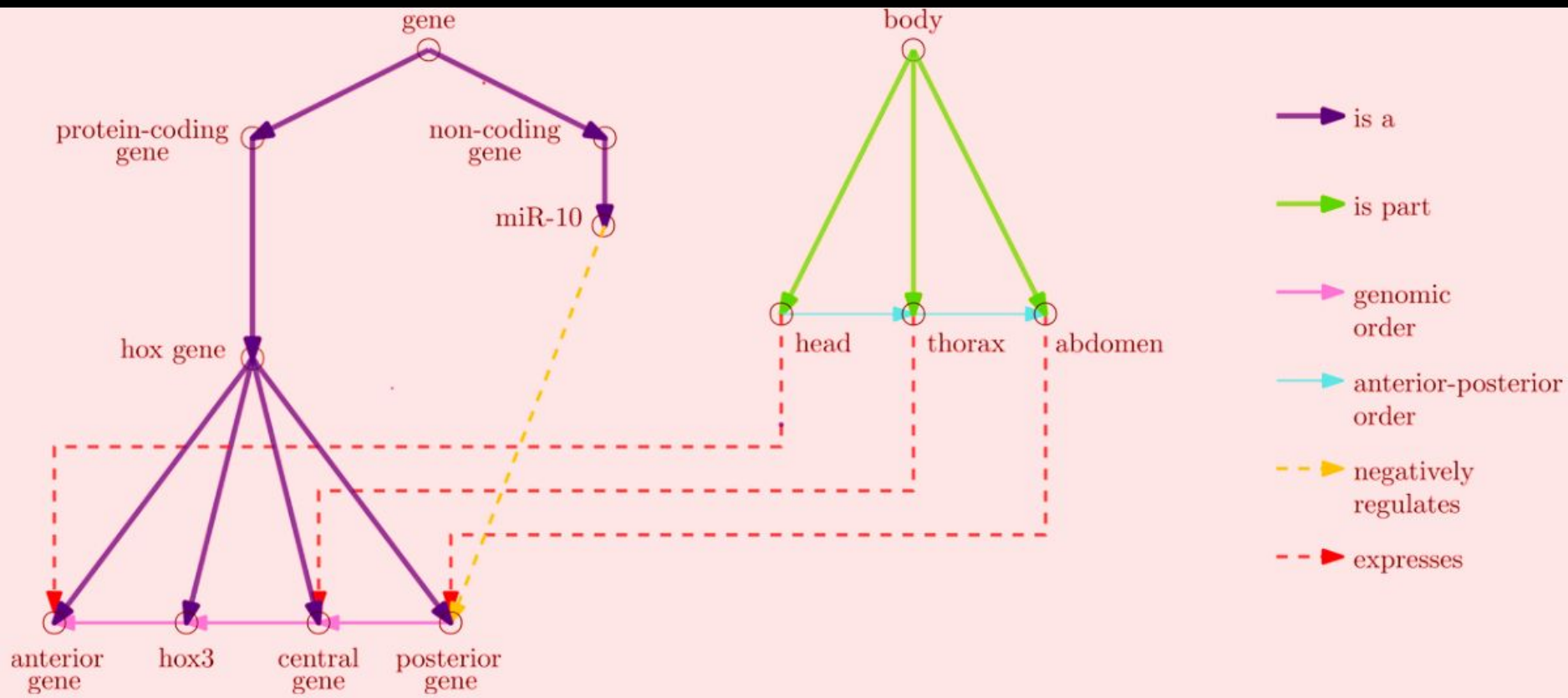


FIGURE 4 Integration of theories T_1 and T_2 formulated in unrelated ontologies requires the construction of a consistent common ontology (shown as red tree) capturing the relevant concepts of both domains. Only then a unified theory $T_1 + T_2$ can be formulated [Color figure can be viewed at wileyonlinelibrary.com]



In practice, ontologies are usually specified in special ontology languages such as OBO, which is most commonly used in biological and biomedical sciences, and is used for the well-known Gene Ontology GO (GO Consortium, 2009). The practical organization of empirical knowledge—that is, data—in a particular domain is strongly influenced by the underlying ontology: the relationships among objects,

The challenges and scope of theoretical biology

David C. Krakauer^{a,*}, James P. Collins^b, Douglas Erwin^{a,c}, Jessica C. Flack^a, Walter Fontana^{a,d}, Manfred D. Laubichler^b, Sonja J. Prohaska^e, Geoffrey B. West^a, Peter F. Stadler^{a,f,g}

^a Santa Fe Institute, Santa Fe, NM, United States

^b School of Life Sciences, Arizona State University, Tempe, AZ, United States

^c Smithsonian Museum of Natural History, Washington, DC, United States

^d Harvard Medical School, Boston, MA, United States

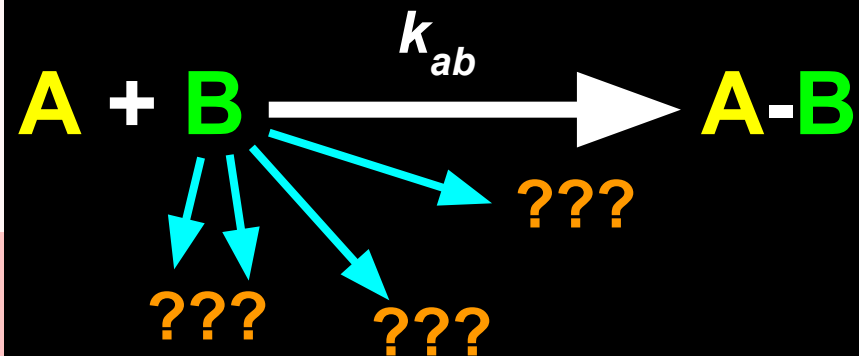
^e Bioinformatics Group, Department of Computer Science, University of Leipzig, Germany

^f Fraunhofer Institute IZI, Leipzig, Germany

^g Max-Planck Institute for Mathematics in the Sciences, Leipzig, Germany

2011

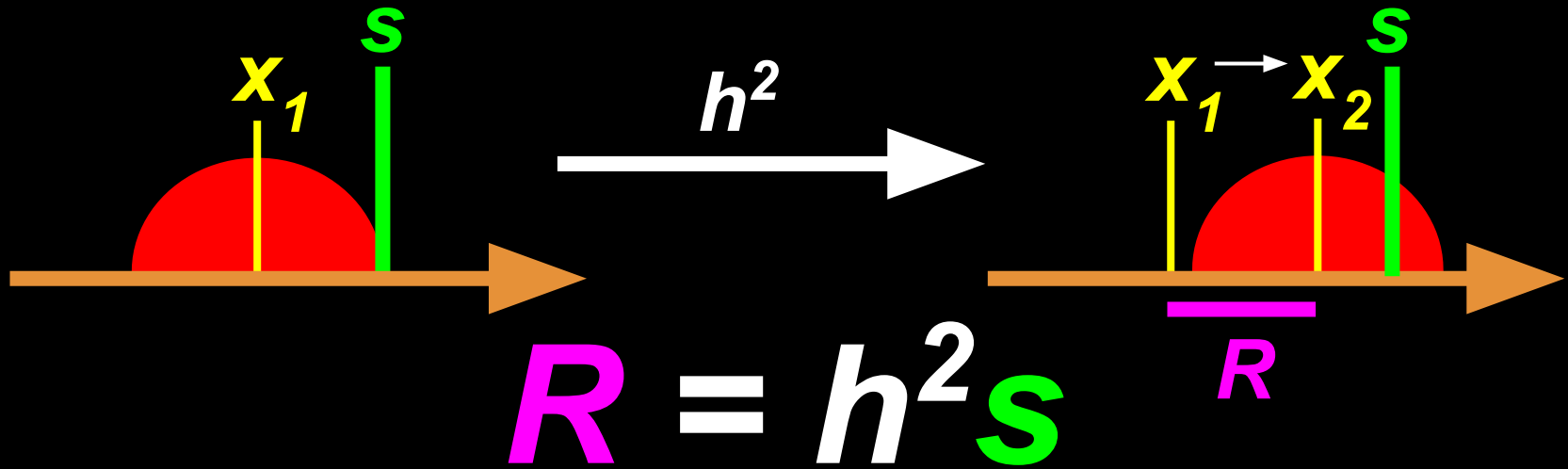
Whereas chemical (reaction) equations again describe relationships of sets of observables (in this case the educts and products of a chemical reaction), the algorithmic *transformation rules* provide a means of predicting what novel entities might be produced. The price we have to pay for the convenient high-level description—for not being derailed by details of electron densities and nuclear movements in physical space—is twofold: First, we have to memorize quite a few rules, not just a single, beautiful and fundamental equation. And secondly, the predictive power of the rules is limited: For instance, to decide which of the (potentially many) applicable rules describes the chemical reaction that is going to take place in a certain situation requires recourse to the underlying physics



First issue: Complex biological patterns, no “rules”....

(e.g. not just “entropy” or ψ)

Second issue: Which rules apply for a specific situation? How do we compute or apply these rules/patterns?



Simple state models in Biology....

Theoretical assumptions are violated in nature (H-W, additivity)

No insights/inferences into mechanisms or counterfactuals

Hard to apply to real data (or limited plausible sample size)

$$R = h^2 s$$

Is like a “F=MA” of Biology.

Like Fundamental Theorem of NS, or Price Eq., or Indirect/Kin...

State models don't make assumptions about underlying processes.

We don't think that F=MA is (or, “needs to be”) hard-coded into our universe. F=MA is a pattern that applies to varying degrees of accuracy for certain spatial temporal scales.

What is “hard-coded” below F=MA?

frontiers
in Systems Neuroscience

HYPOTHESIS AND THEORY
published: 07 June 2016
doi: 10.3389/fpsyg.2016.00049

Universal Darwinism As a Process of Bayesian Inference

John O. Campbell*

Independent Researcher, Victoria, BC, Canada

2016

$$P(h_i | I, m) = P(h_i | m) \frac{P(I | h_i m)}{P(I | m)}$$

At the core of Bayesian inference, underlying both the Price equation and the principle of free energy minimization we find an extremely simple mathematical expression: Bayes' theorem:

$$q_i' = q_i \frac{w_i}{w}$$

Biology as Information Dynamics



John Baez

Stanford Complexity Group
April 20, 2017

2016

Biswa Sengupta^{1*}, Arturo Tozzi², Gerald K. Cooray³, Pamela K. Douglas⁴, Karl J. Friston¹



frontiers
in Systems Neuroscience

HYPOTHESIS AND THEORY
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Biology as Information Dynamics



John Baez

Stanford Complexity Group
April 20, 2017

Towards a Neuronal Gauge Theory 2016

Biswa Sengupta^{1*}, Arturo Tozzi², Gerald K. Cooray³, Pamela K. Douglas⁴, Karl J. Friston¹

Approximate Bayesian inference as a gauge theory

Biology as Information Dynamics

Biswa Sengupta^{1 2 3} Karl Friston⁴

2017

Recent work
on Gauge
theories and
Information
Entropy in
Biology....

$$P(h_i | I, m) = P(h_i | m) \frac{P(I | h_i m)}{P(I | m)}$$

At the core of Bayesian inference, underlying both the Price equation and the principle of free energy minimization we find an extremely simple mathematical expression: Bayes' theorem:

$$q'_i = q_i \frac{w_i}{w}$$



John Baez

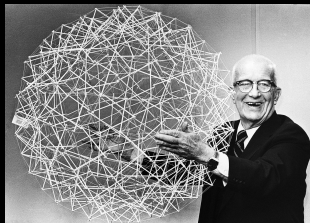
Stanford Complexity Group
April 20, 2017

VNE

Variational
Neuro-
Ethology

Ramstead,
Badcock &
Friston
2017

RBF



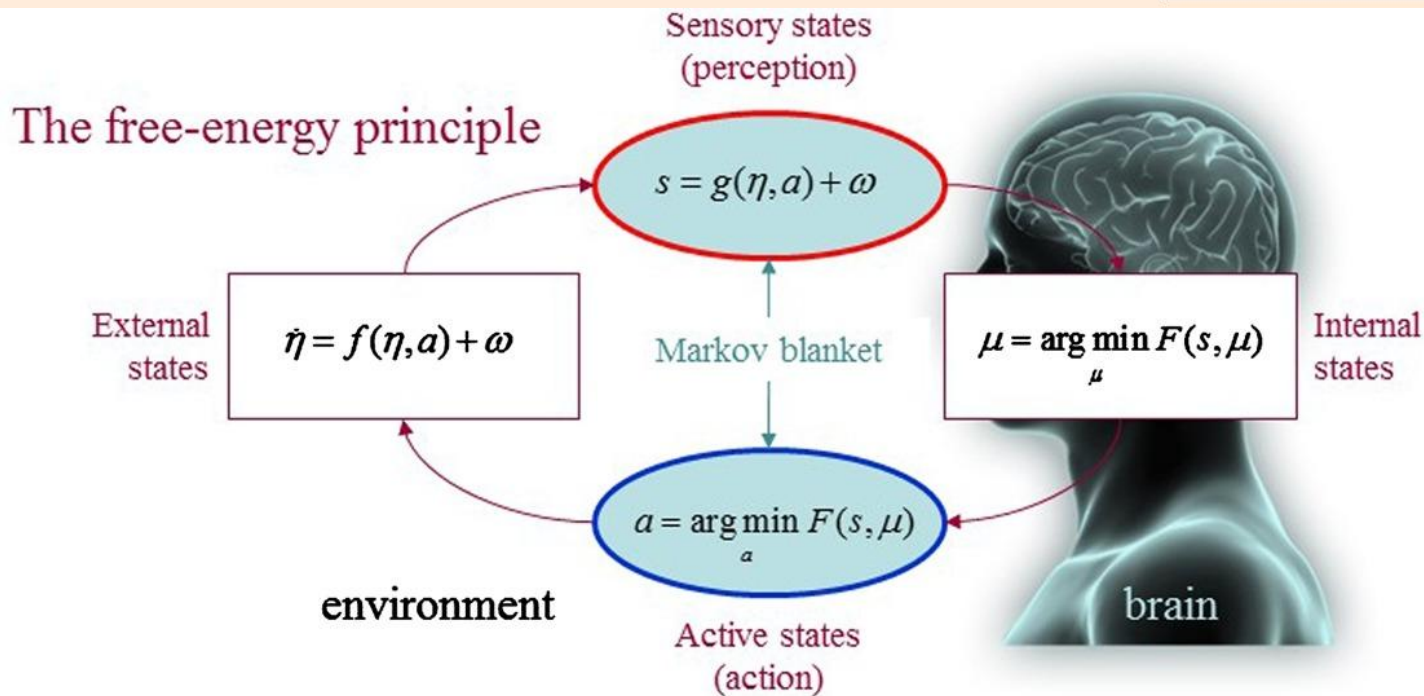
"just a coincidence"??

Review

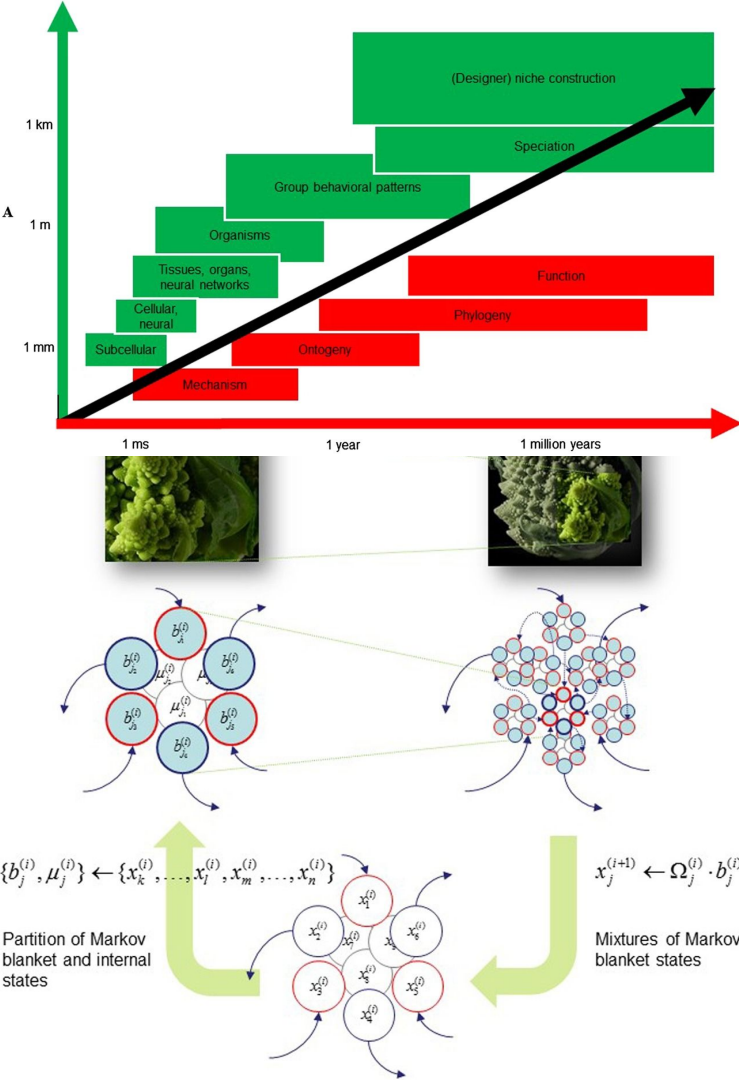
Answering Schrödinger's question: A free-energy formulation

Maxwell James Désormeau Ramstead^{a,b,*}, Paul Benjamin Badcock^{c,d,e},
Karl John Friston^{f,1}

PHYSICS of LIFE
reviews



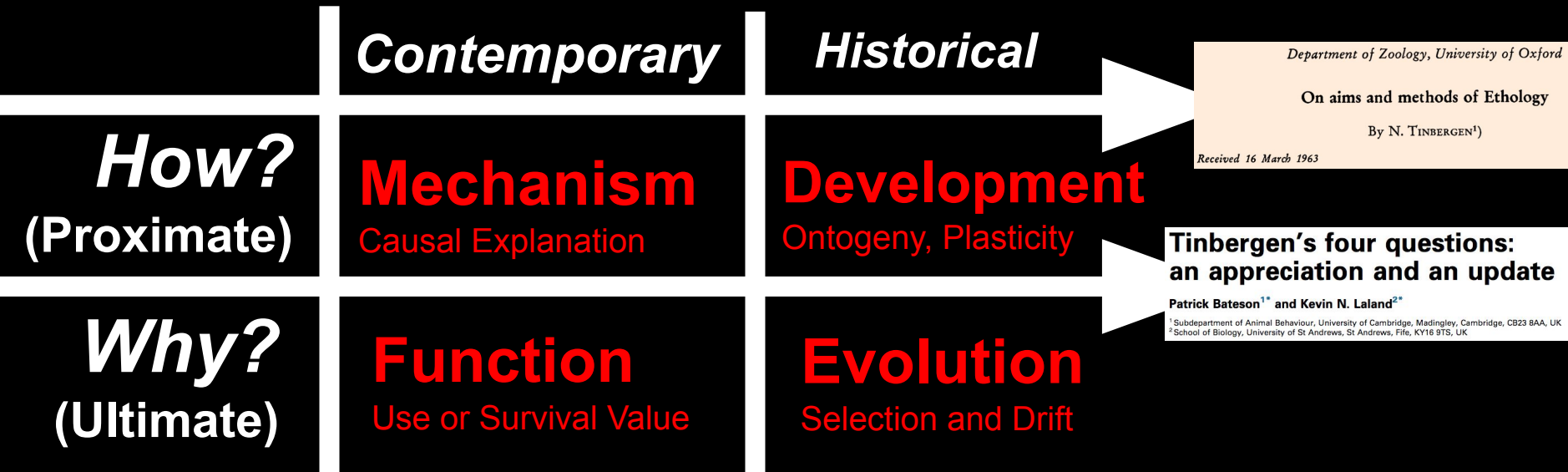
$$F = \text{Energy} - \text{Entropy} = -\langle \ln p(s, \eta) \rangle_q + \langle \ln q(\eta) \rangle_q$$



VNE applies to biological systems across many orders of magnitude of spatio-temporal variation.

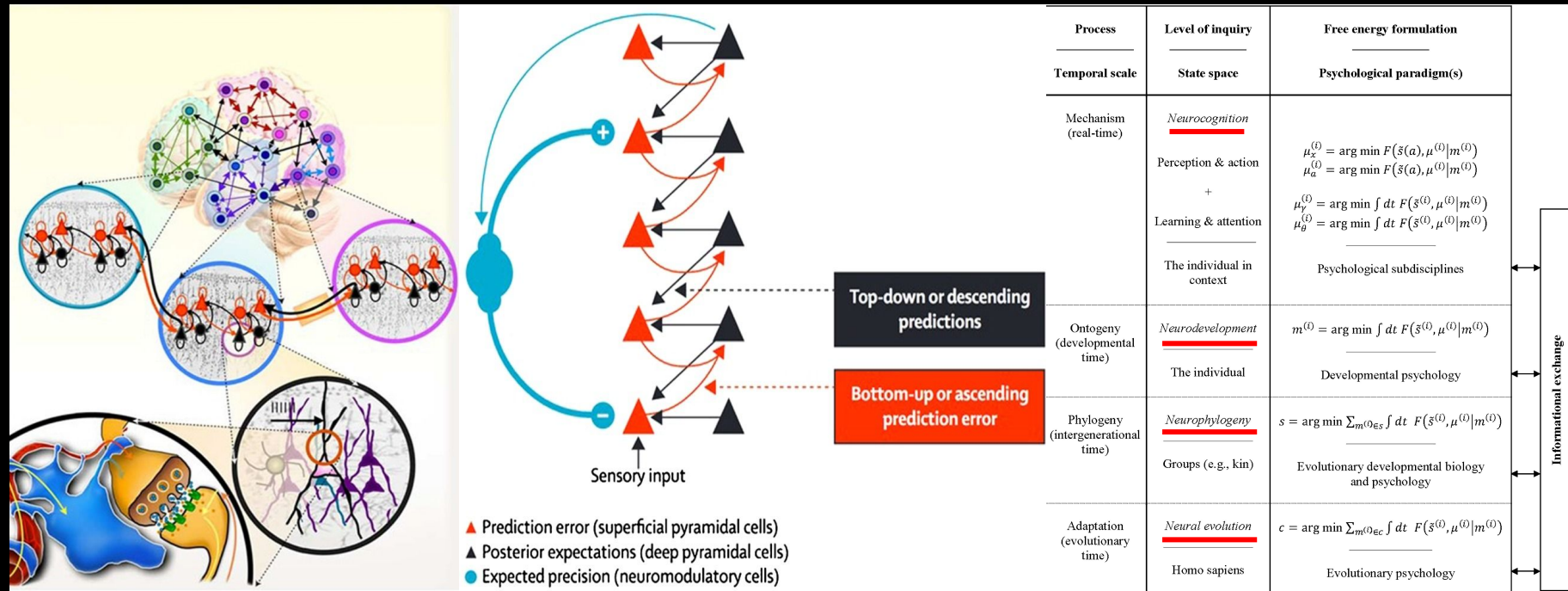
VNE is an **E**volutionary **S**ystems Theory about how hierarchically-nested Markov blankets performing active inference inextricably (statistically and mechanistically) link internal and external states through action and perception among, and across, biological spatio-temporal scales.

RBF 2017: “Given the success of this explanatory framework in biology, we suggest that Tinbergen’s levels of inquiry might be apt to elucidate structural laws that supplement the general principles provided by the FEP....the FEP describes a [general biological modeling imperative], while Tinbergen has offered a distinctive but complementary framework that allows us to develop substantive explanations for the phenotypic traits and behaviors of any given species or organism...”



RBF 2017 work through only one example in their paper:

How the “Hierarchically Mechanistic Minds” EST can be used within the Variational Neuroethology framework to study all scales of human socio-biocultural evolution in Humans.



Other people are already critiquing and building on VNE.



Physics of Life Reviews
Available online 20 September 2017
In Press, Corrected Proof



Review

Answering Schrödinger's question: A free-energy formulation

Maxwell James Désormeau Ramstead^{a, b, ✉, 1}, Paul Benjamin Badcock^{c, d, e}, Karl John Friston^{f, 1}

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Referred to by Michael Kirchhoff [open access](#)

Hierarchical Markov Blankets and Adaptive Active Inference
Physics of Life Reviews, Available online 2 January 2018, Pages
[PDF \(275KB\)](#)

Laurence J. Kirmayer
Ontologies of life: From thermodynamics to teleonomics
Physics of Life Reviews, Available online 2 December 2017, Pages
[PDF \(218KB\)](#)

Jean Daunizeau
A plea for "variational neuroethology"
Physics of Life Reviews, Available online 24 November 2017, Pages
[PDF \(208KB\)](#)

Giovanni Pezzulo, Michael Levin
Embodying Markov blankets
Physics of Life Reviews, Available online 24 November 2017, Pages
[PDF \(286KB\)](#)

Jelle Bruineberg, Casper Hesp
Beyond blanket terms: Challenges for the explanatory value of vari...
Physics of Life Reviews, Available online 14 November 2017, Pages
[PDF \(235KB\)](#)

Leonid M. Martyushev
Living systems do not minimize free energy
Physics of Life Reviews, Available online 10 November 2017, Pages
[PDF \(185KB\)](#)

Loet Leydesdorff
Lifting the Markov blankets of socio-cultural evolution
Physics of Life Reviews, Available online 3 November 2017, Pages
[PDF \(282KB\)](#)

John O. Campbell
Towards a unification of evolutionary dynamics
Physics of Life Reviews, Available online 3 November 2017, Pages
[PDF \(321KB\)](#)

Samuel Veissière
Cultural Markov blankets? Mind the other minds gap!
Physics of Life Reviews, Available online 3 November 2017, Pages
[PDF \(217KB\)](#)

Nicola Bellomo, Ahmed Elaiw
Dynamics and equilibria of living systems
Physics of Life Reviews, Available online 19 October 2017, Pages
[PDF \(185KB\)](#)

Arturo Tozzi, James F. Peters
Critique of pure free energy principle
Physics of Life Reviews, Available online 16 October 2017, Pages
[PDF \(252KB\)](#)

As of
1/3/2018
12 comments

1. The case study in VNE on human cognition is still not operationalized in a way that allows usage of actual data:
2. And it is even more unclear how the VNE approach could be deployed in other, arbitrary evolutionary systems.....
Especially using real data!

Process	Level of inquiry	Free energy formulation
Temporal scale	State space	Psychological paradigm(s)
Mechanism (real-time)	<u>Neurocognition</u> Perception & action + Learning & attention <hr/> The individual in context	$\mu_x^{(i)} = \arg \min F(\tilde{s}(a), \mu^{(i)} m^{(i)})$ $\mu_a^{(i)} = \arg \min F(\tilde{s}(a), \mu^{(i)} m^{(i)})$ $\mu_\gamma^{(i)} = \arg \min \int dt F(\tilde{s}^{(i)}, \mu^{(i)} m^{(i)})$ $\mu_\theta^{(i)} = \arg \min \int dt F(\tilde{s}^{(i)}, \mu^{(i)} m^{(i)})$ <hr/> Psychological subdisciplines
Ontogeny (developmental time)	Neurodevelopment <hr/> <u>The individual</u>	$m^{(i)} = \arg \min \int dt F(\tilde{s}^{(i)}, \mu^{(i)} m^{(i)})$ <hr/> Developmental psychology
Phylogeny (intergenerational time)	Neurophylogeny <hr/> <u>Groups (e.g., kin)</u>	$s = \arg \min \sum_{m^{(i)} \in s} \int dt F(\tilde{s}^{(i)}, \mu^{(i)} m^{(i)})$ <hr/> Evolutionary developmental biology and psychology
Adaptation (evolutionary time)	Neural evolution <hr/> <u>Homo sapiens</u>	$c = \arg \min \sum_{m^{(i)} \in c} \int dt F(\tilde{s}^{(i)}, \mu^{(i)} m^{(i)})$ <hr/> Evolutionary psychology

Informational exchange



“Read Dennett (1995) and Noble (2016) and J&L (2005) & Akçay & Van Cleve (2016) and EFK (2000) and”



Processes, Interactions, Context (1992,2011,2014,2016)



“Keep it rational and measurable”



Free Energy

Pragmatic...Empirical...Quantitative...Pluralistic...

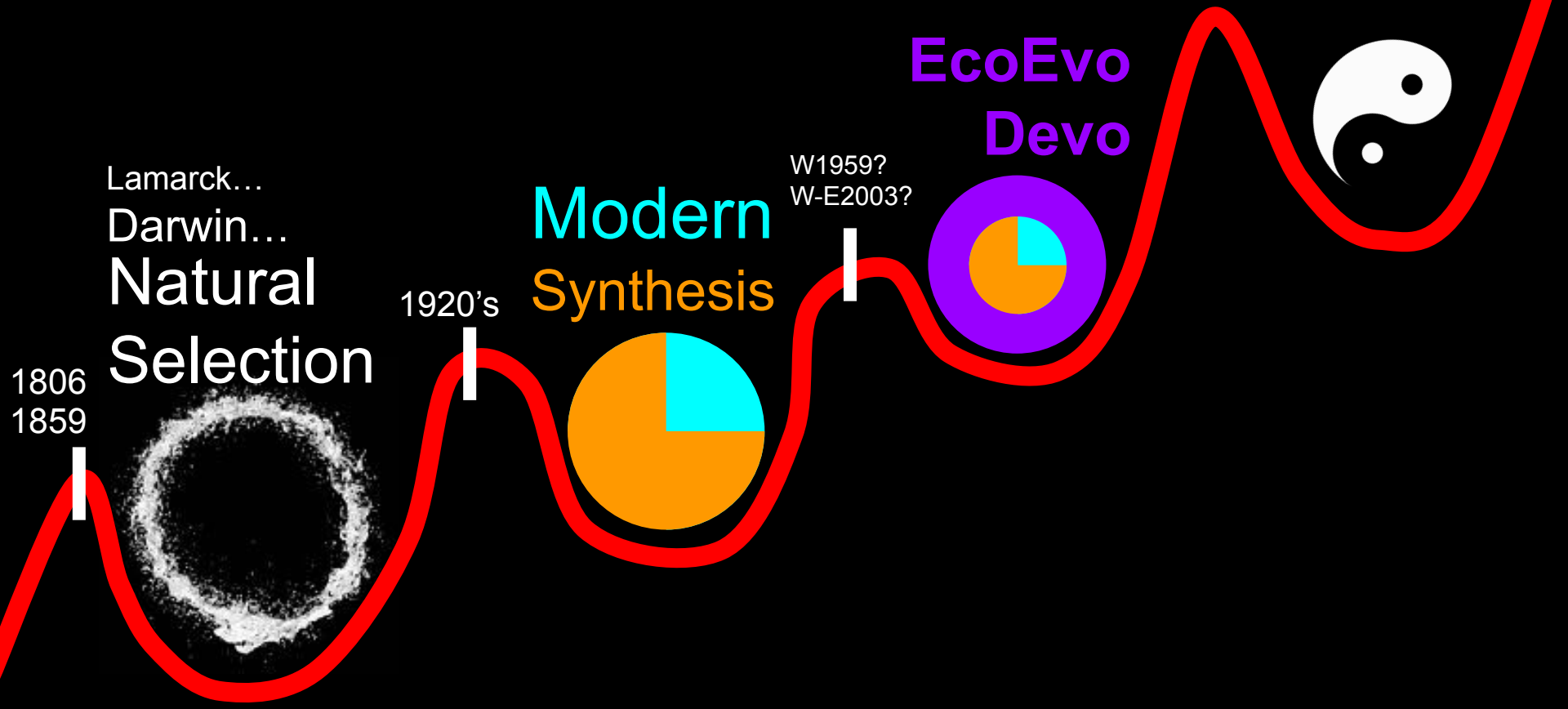
Make predictions.....Accommodate Complexity...

Claim 2:

The data, theory, and philosophy already exist to synthesize a tractable generalized model of evolution!

The challenge lies in finding how to integrate the VNE with classical evolutionary theory and apply it to real systems using limited empirical data.

MVEE- A Way Forward...

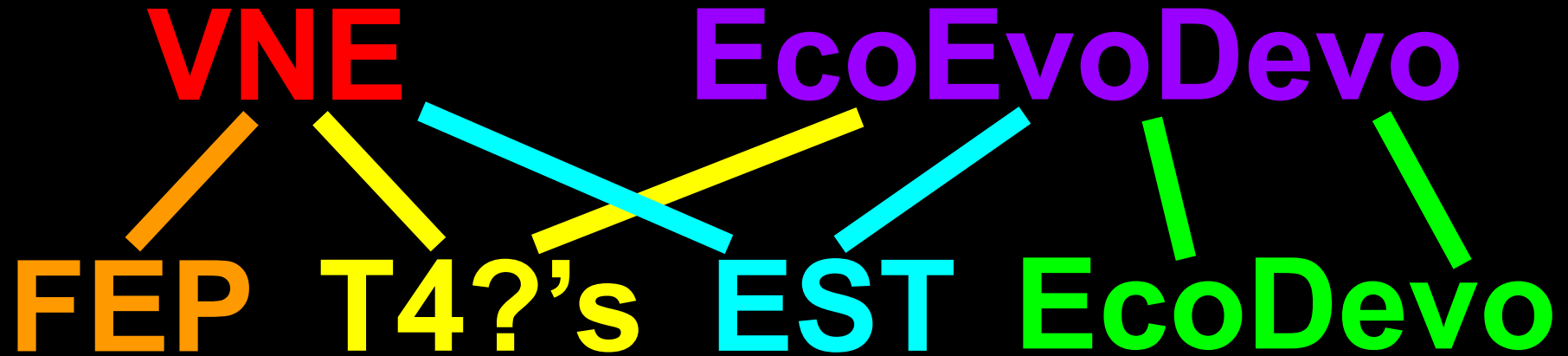


EcoEvoDevo

T4?'s

EST

EcoDevo



MVEE

```
graph TD; MVEE[MVEE] -- red --> VNE[VNE]; MVEE -- purple --> EcoEvoDevo[EcoEvoDevo]; VNE -- orange --> FEP[FEP]; VNE -- yellow --> T4[T4?'s]; EcoEvoDevo -- cyan --> EST[EST]; EcoEvoDevo -- green --> EcoDevo[EcoDevo]; VNE -- cyan --> EST; T4 -- yellow --> EST;
```

VNE

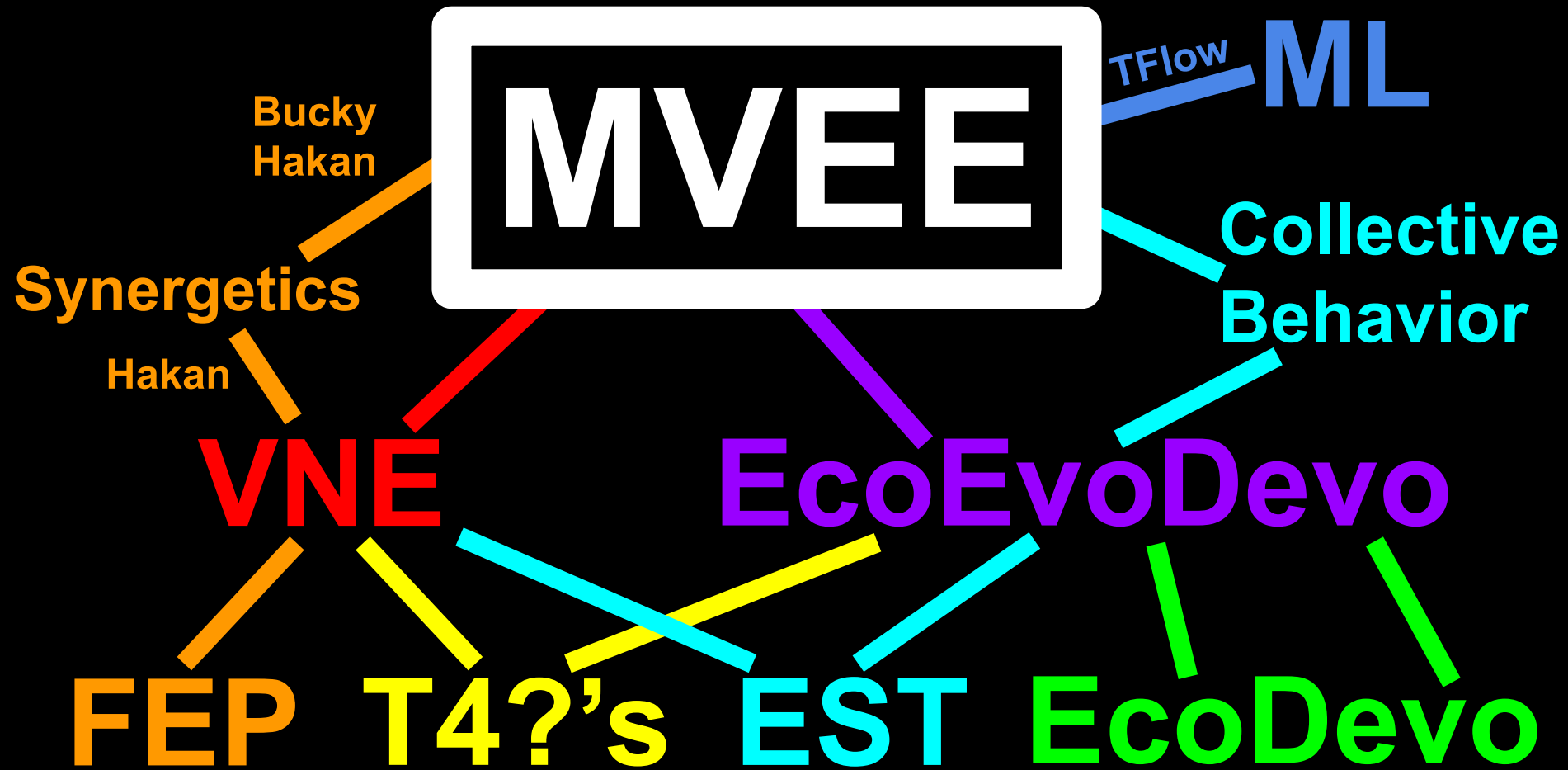
EcoEvoDevo

FEP

T4?'s

EST

EcoDevo



Multilevel Variational Evolutionary Ecology (MVEE)

“**Variational**” in the Darwinian sense refers to “Natural Variation”, for example in Lewontin 1983. However “**Variational**” also is technically used to refer to variational (ensemble) Bayesian models, for example in the Variational Free Energy Principle. **MVEE** draws on both these definitions.

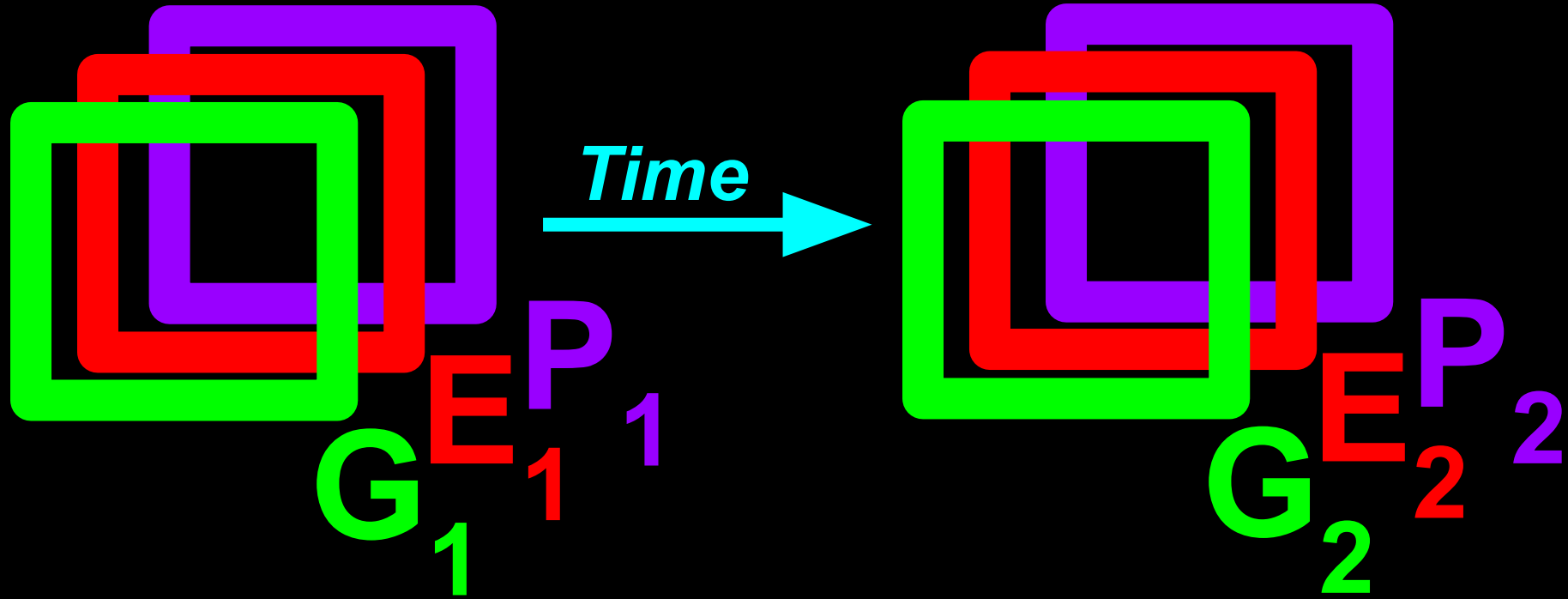
MVEE also has another embedded meaning:

Minimum Viable Evolutionary Explanation.

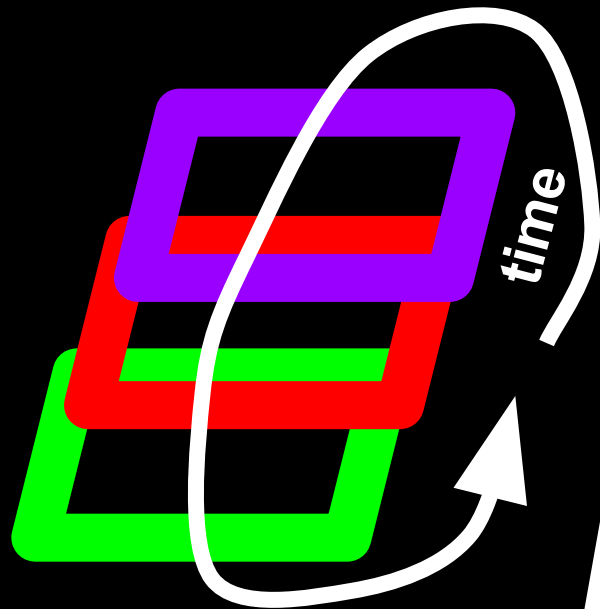
As it turns out, **MVEE** is the framework for formulating **MVEE**’s!

- Is MVEE consistent with prior Biological theory?
 - Yes, I believe MVEE is at worst equivalent to EcoEvoDevo at best.
- Is MVEE a Gauge Theory?
 - Yes, it only deals with observables and follows RBF 2017.
- Can MVEE deal with theoretical (analytical) evolution?
 - Yes, and may provide atemporal formal solutions to these systems.
- Can MVEE deal with empirical (open) evolution?
 - Yes, and at least can provide statistically-optimal estimates and maximally-informed hypotheses about real biological systems.
- What is the computational architecture of MVEE?
 - By using a single integrated machine learning framework on pre-existing biological data (TensorFlow/compute-graph), MVEE jointly and optimally considers coarse-grained state and process models across scales.

No “Fitness”....
Only measurable things:
G, E, P, and Time

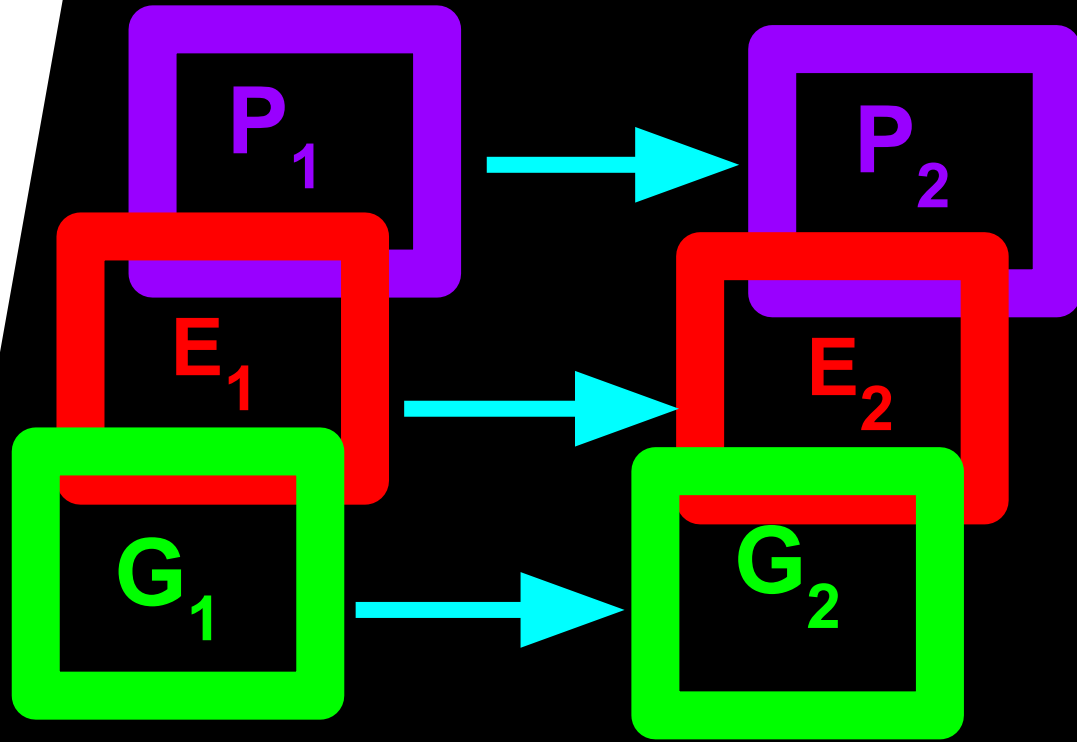


PROCESS MODELS



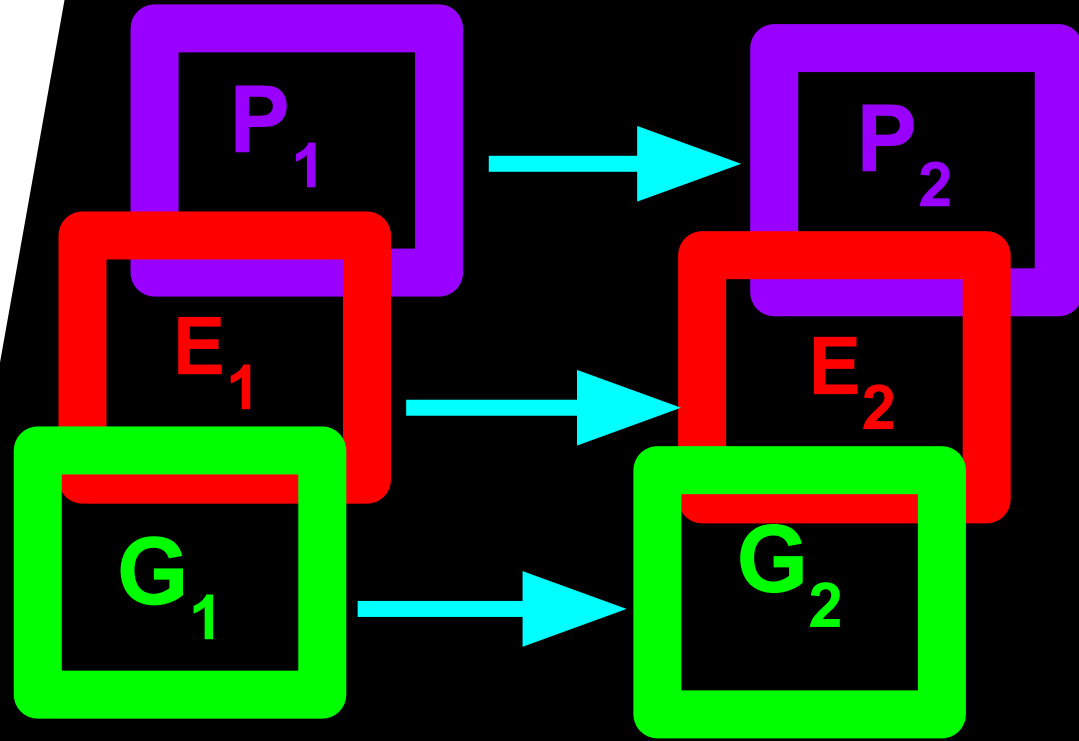
Collective Behavior
Decent. Algorithms

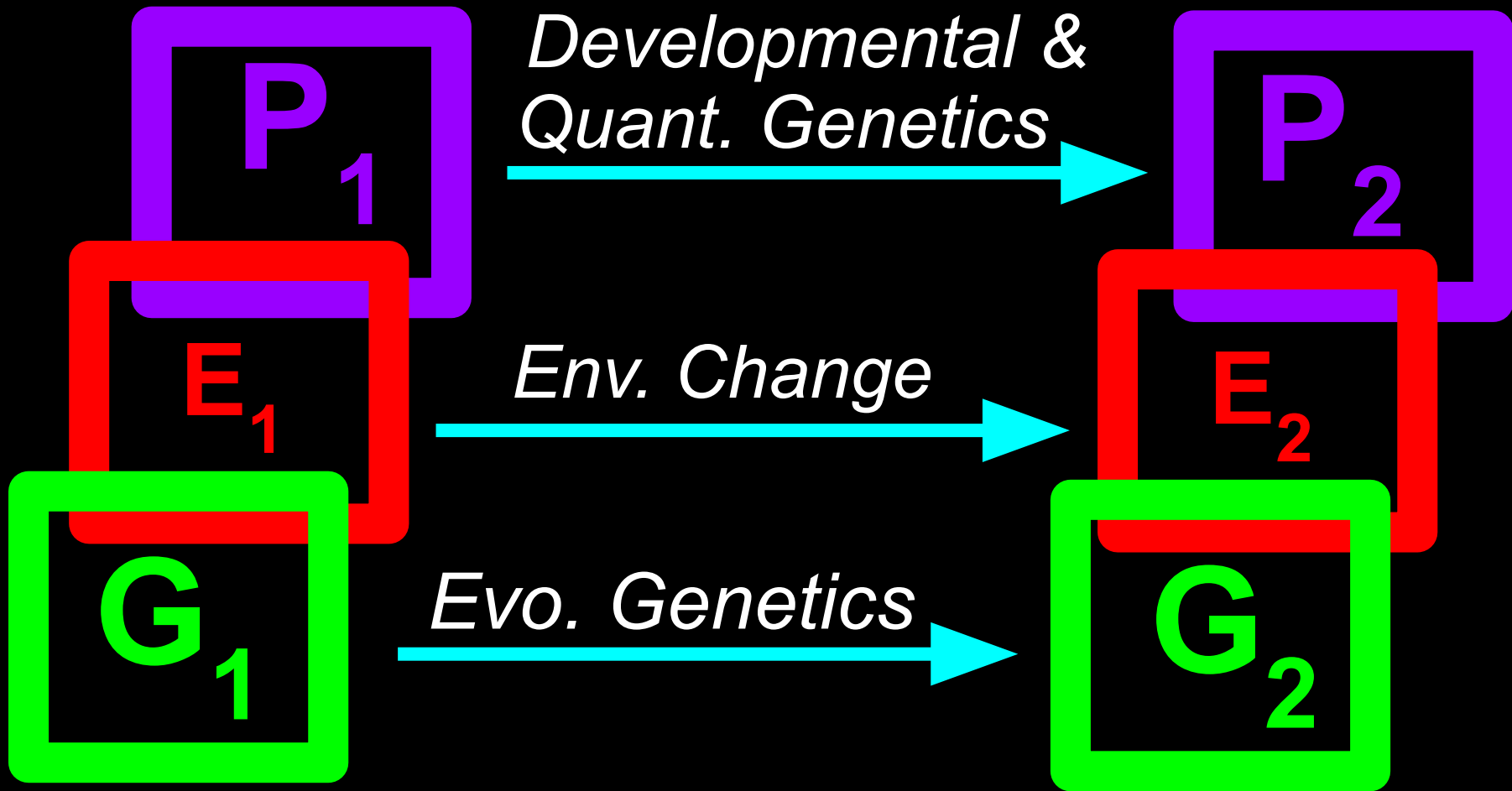
STATE MODELS

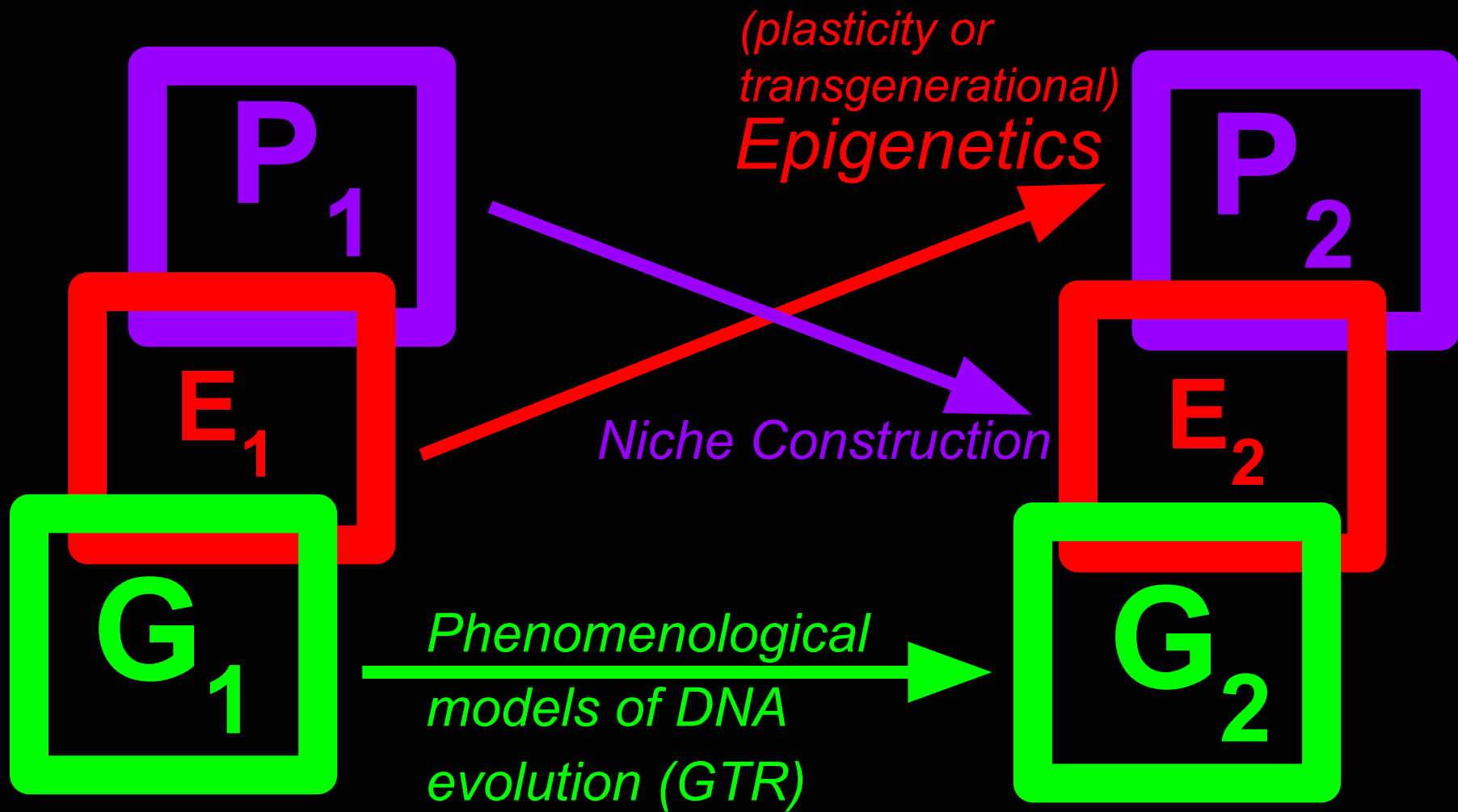


Use what
works!

STATE MODELS





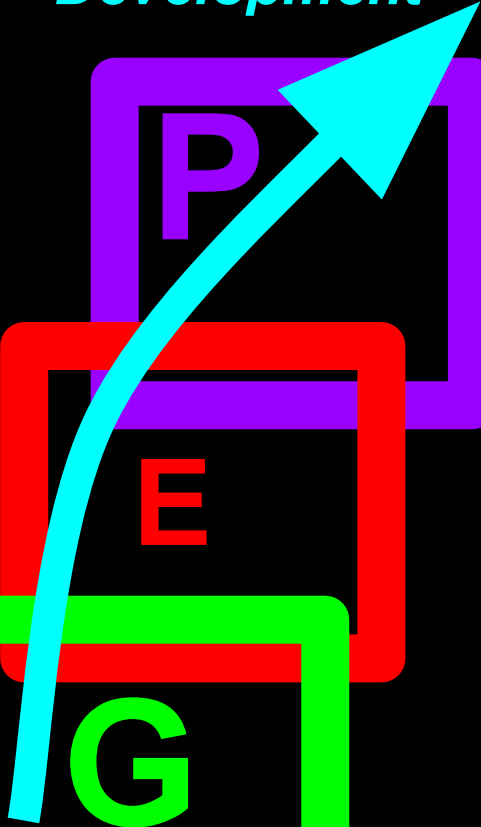


Development

P

E

G



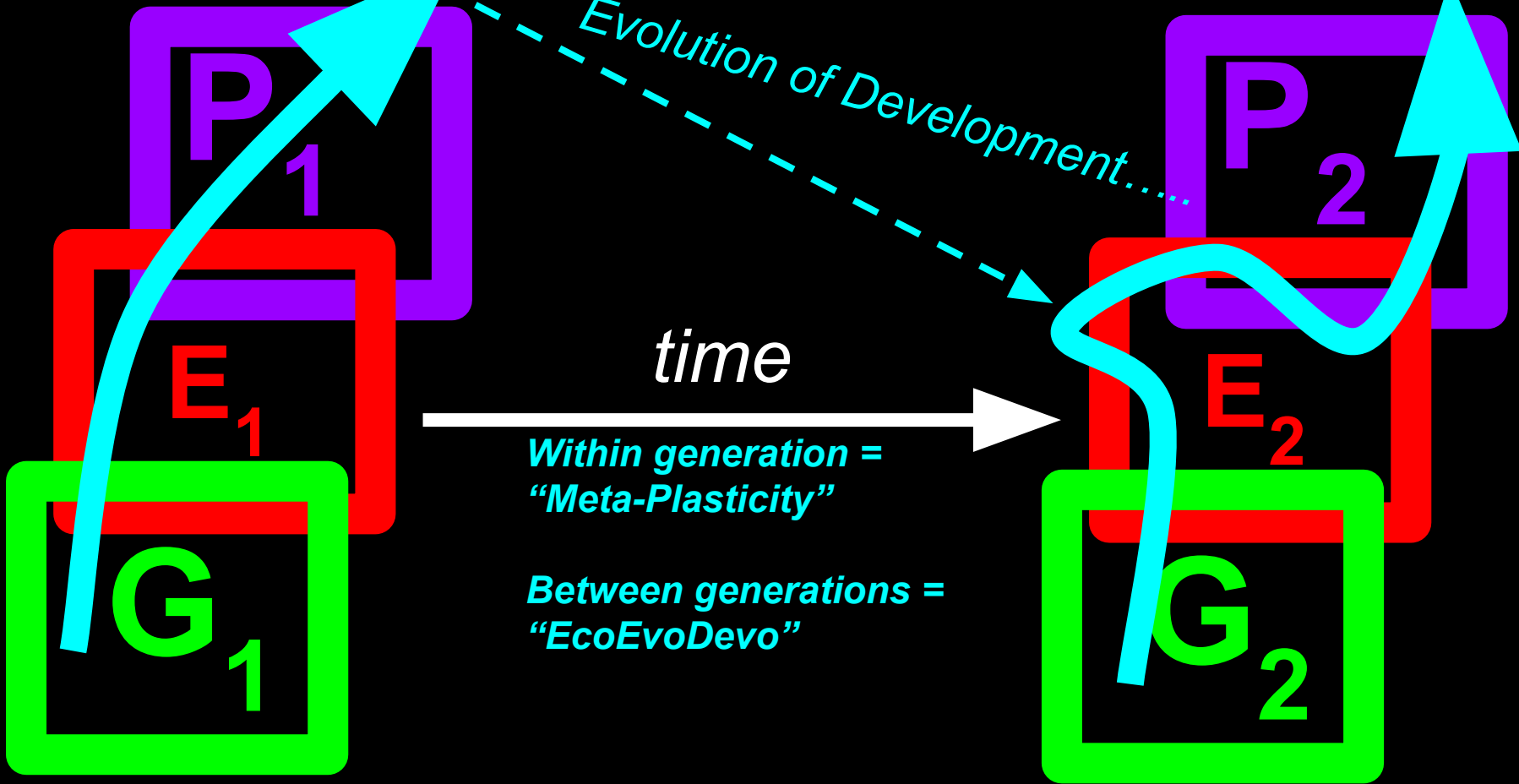
Development

Evolution of Development...

time

*Within generation =
"Meta-Plasticity"*

*Between generations =
"EcoEvoDevo"*



PROCESS MODELS

Collective Behavior

Local computation

Predictive/Adaptive

Multilevel Feedback loops

Robustness & Evolvability

Emergence/Self-Organization

What is the Algorithm?

What does each agent perceive?

What can each agent do?

How do group outcomes arise?



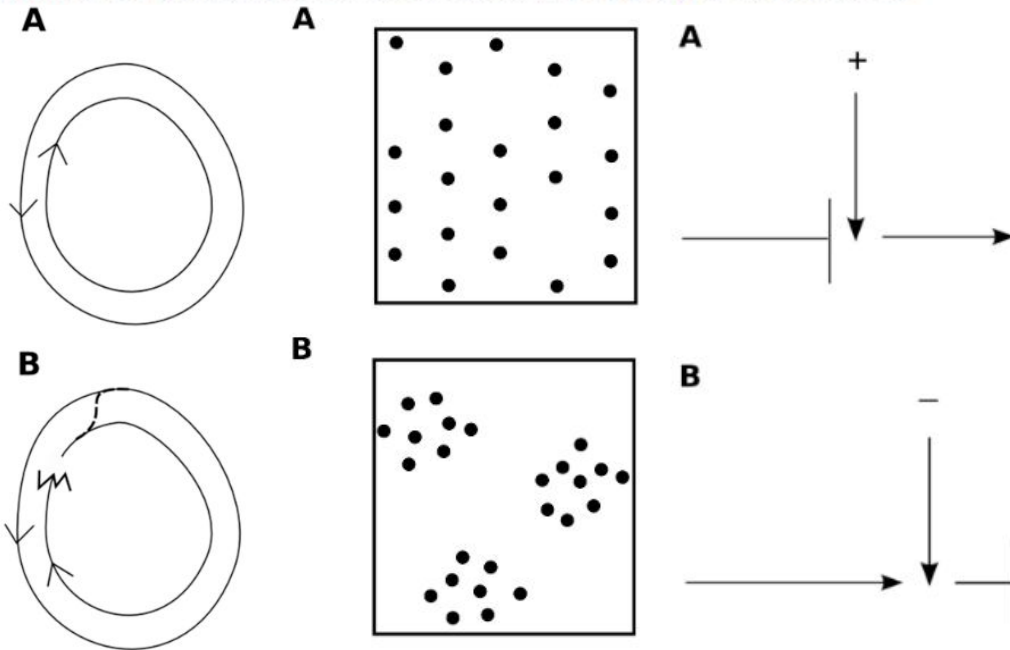
Formalizing a decentralized process implies formalizing the environmental dynamics:

The Ecology of Collective Behavior

2014

Deborah M. Gordon*

Department of Biology, Stanford University, Stanford, California, United States of America



The Evolution of the Algorithms for Collective Behavior

2016

Deborah M. Gordon^{1,*}

¹Department of Biology, Stanford University, Stanford, CA 94305, USA

*Correspondence: dmgordon@stanford.edu

<http://dx.doi.org/10.1016/j.cels.2016.10.013>



Also see Collective Behavior Appendix

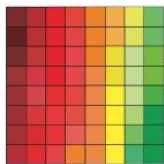
tensor = multidimensional array

vector



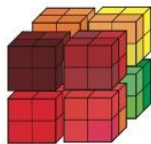
$$\mathbf{v} \in \mathbb{R}^{64}$$

matrix



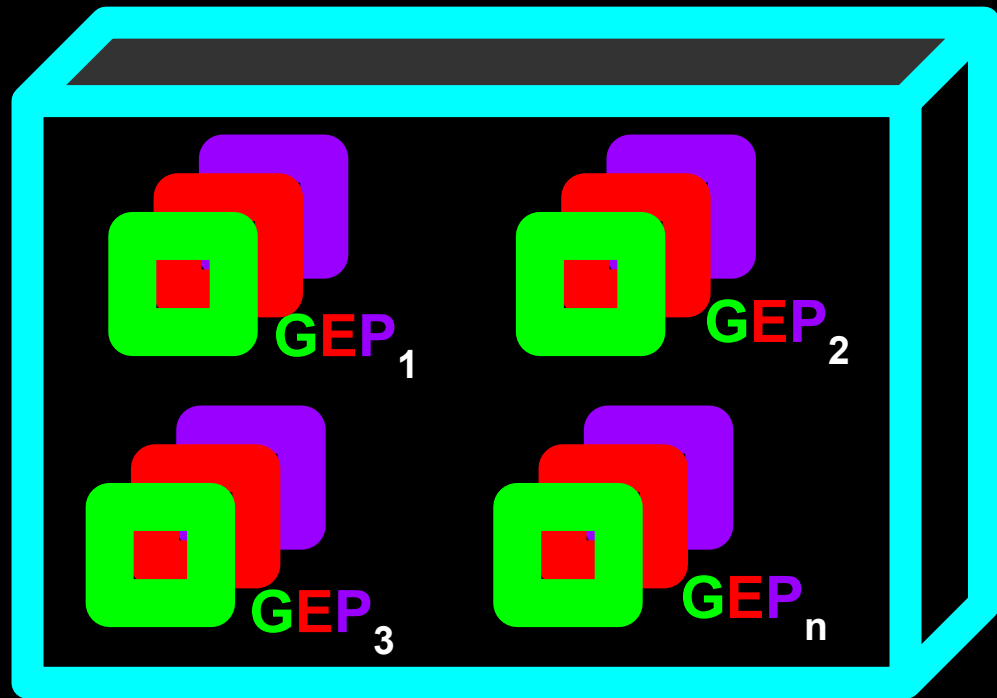
$$\mathbf{X} \in \mathbb{R}^{8 \times 8}$$

tensor



$$\mathbf{X} \in \mathbb{R}^{4 \times 4 \times 4}$$

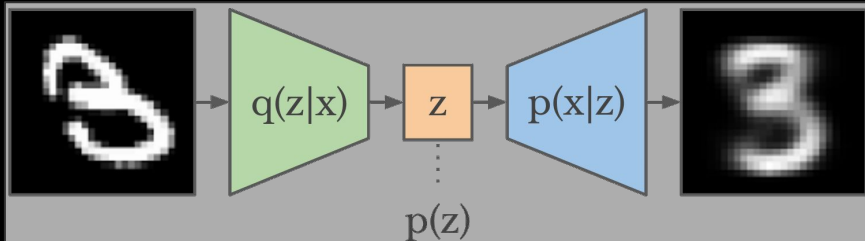
Biology $\in \mathbb{R}^{\text{GEP}_t}$



Generalized, Dynamic, multiscale
Tensor representation of Any Evolving System.

Free from “Fitness”!





Danijar Hafner

Publications Projects Materials About

Building Variational Auto-Encoders in TensorFlow

TensorFlow: Biology's Gateway to Deep Learning?

Ladislav Rampasek^{1,2} and Anna Goldenberg^{1,2,*}

¹SickKids Research Institute, 686 Bay Street, Toronto, ON M5G 0A4, Canada

²Department of Computer Science, University of Toronto, 40 St. George Street, Toronto, ON M5S 2E4, Canada

*Correspondence: anna.goldenberg@utoronto.ca

<http://dx.doi.org/10.1016/j.cels.2016.01.009>

TensorFlow Enabled Genetic Programming

Kai Staats, Edward Pantridge, Marco Cavaglia, Iurii Milovanov, Arun Aniyan

(Submitted on 10 Aug 2017)

TOWARDS EVOLUTIONARY DEEP NEURAL NETWORKS

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UK

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- BayesFlow Entropy (contrib)
- BayesFlow Monte Carlo (contrib)
- BayesFlow Stochastic Graph
- (contrib)
- BayesFlow Stochastic Tensors
- (contrib)
- BayesFlow Variational Inference
- (contrib)

And more...

$$E = MVEE \otimes t$$

Evolution is (described by)

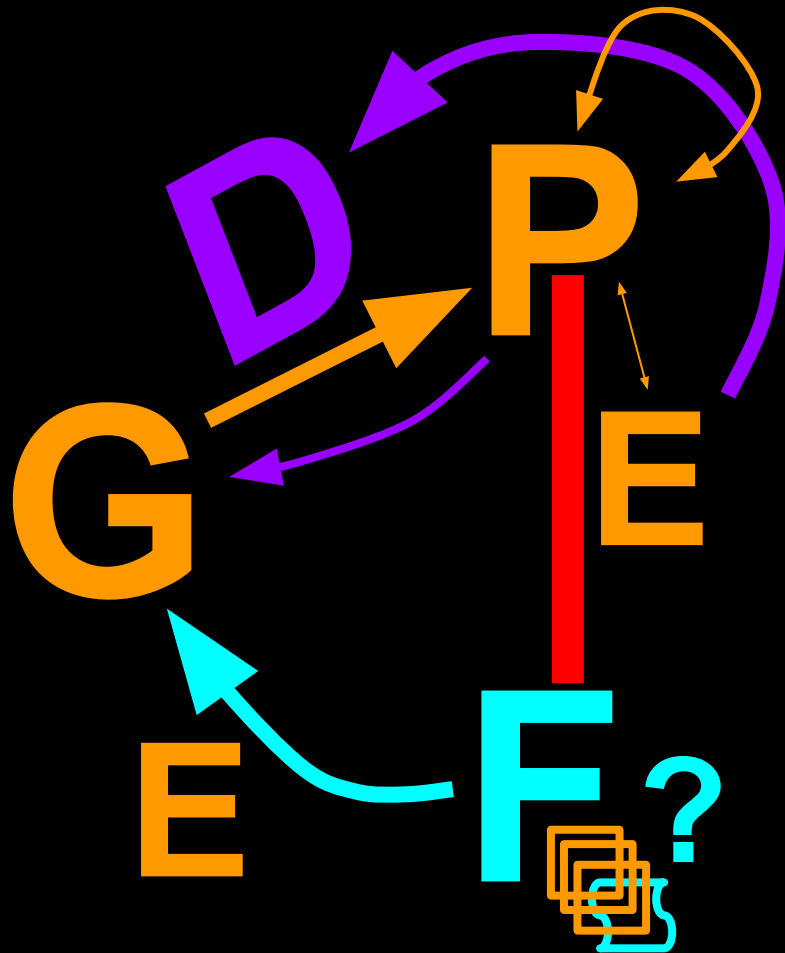
Multilevel Variational Evolutionary Ecology

tens \otimes rized through **time**

Summary

In Two Breaths

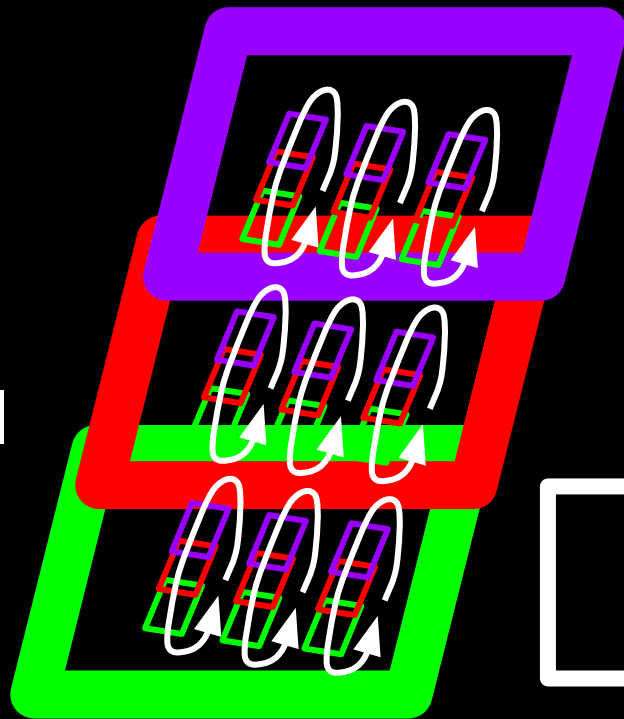
1.



FEED

is a
mess...

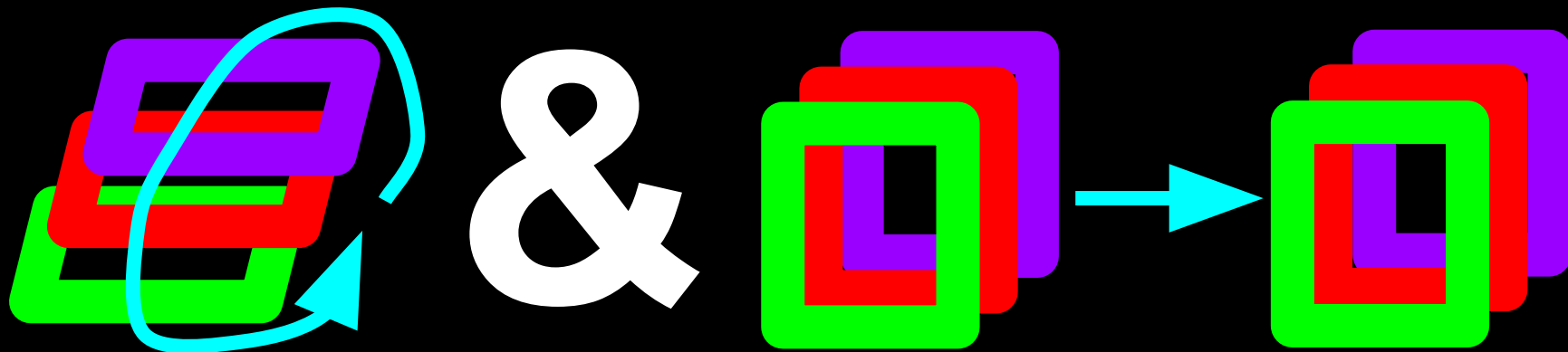
2.



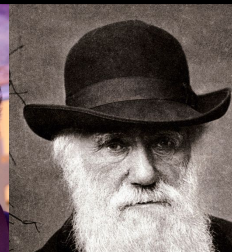
$$\text{Biology} \in \mathbb{R}^{\text{GEP}}_t$$

$$\mathbf{E} = \mathbf{MVEE} \otimes \mathbf{t}$$

MVEE draws on many sources, especially VNE, to potentially overcome some of the fundamental weaknesses in current evolutionary studies.



$$E = MVEE \otimes t$$



$$\text{Biology} \in \mathbb{R}^{\text{GEP}_t}$$

Chreods, homeorhesis and biofields: Finding the right path for science through Daoism ☆

Arran Gare ✉

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<https://doi.org/10.1016/j.pbiomolbio.2017.08.010>

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Linking the Tao, biomathics and information through the logic of energy

Joseph E. Brenner ✉

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<https://doi.org/10.1016/j.pbiomolbio.2017.08.006>

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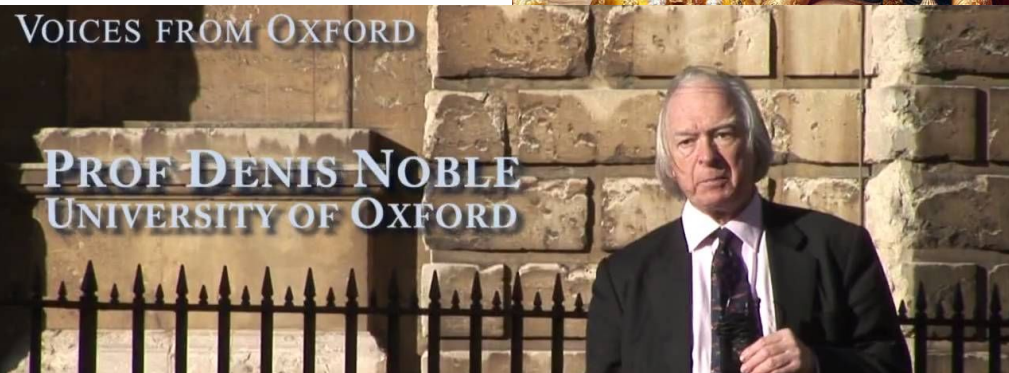
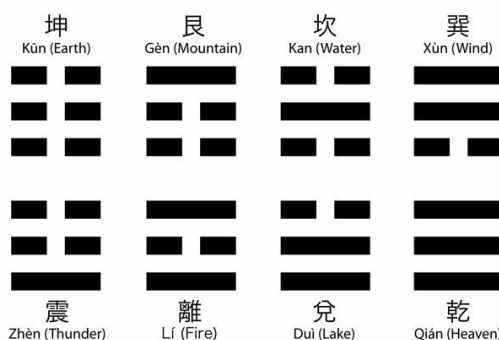
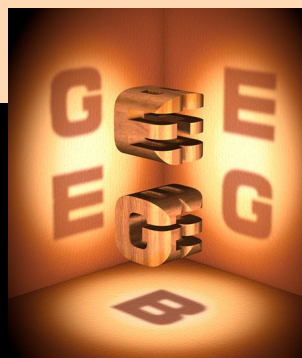
East-West paths to unconventional computing

Andrew Adamatzky ^{a, b, ✉}, Selim Akl ^c, Mark Burgin ^d, Cristian S. Calude ^e, José Félix Costa ^f, Mohammad Mahdi Dehshibi ^g, Yukio-Pegio Gunji ^h, Zoran Konkoli ⁱ, Bruce MacLennan ^k, Bruno Marchal ^j, Maurice Margenstern ^l, Genaro J. Martinez ^m, ^a, Richard Mayne ^a, Kenichi Morita ⁿ, Andrew Schumann ^o, Yaroslav D. Sergeyev ^p, Georgios Ch. Sirakoulis ^q, Susan Stepney ^r ... Hector Zenil ^t

[Show more](#)

<https://doi.org/10.1016/j.pbiomolbio.2017.08.004>

Hankey, Igamberdiev, Hu/Petoukhov², Islami, Rosen, Longo.....



Stepping Beyond the Newtonian Paradigm in Biology

Towards an Integrable Model of Life: Accelerating Discovery in the Biological Foundations of Science
INBIOA White Paper

Plamen L. Simeonov, Integral Biomathics, Germany

plamen@simeio.org

Appendix 1

Collective Behavior

Appendix 2

Synergetics

Appendix 3

Gauge and
Coarse-Graining.

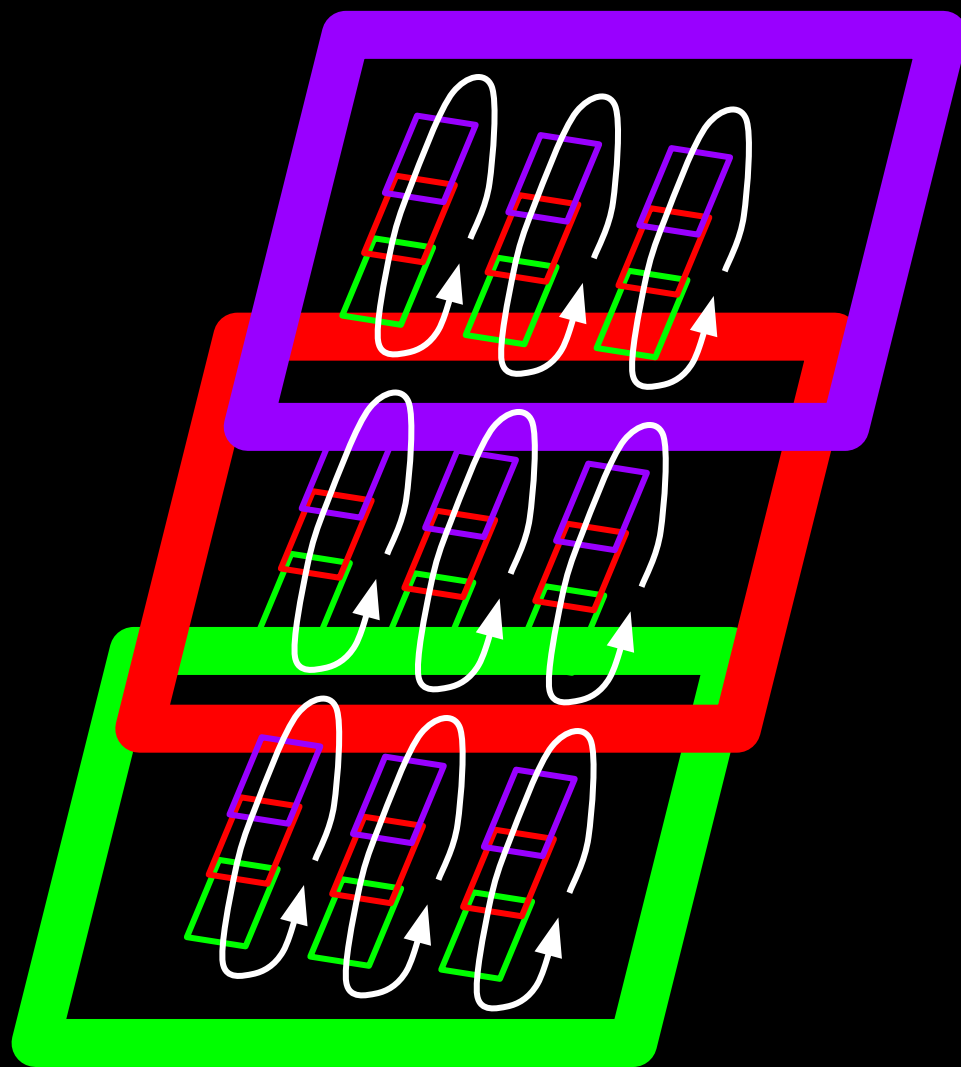
Appendix 1

Collective Behavior

Define “Behavior”:

Pragmatically, Pluralistically,
Algorithmically, Empirically,
Parsimoniously, etc

A **multilevel**,
Coarse-Grained,
Mechanism-Flexible
taxonomy is our manifold
map to effectively navigate
the multilevel $(\mathbf{G-E-P})_t$
Tensor construct.



“Hallmarks of Life”

Heredity

Development

Reproduction

Response to Stimuli

Metabolism

Homeostasis

Adaptation/Evolution

Negentropy Generation (S. 1944)

Aperiodic Crystal Structure (S. 1944)



Wittgenstein and Ant-Watching

DEBORAH M. GORDON

*Department of Biological Sciences
Stanford University
Stanford, CA 94305
U.S.A.*

1992



ABSTRACT: Research in animal behavior begins by identifying what animals are doing. In the course of observation, the observer comes to see animals as performing a particular activity. How does this process work? How can we be certain that behavior is identified correctly? Wittgenstein offers an approach to these questions, looking at the uses of certainty rather than attempting to find rules that guarantee it. Here two stages in research are distinguished: first, watching animals, and second, reporting the results to other scientists. Certainty about what animals are doing, has different uses at each stage.

KEY WORDS: Animal behavior, certainty, description, observation, seeing.

“Hallmarks of Life”

Heredity

Development
Reproduction

Response to Stimuli
Metabolism

Homeostasis

Adaptation/Evolution

Negentropy Generation (S. 1944)

Aperiodic Crystal Structure (S. 1944)

“Hallmarks of Life”	“Algorithms of Life!!”	
Heredity	Maintain Information/Material	
Development	Intra-Generational Change	Eco
Reproduction	Inter-Generational Change	Evo Devo
Response to Stimuli	Process Information	
Metabolism	Process Resources	
Homeostasis	Resilience, Robustness, Persistence	
Adaptation/Evolution	Learning & Inference	(Implied from above)
Negentropy Generation (S. 1944)	Local organization	(e.g. Stigmergy)
Aperiodic Crystal Structure (S. 1944)	Physical-Informational Nexus	

The “Algorithms of Life” are coarse-grained or simulated algorithmic models, providing biologically-plausible manifolds to explore the **GEP tensor** over any time scale....

The compute graph (TensorFlow) model allows arbitrary, modular, and tractable use of current data/models.



The “Algorithms of Life” are coarse-grained or simulated algorithmic models, providing biologically-plausible manifolds to explore the **GEP tensor** over any time scale....

In other words, we use information about the species/time-specific processes to preferentially explore functional manifolds that are reachable under informed models but implausible under incorrect models (e.g. Parsimony vs. GTR+I+G).....

We know that bone morphogenetic processes and allometric scaling allow us to understand biases of morphological evo. (Gould’s Antlers, Wagner, Turing)
.....We need something like this for collective behavior!

Department of Zoology, University of Oxford

On aims and methods of Ethology

By N. TINBERGEN¹⁾

Received 16 March 1963

¹⁾ Dedicated to Professor KONRAD LORENZ at the occasion of his 60th birthday.

Tinbergen's four questions: an appreciation and an update

Patrick Bateson^{1*}

and Kevin N. Laland^{2*}

TREE, 2013

¹ Subdepartment of Animal Behaviour, University of Cambridge, Madingley, Cambridge, CB23 8AA, UK

² School of Biology, University of St Andrews, St Andrews, Fife, KY16 9TS, UK

Contemporary

Historical

How?
(Proximate)

Mechanism
Causal Explanation

Development
Ontogeny, Plasticity

Why?
(Ultimate)

Function
Use or Survival Value

Evolution
Selection and Drift

Appendix 2

Synergetics

SYNERGETICS

Explorations in the Geometry of
Thinking

by

1975

R. Buckminster Fuller

in collaboration with E. J. Applewhite

First Published by Macmillan Publishing Co. Inc. 1975, 1979.

Further
Explorations
in the Geometry
of Thinking

SYNERGETICS

2

1979

**R. BUCKMINSTER
FULLER**

+ Hakan (1983) :
"Nonequilibrium Nonlinear
Statistical Physics"

Complexity:
"Self-Organization"
"Chaos and Order"
(Phase transitions, etc...)

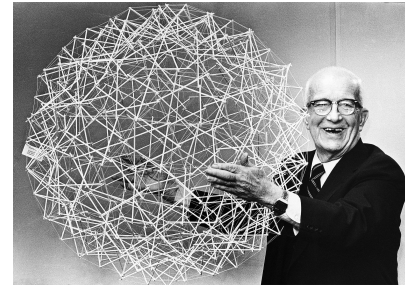
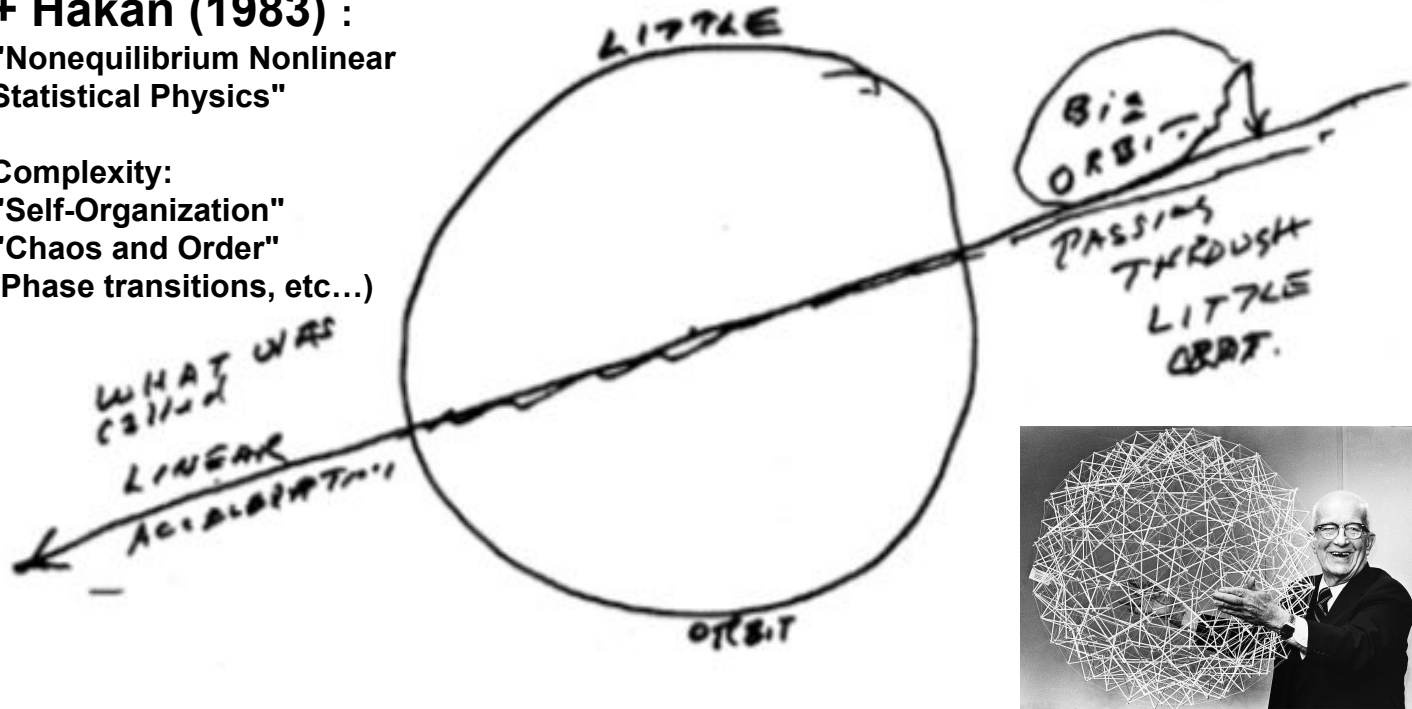
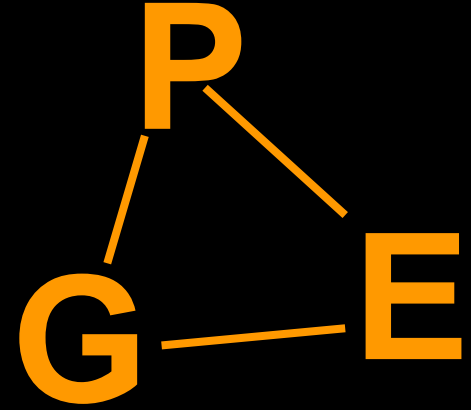
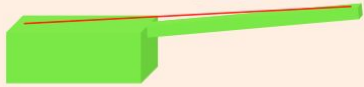


Fig. 1009.57B Big Orbit Passing through Little Orbit: What was called linear acceleration is an unrecognized arc of a bigger system.

RBF's K-Shell Class of Tensegrity Structures exhaustively and hierarchically describes structural dynamics among K items.

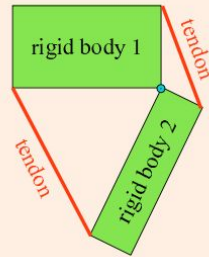


class 1 tensegrity system



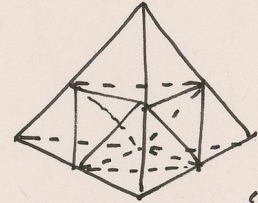
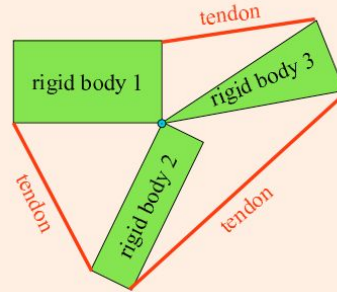
class 2 tensegrity system

2 rigid bodies
2 **tensile** elements



class 3 tensegrity system

3 rigid bodies
3 **tensile** elements



"Triangulation" is the
nature of nature

Buckminster Fuller

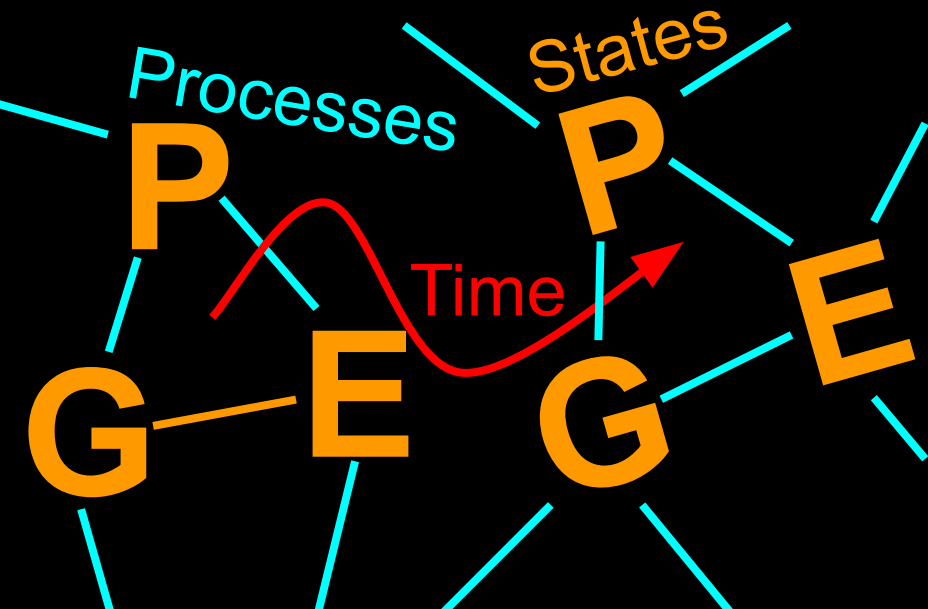
An **MVEE** object is a formalized dynamic multiscale Synergetic equilibrium:

Class 3 + 1

Tensegrity system

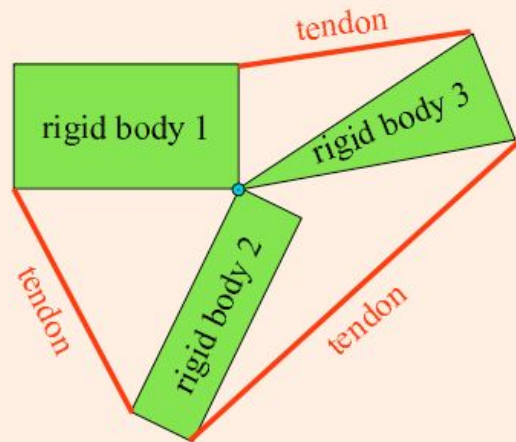
(open ended)

Szathmary et al. 2016/2017, Infinite Semiosis/Novelty



class 3 tensegrity system

3 rigid bodies
3 **tensile** elements

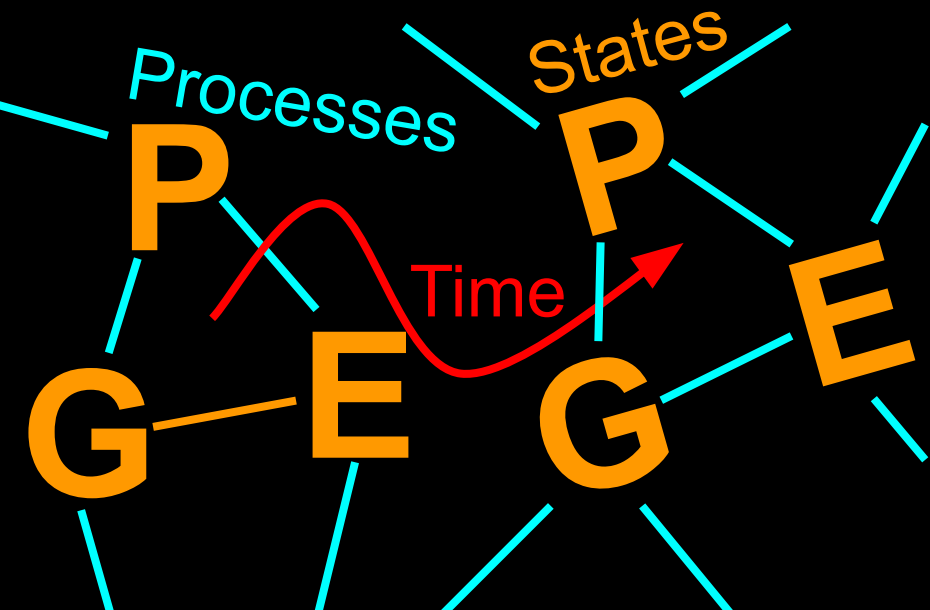


An **MVEE** object is a formalized dynamic multiscale Synergetic equilibrium:

Class 3 + 1

Tensegrity system

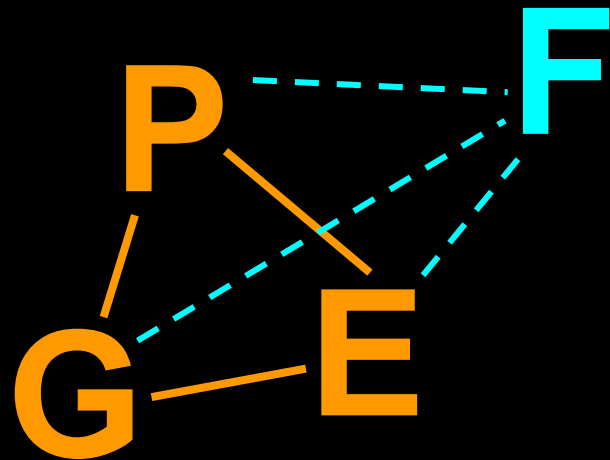
(open ended Szathmary et al. 2016/2017, Infinite Semiosis/Novelty)



Class 4

Tensegrity system

(closed-form Nowak / Game Theory, limited syntactic Novelty)
(Mechanism under strong closure)



Formal, timeless relationships
as in Newtonian physics

Appendix 3

Gauge and
Coarse-Graining.

If you printed and crystallized the single-stranded DNA of all possible sequences of a 100-basepair genome, the required volume would be:



If you printed and crystallized the single-stranded DNA of all possible sequences of a 100-basepair genome, the required volume would be **10 billion times the volume of Jupiter.**

($1.76 \times 10^{25} \text{ km}^3 \approx (1.1 \times 10^{-26} \text{ m}^3 \text{ displaced per 100-bp DNA helix}) * (1.6 \times 10^{60} \text{ oligomers, representing the } 4^{100} \text{ combinations in sequence space})$).

Every specific genomic configuration is novel.

The same could probably be said for **Phenotype** or **Environment**, which are both endlessly dynamic and infinitely describable (cue Borges story.....). So.....

We use abstract lower-dimensional state spaces (manifolds).

Broadly we can consider two types of theory -- *State* and *Process* theories:

State = What?

$$PV = nRT \dots\dots E = mc^2 \dots\dots R = h^2S \dots\dots$$

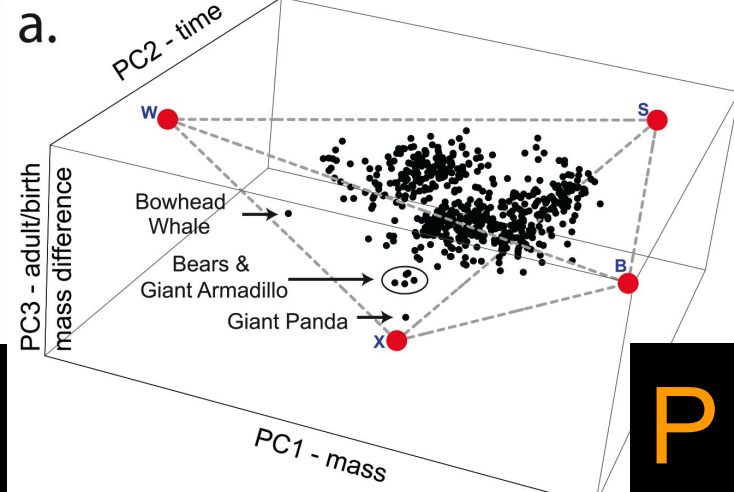
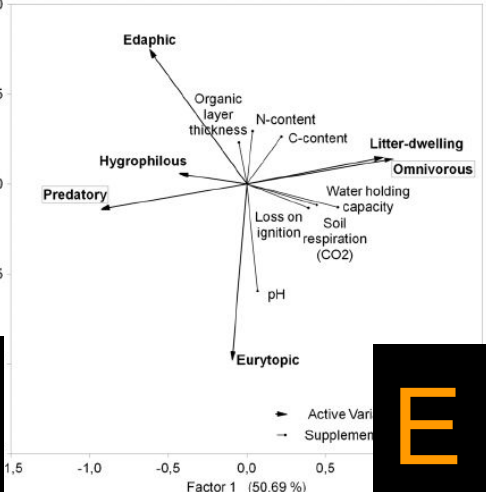
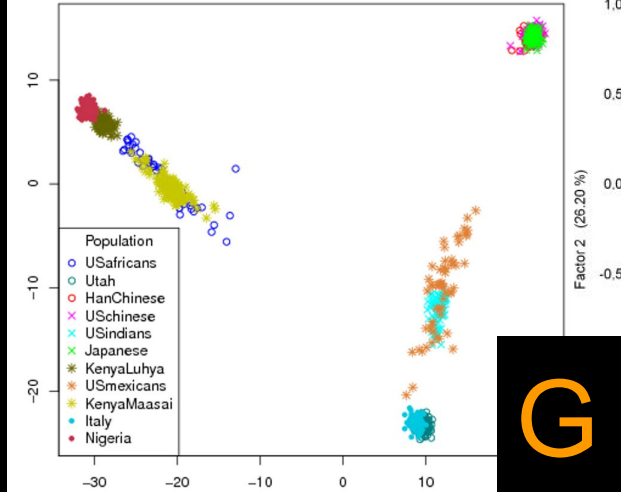
These are *State* theories because they describe how aspects of the system (measured or calculated) are instantaneously related to one another. They are predictive and mechanistically agnostic.

Process = How?

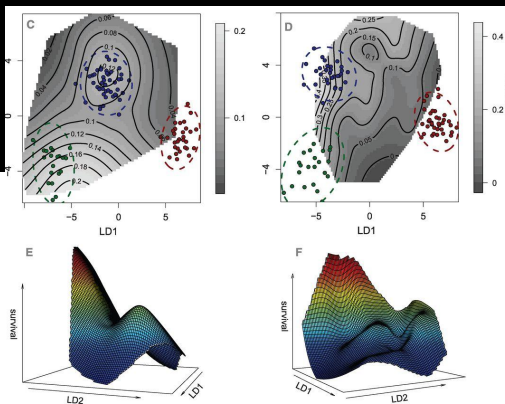
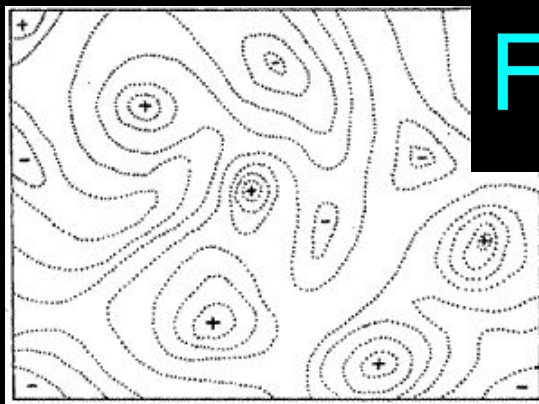
Natural Selection....Thermodynamics....Semiotics....

These are *Process* theories because they describe algorithmic, procedural, or mechanistic relationships and becomings. They are not predictive unless coupled to a state theory as well.

For example, $R = h^2S$ is a simple state model following the process model of Darwin 1859.



**Dimensional reduction ...
(Coarse-Graining of Data)**





“Gauge” =
“Measurement”



“Dirac defines **gauge** as under-determination of the **variables’ evolution**, and observes that....**only gauge-invariant quantities can be physical**, by definition...”



Why Gauge?

Carlo Rovelli

Aix Marseille Université, CNRS, CPT, UMR 7332, 13288 Marseille, France.

Université de Toulon, CNRS, CPT, UMR 7332, 83957 La Garde, France.

(Dated: November 15, 2013)

The world appears to be well described by gauge theories; why? I suggest that gauge is more than mathematical redundancy. Gauge-dependent quantities can not be predicted, but there is a sense in which they can be measured. They describe “handles” through which systems couple: they represent real relational structures to which the experimentalist has access in measurement by supplying one of the relata in the measurement procedure itself. This observation leads to a physical interpretation for the ubiquity of gauge: it is a consequence of a relational structure of physical quantities.

“Dirac defines gauge as under-determination of the **variables’ evolution**, and observes that....**only gauge-invariant quantities can be physical**, by definition...”

Coarse-graining

Mainstream:

Coarse-Graining Parameterization and Multiscale Simulation of Hierarchical Systems. Part I: Theory and Model Formulation

Steve Cranford and Markus J. Buehler

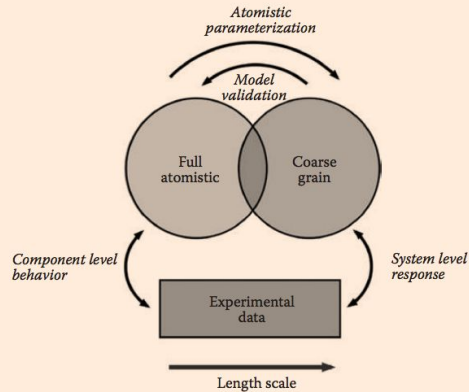


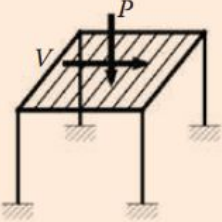
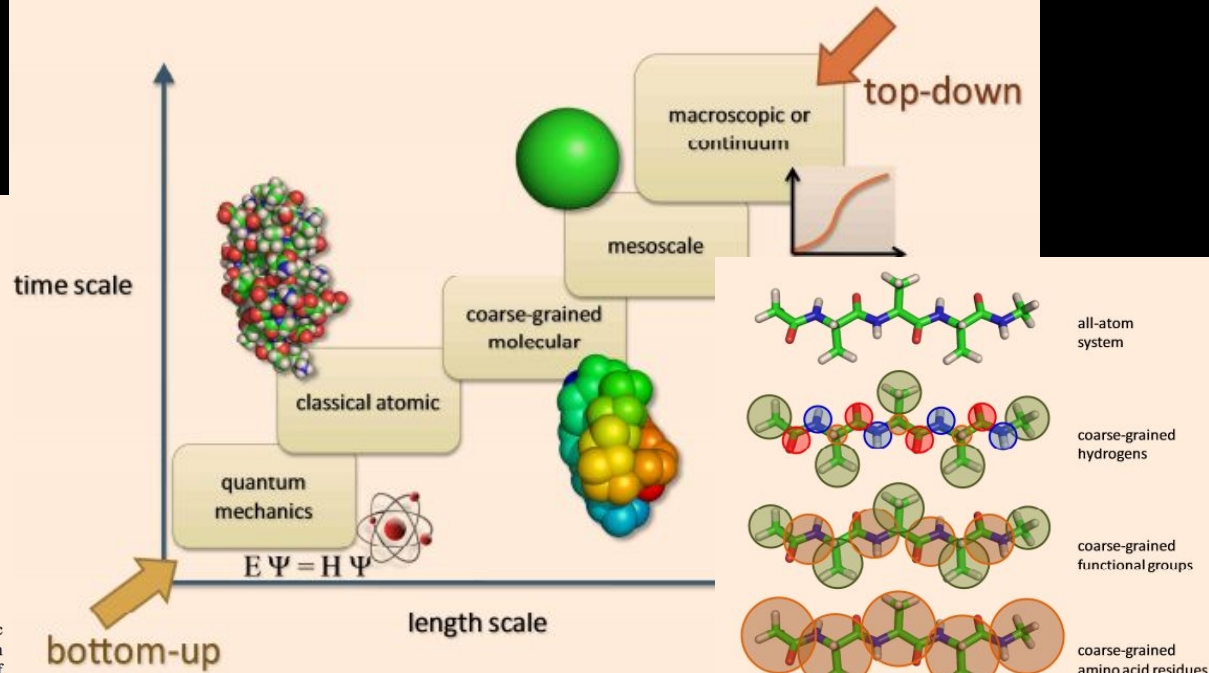


FIGURE 2.6 Validation of coarse-grain model through component behavior at atomistic scale and system characterization from experimental data. Experimental data ranges from component (molecular) to system (mesoscopic) length scales, providing a reciprocal loop of validation with both atomistic and coarse-grain models.

	Detailed model of constituent material(s) and structures(s)	Development of representative model for relevant behavior	Simplified system-level analysis
<i>Structural analysis</i>	 <p>Steel joist girder with known member properties (Yield stress, Young's modulus, etc.) and geometry.</p>	 <p>Joist girder represented by a beam element with known behavior and load response from analysis of joist girder; assumed linear elastic beam theory valid.</p>	 <p>Beam elements used in analysis of structural frame.</p>



Fringe:

2013

Causal Entropic Forces

A. D. Wissner-Gross^{1,2,*} and C. E. Freer^{3,†}

¹*Institute for Applied Computational Science, Harvard University, Cambridge, Massachusetts 02138, USA*

²The Media Laboratory, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, USA

³Department of Mathematics, University of Hawaii at Manoa, Honolulu, Hawaii 96822, USA

Recent advances in fields ranging from cosmology to computer science have hinted at a possible deep connection between intelligence and entropy maximization, but no formal physical relationship between them has yet been established. Here, we explicitly propose a first step toward such a relationship in the form of a causal generalization of entropic forces that we find can cause two defining behaviors of the human “cognitive niche”—tool use and social cooperation—to spontaneously emerge in simple physical systems. Our results suggest a potentially general thermodynamic model of adaptive behavior as a nonequilibrium process in open systems.

DOI: [10.1103/PhysRevLett.110.168702](https://doi.org/10.1103/PhysRevLett.110.168702)

PACS numbers: 05.65.+b, 05.70.-a, 07.05.Mh, 45.80.+r

COLLECTIVE COMPUTATION GROUP @ SFI

C4: Center for Complexity and Collective Computation

$$I[Z: X] + I[Z: Y] - I[Z: X \cap Y] = I[Z: X] + I[Z: Y] - I[Z: X \cap Y] =$$
[illegible]

Modeling Interaction via the Principle of Maximum Causal Entropy

Brian D. Ziebart
J. Andrew Bagnell
Anind K. Dey

School of Computer Science, Carnegie Mellon University, Pittsburgh, PA 15213, USA

2016

BZIEBART@CS.CMU.EDU
DBAGNELL@RI.CMU.EDU
ANIND@CS.CMU.EDU

Coarse-graining

I personally don't care about philosophical issues of top-down causation but I am bolstered by knowing that some people heartily endorse this principle as transcendent.

I am interested in how we can formalize optimal *State* and *Process* model/data coarse-graining, given our available information about the states and processes of the world.

Example *state/process* + coarse-graining for “Pogo Foraging”

For the scale of one ant colony over one day:

State: Dynamic model (any type) with colony-, time- and environment-effects, e.g. Prab.2012

Process: an agent-based model like e.g. G.G.2013 + Davidson.2016

For the scale of a population of colonies over a summer:

State: An ensemble characterization of foraging dynamics using the *State* model above. Calculated on a realized ecological trajectory, or over a distribution of trajectories.

Process: A parametric or non-parametric descriptor of ensembles of the *Process* model above, allowing for natural variation in colony-specific “sensitivity”, iterated over a summer.

For the scale of populations over intergenerational time:

State: Something like Fisher’s Fundamental Theorem or $R = h^2S$ (but see Ewens/Lessard 2015 and Plutynski 2006), applied to the simulated/actual Phenotype-Fitness mappings from the above *State* model.

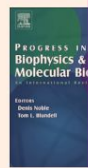
Process: A life history table showing how colony behavior, colony developmental stage, and ecological context influence the likelihood that a colony leaves offspring....**AND**..... a mechanistic neurophysiological model explaining how statistical heritability arises via vertical transmission of molecular variation.....Make Darwin Proud Again!!!

2017

Progress in Biophysics and Molecular Biology

journal homepage: www.elsevier.com/locate/pbiomolbio

Contents lists available at ScienceDirect



Universal Darwinism As a Process of Bayesian Inference

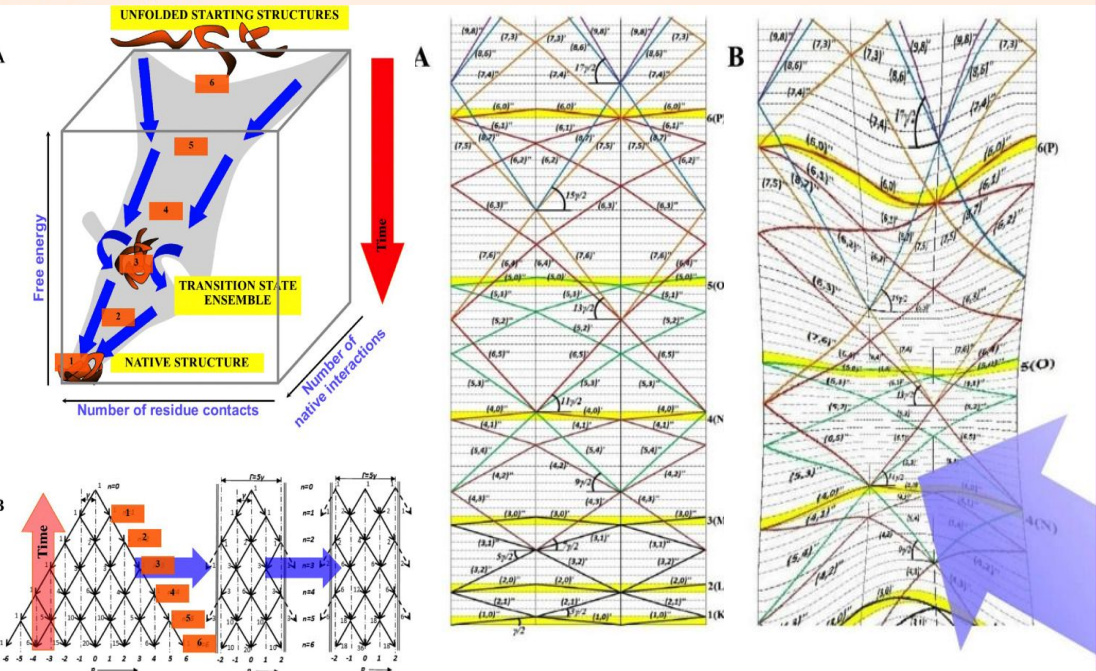
John O. Campbell *

Independent Researcher, Victoria, BC, Canada

2016

Cellular gauge symmetry and the Li organization principle: General considerations

Arturo Tozzi ^{a, b}, James F. Peters ^{c, d, e}, Jorge Navarro ^f, Wu Kun ^g, Bi Lin ^{g, **}, Pedro C. Marijuán ^{f, *}



$$F(s, u) = D_{KL} [q(\psi|\mu) || p(\psi|m)] - E_q [\log p(s|\psi, m)]$$

Free Energy = Complexity-Accuracy

$$P(h_i | I, m) = P(h_i | m) \frac{P(I | h_i m)}{P(I | m)}$$

At the core of Bayesian inference, underlying both the Price equation and the principle of free energy minimization we find an extremely simple mathematical expression: Bayes' theorem:

$$q'_i = q_i \frac{w_i}{w}$$

Better living through physics

David C. Krakauer & Jessica C. Flack

Nowak and colleagues' explanation of the evolution of altruism (*Nature* **466**, 1057–1062; 2010) in terms of individual-level selection might be reconciled with the views of their kin-selection opponents by striking an analogy with statistical mechanical and thermodynamic treatments in physics.

Statistical mechanics provides the microscopic basis for the macroscopic variables in thermodynamics, which is an equilibrium theory treating aggregate variables. As with thermodynamics, traditional multilevel selection theory is based on equilibrium solutions operating on nominal, aggregate variables. In the Hamilton kin-selection framework, variables correspond to the terms benefit, cost and relatedness. But because that treatment is not fundamentally mechanistic, it is often unclear what the units of these variables are, and how best to measure them.

Population genetics presents an evolutionary analogue of statistical mechanics that complements Hamilton's evolutionary thermodynamics. Hamilton's rule – which expresses relatedness between the helped and the helper in terms of cost and benefit to the fitness of both – and its related inequalities all express dependencies among macroscopic variables of state in structured populations.

The greater complexity of biological systems over physical ones, and their strong interdependency, make for a zoo of biological macroscopic laws with many multilevel selection principles, each with its adherents and disciples.

The great promise of evolutionary statistical mechanics is that it should allow us to enumerate the full space of possible fundamental evolutionary inequalities and the mechanistic conditions under which they apply, thence identifying those with the greatest empirical generality.