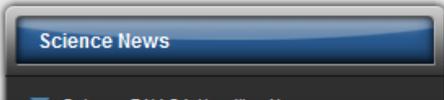




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MYSTERY OF THE MISSING WAVES ON TITAN

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Cassini Spies Wind-Rippled Waves on Titan

By Irene Klotz, Discovery News | March 23, 2014 10:15am ET

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Cassini VIMS image showing specular reflections in one of Titan's many lakes during the T85 flyby on July 24, 2012.
Credit: NASA/JPL-CALTECH/SSI/JASON W. BARNES ET AL.
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New observations from NASA's Saturn-orbiting Cassini spacecraft show what appear to be glints of sunlight bouncing off a wind-rippled lake on the moon Titan.

"If correct, this discovery represents the first sea-surface waves known outside of Earth," University of Idaho planetary scientist Jason Barnes wrote in an abstract of a paper presented at the Lunar and Planetary Science Conference in Houston this week.

of the most shocking discoveries of the past 10 years is how much the landscape of Titan resembles Earth. Like our own blue planet, the surface of Titan is dotted with lakes and channels, islands, mud, rain clouds and maybe even rainbows. The giant moon is not, however, H₂O. With a surface temperature dipping 290 degrees F below zero, Titan has no liquid water. Instead, researchers believe the fluid that sculpts Titan is an unknown hydrocarbon, and other hard-to-freeze hydrocarbons.



**WE KNOW THE WAVES ON THE OCEAN
OF TITAN ARE MISSING BECAUSE THERE
IS A GENERAL THEORY OF TWO-PHASE
FLUID FLOW INTERFACES THAT
PREDICTS WAVES AND THEIR
DISPERSION CHARACTERISTICS**





Science News

Mystery of the Missing Life on Titan

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Cassini Spies Long-sought Life on Titan

By Irene Klotz, Discovery News | March 23, 2014 10:15am ET

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WE DON'T KNOW IF THERE IS "MISSING LIFE" BECAUSE WE DO NOT HAVE A THEORY THAT PREDICTS THE EXISTENCE OF LIFE AS A PHYSICAL PHENOMENON, NOR DO WE UNDERSTAND WHAT SORT OF LIFE CAN ARISE IN DIFFERENT ENVIRONMENTS



THE GOAL OF OUR WORK IS TO COME CLOSER TO SUCH A THEORY

BECAUSE WE ARE INTERESTED IN GENERAL PRINCIPLES AND
NOT SPECIFIC CARBON CHEMISTRY DETAILS, WE NEED TO
DEVELOP A THEORY OF UNIVERSAL BIOLOGY, DIVORCED
FROM IDIOSYNCRATIC DETAILS



Universal Biology

- To understand what we mean by universal biology, let us think instead about “universal computation”.
- **Historical note:** the abstract theory of computation was developed by Alan Turing and others before there were real computers.
 - And real computers were designed by John Von Neumann’s team at IAS to instantiate the theory
- **Inverse problem:** If you were given a modern computer, could you work backwards and deduce the abstract theory of computation?
 - In biology, we have the inverse problem: the biology is already created and we want to understand what is the abstract theory of which it is an instantiation!



Universal Computation



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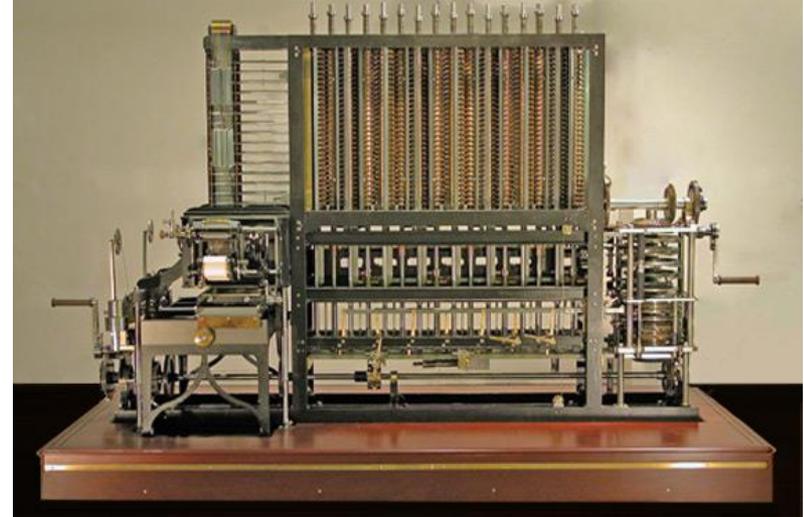
Universal Computation



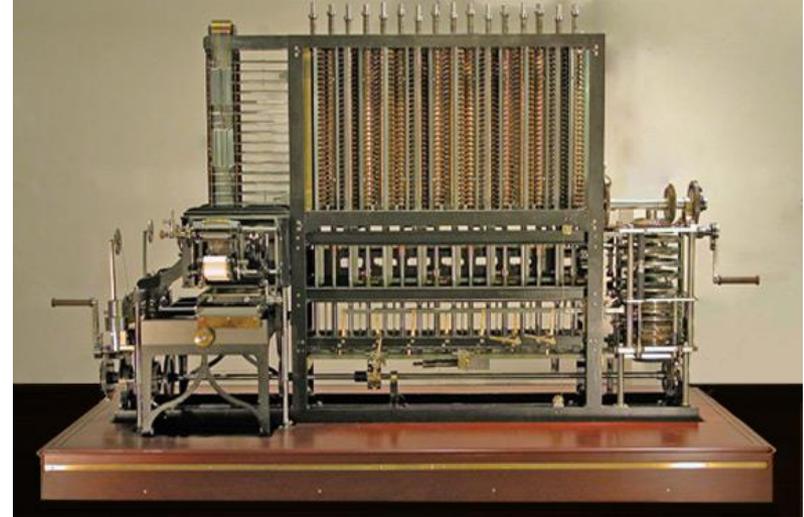
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Universal Computation



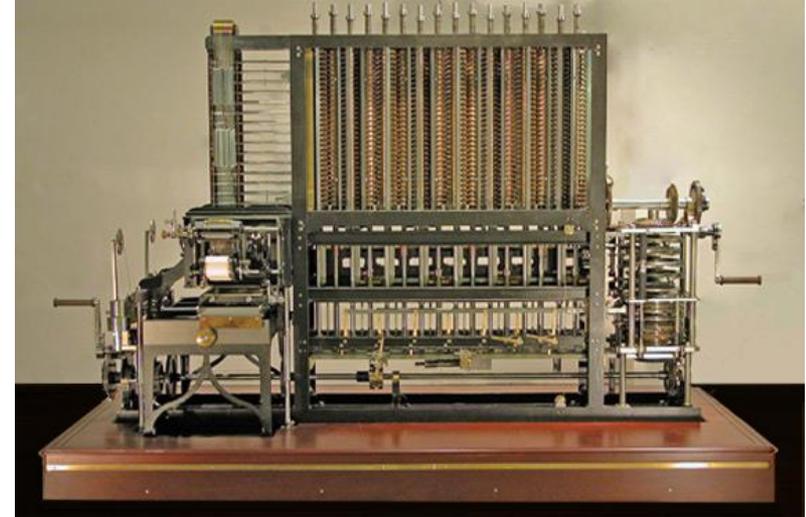
Universal Computation



Universal Computation



=



- A computer is neither a shiny chunk of glass, plastic and silicon nor a bunch of cog wheels, springs and levers.
- It is an abstract concept (Turing machine with a von Neumann architecture etc.) that can be instantiated in many ways.



Universal Biology

- **Universal Biology** is the set of general principles that govern living matter without specific reference to how that living material is instantiated
- Translation, transcription, replication are all aspects of living systems that are likely to be universal



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- **The existence of a genetic code is universal**
- **Our *specific* genetic code is an instantiation of this abstraction**



Universal Biology

- Universal Biology is the set of general principles that govern living matter without specific reference to how that living material is instantiated
- Translation, transcription, replication are all aspects of living systems that are likely to be universal
- The existence of a genetic code is universal
- Our specific genetic code is an instantiation of this abstraction
- **Claim:** the dynamics of genetic codes is universal and leads to an inexorable pattern of the emergence of life.



THE PHASE DIAGRAM OF LIFE ...

... as inferred from the collective dynamics of innovation-sharing protocols

PNAS PNAS

Collective evolution and the genetic code

Kalin Vetsigian*, Carl Woese^{†‡§}, and Nigel Goldenfeld^{**†¶}

Departments of *Physics and †Microbiology and ‡Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801

A dynamical theory for the evolution of the genetic code is presented, which accounts for its universality and optimality. The central concept is that a variety of collective, but non-Darwinian, mechanisms likely to be present in early communal life generically lead to refinement and selection of innovation-sharing protocols, such as the genetic code. Our proposal is illustrated by using a simplified computer model and placed within the context of a sequence of transitions that early life may have made, before the emergence of vertical descent.

10696–10701 | PNAS | July 11, 2006 | vol. 103 | no. 28



Darwinian transition

~ 3.8Gya

Competing
genetic
codes

Translational
machinery too
complex to be
deformable

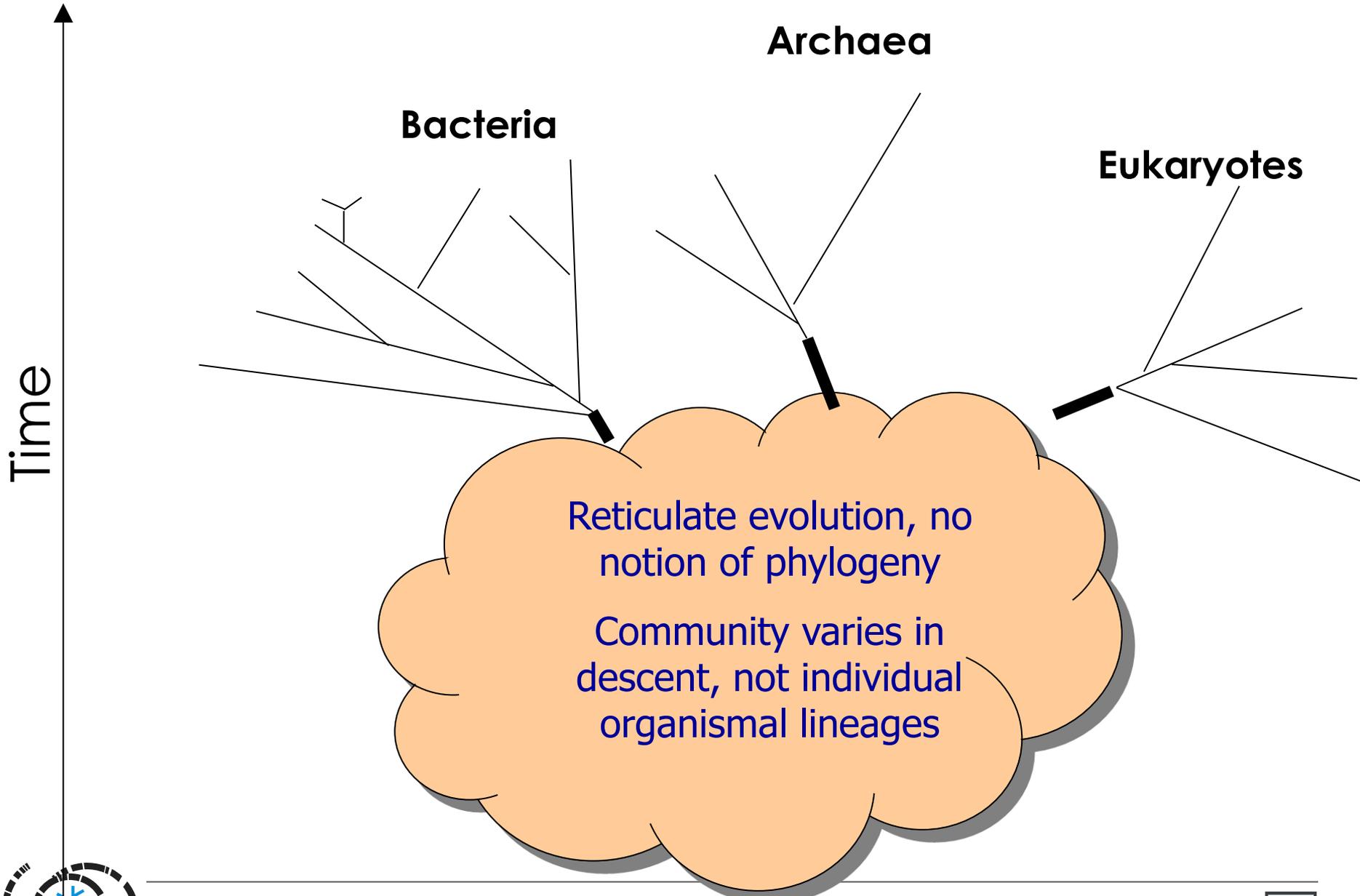


Universal
Genetic
Code and
HGT

Lineages defined
by slow evolution
of translation

The “Progenote” state

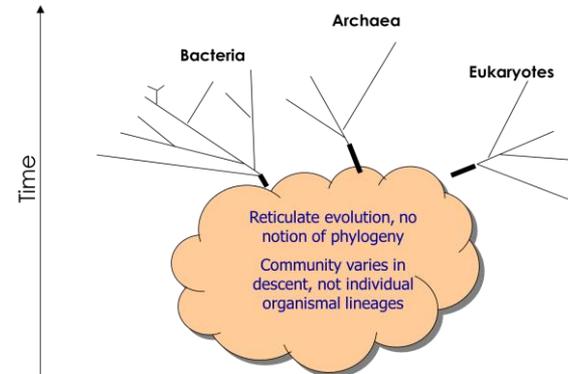




The Progenote

- **Originally conjectured by Woese (1972) as a phase of life where:**

- Genotype/phenotype distinction was still emerging
- Cells not yet sharply-defined
- Massive endosymbiosis



- **An emergent state whose dynamics generates the evolution of the canonical genetic code (VWG 2006)**

- Collective due to HGT of translation and other developing cell machinery
- Translation machinery generates statistical distribution of proteins
- Dynamical consequence is uniqueness and error-minimization property of genetic code



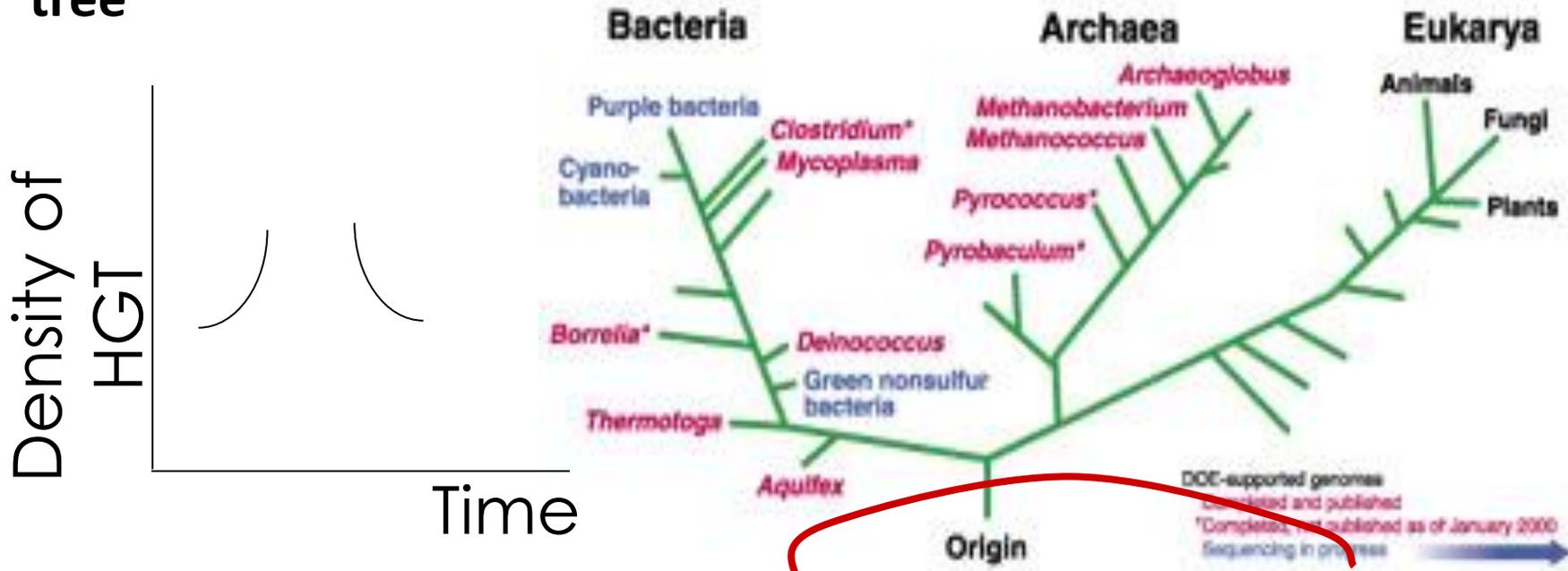
Our Big Questions

- **What are the universal principles governing evolving matter and the existence of the phenomenon of life?**
- **What evolutionary dynamics allowed life to go from nothing to LUCA in < 1 billion years?**
- **Is there evidence for the progenote state embedded in genomes?**
- **How did the progenote state break down ~ 3.8 billion years ago?**
- **What determines the speed of evolution? Collective effects? Environmental stress?**



Experimental predictions

- Collective phase may explain the origin of genes, viruses, gene transfer agents
- Density of HGT events may show near-transitional behavior
- Map density of HGT events onto the ribosomal phylogenetic tree



Goals of our NAI

- **Goal 1: to understand whether life is an inevitable outcome of the laws of physics, or if it is an “accident”.**
 - If life is a generic physical phenomenon then we can reasonably expect it to exist elsewhere.
- **Goal 2: to find direct evidence of the collective state of life: the progenote**
 - Our analysis of the genetic code can only be explained by appealing to collective effects, but we want direct evidence



Goals of our NAI

- **Goal 3: to understand why are there three Domains of life?**
 - Why not 1000? Why such a small number? Does this reflect general principles or just an accident?
 - How does the progenote state break down?
- **Goal 4: to understand how cells sense and interact with their environment**
 - Can environmental stress accelerate rate of evolution?



Goal 1: Universal Biology: new physical laws?

- **Schrodinger, Delbruck, ... earliest physicists to work in biology**
 - Partial motivation was to find new physical laws!
- **Where would such laws lie?**
 - Our answer: emergence and existence of life itself
 - How does matter self-organize hierarchically to create replicating, evolvable structures?
 - How do molecules come to life?
- **To understand biology in the same sense that we understand physical phenomena, we need to understand why the phenomenon occurs**
 - Dynamics of systems that can reprogram themselves



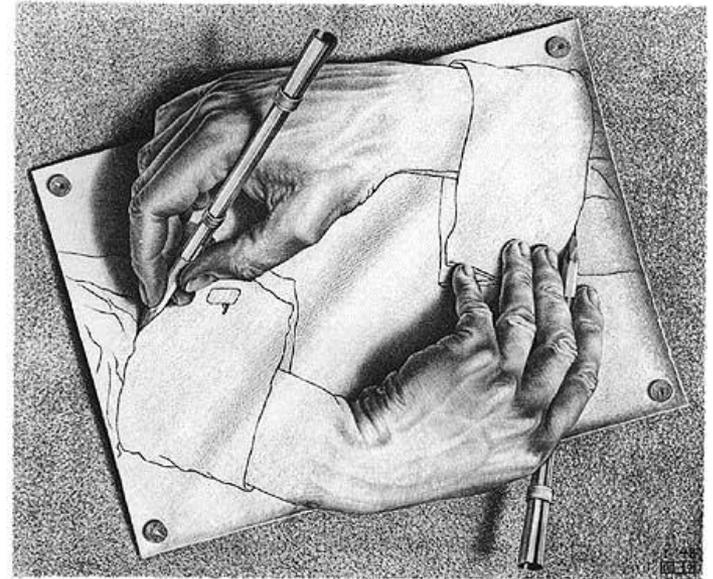
Evolving Dynamical System

- **Self-referential property of prebiotic evolution:**

- Agents are molecules
- Agents' function is to modify agents
- The modified agents can in turn modify other agents

- **Open ended growth of complexity:**

- Dynamical systems with above property can produce agents with new functions
- Formation of new functions is a necessary condition for open ended growth of complexity



Drawing Hands by M. C. Escher

- **Our goal is to find the simplest model of evolving dynamical systems with above property that can be quantitatively analyzed**

- Find the conditions for the transition between a simple state (fixed points/periodic) and a state of open ended growth of complexity.

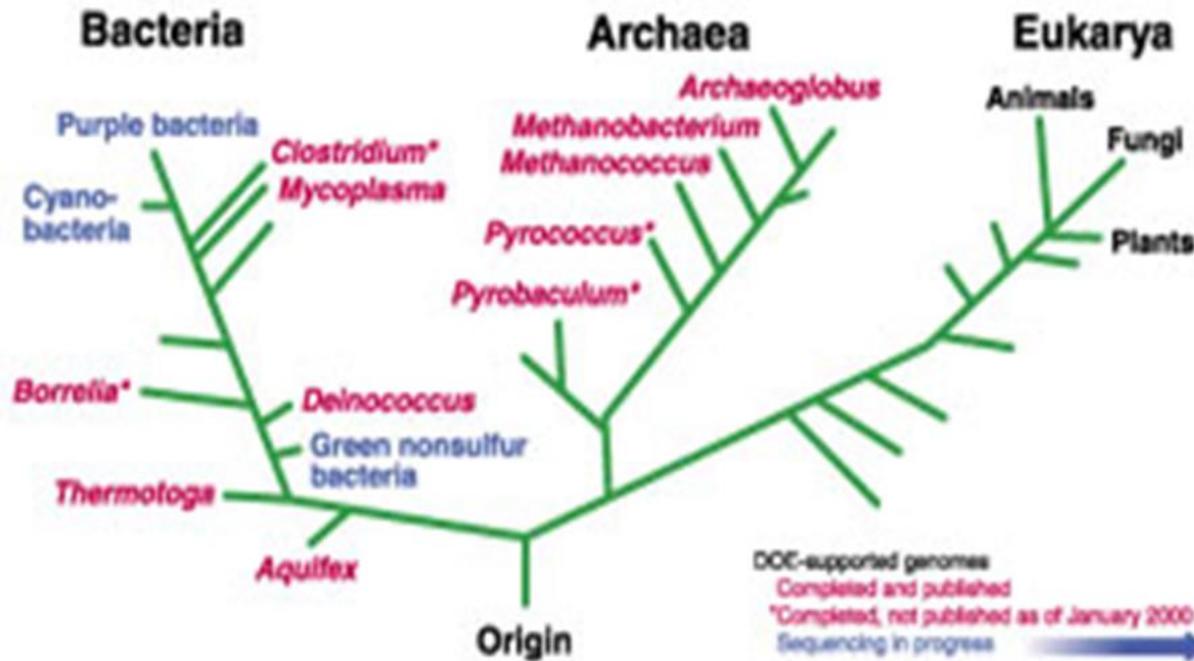


Goal 2: Windows on the progenote

- **Underlying idea: look at core cellular machinery that will be most reflective of collective effects**
 - Amino-acyl-tRNA synthetases, the least conserved elements of translational machinery
 - Rich structure: two classes, complex relatedness groups
 - Deviations from canonical phylogenetic pattern of rRNA, elongation factors, transcriptional machinery
- **Evidence for ancient HGT events?**
- **Action plan: comparative phylogenomics of these ancient proteins to look for HGT events, map out the density of these correlated to rRNA phylogeny; extend to other proteins; attempt to understand the order in which transitions of evolutionary structure took place**



Goal 3: Breakdown of the progenote state and the transition to vertical evolution



- Theory suggests that a progenote state is an inevitable feature of the growth of complexity. Why does it break down to vertical evolution?



Lineages are patterns in gene space

- **Genomes are sequences of strings in a finite alphabet**
 - E.g. sequences of zeroes and ones
- **The abundance distribution of these strings defines a population**
- **Closely-related organisms have similar strings**
 - We can define distance metrics to quantify similarity, e.g. Hamming distance is number of different entries between two strings
- **Dynamics can be calculated using extensions of quasi-species theory**



Lineages are patterns in gene space

- Dynamics can be calculated using extensions of quasi-species theory

$$\frac{dX_I}{dt} = \sum_J (R_{IJ} W_J X_J - G_{IJ} W_J X_I X_J) + \text{HGT} + \text{noise}$$

Abundance of genome I

Reproduction and mutation from J to I

Fitness

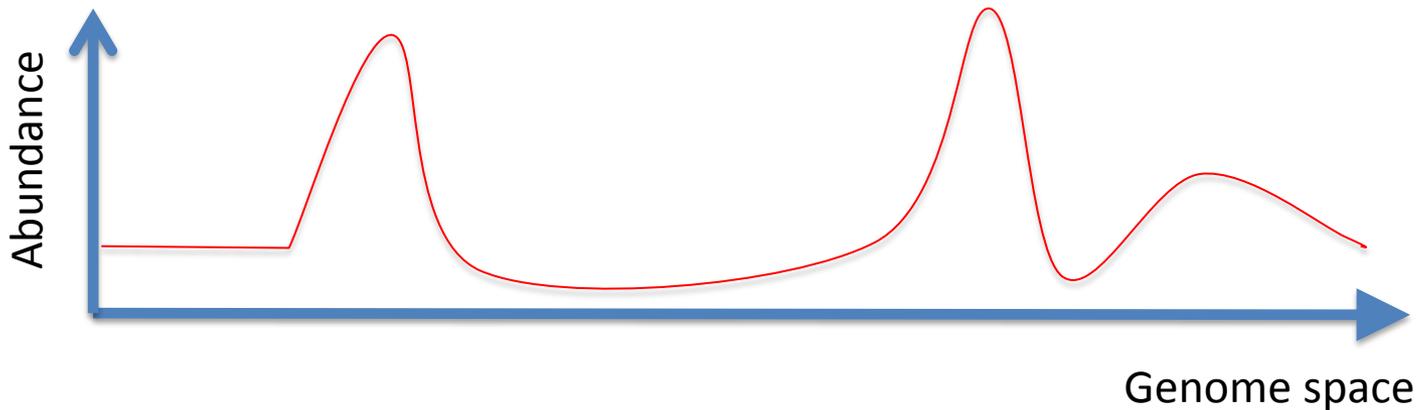
Competition

- Dynamics and fluctuations calculated using master equation techniques



Lineages are patterns in gene space

- Species correspond to clusters in gene space

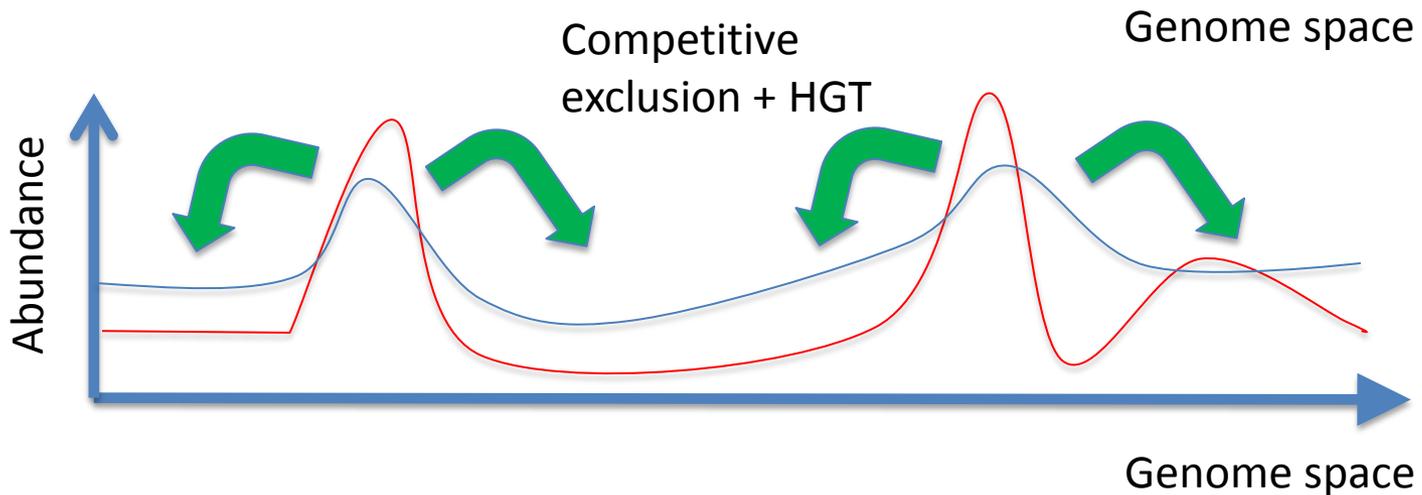
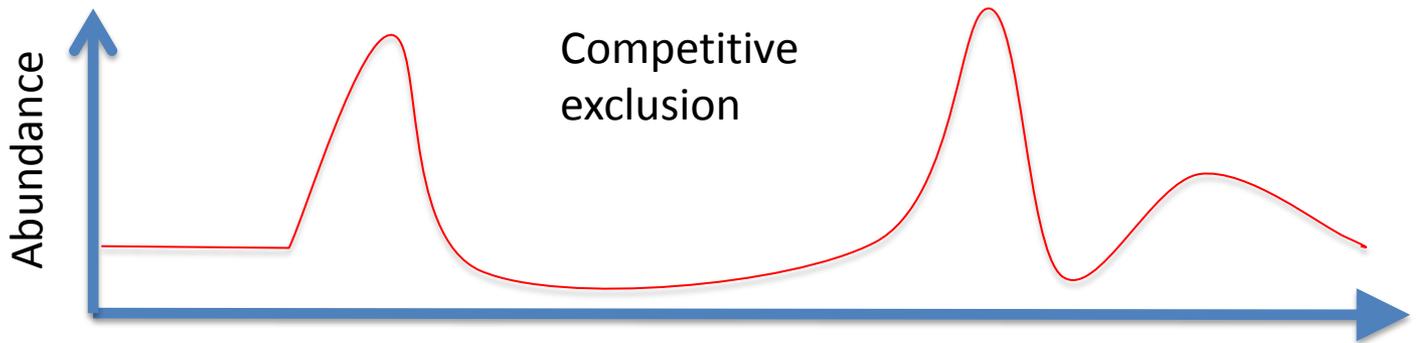


- **Competitive exclusion leads to pattern-forming instabilities**
 - Similar organisms try to occupy same niche
 - Organisms between two peaks will experience double the inhibition of growth
 - → peaks tend to become more pronounced



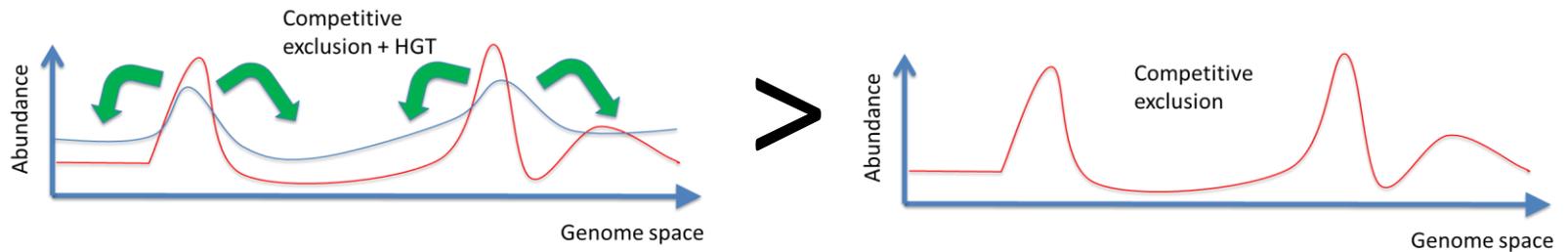
Lineages are patterns in gene space

- HGT tends to redistribute species in genome space

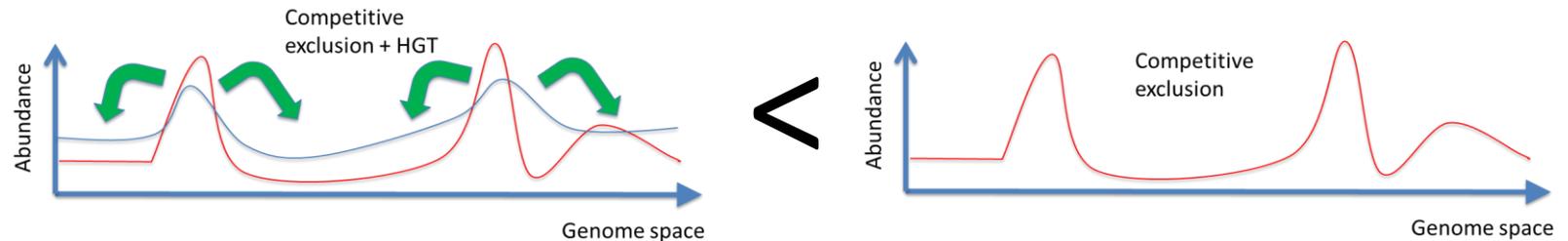


Lineages are patterns in gene space

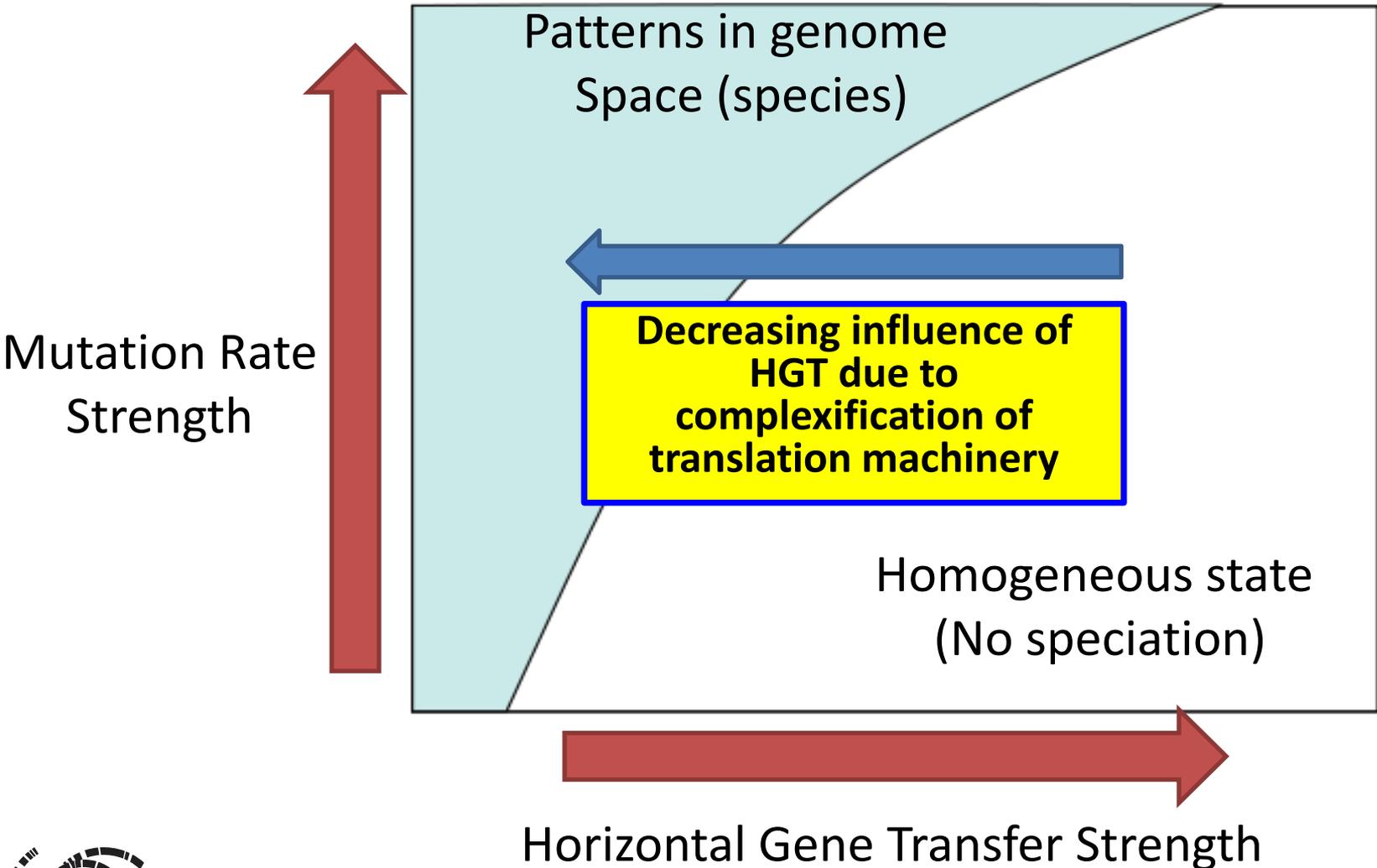
- Progenote/collective phase of life



- Modern lineages/vertical evolution phase of life



Preliminary phase diagram of Darwinian Transition



Nature of the Darwinian threshold

- **Why are there so few Domains of life?**
- **Dynamics of the Darwinian transition will be dominated by principal components of the instability of the progenote state**
 - Technically, fastest growing stability operator eigenvectors
- **Conjecture: these correspond to key aspects of template-directed synthesis (translation, transcription, replication) and metabolism.**
 - Topic of future work



Goal 4: Universal aspects of how life responds to its environment

- **Rapid evolution of life due to:**
 - Collective effects, endosymbiosis, HGT
 - Evolution of evolvability, a core feature of universal biology
- **Characterize modern mechanisms for promoting the ability to evolve under stress**
 - Generation of genomic and genetic diversity
 - Upregulation of mutation rates in space and at specific loci
 - Gene amplification
- **How cells decide to go on path to genome rearrangement as opposed to genome repair**
- **Role of environmental gradients in up-regulating mutation rates, documented by recent experiments in Bacteria**
 - How universal is this? Experiment in Archaea, which have very different metabolism and regulatory mechanisms.



Key project milestones

Theme 1	Explicit construction of self-referential dynamics; predictive calculation of “fitness landscape” and growth of complexity; emergence of trophic layers in Cottrell systems.
Theme 2	Characterization of HGT in AARS; identification of AARS-like patterns in other proteins; final model of early associations and possible identification of extinct lineages; construction of protoribosome.
Theme 3	Determination of evidence for existence of a progenote state; determination of evidence for a Darwinian transition in Archaeal replication machinery; determination of LEACA; determination of evolution of the cell membrane
Theme 4	Demonstration of how a stress response promotes gross chromosomal rearrangement; identification of molecular determinant for stress-induced genomic rearrangement; use of GeoBioCell to induce puromycin resistance in the Archaea <i>M. mazei</i> and <i>M. acetivorans</i> based on environmental gradients.

