

# Introduction to Bioengineering

## BIOE/ENGR.80

### Stanford University

Spring 2020 Class Slides

Day 22  
27 May 2020

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# Week 7 reprise

PROJECT  
SKILL

Impact versus effort mapping

Project topic selection

Communicating clearly

Storytelling for engagement

Performing for impact



# Week 8 look ahead

CONCEPT  
SKILL

Evolution as algorithm


Evolution as service


Evolution 2.0?

<Evolutionary algorithm sandbox>

# Evolution as algorithm\*

Dictionary

Search for a word 

 **al·go·rithm**  
/'algə,riTHəm/

*noun*

a process or set of rules to be followed in calculations or other problem-solving operations, especially by a computer.  
"a basic algorithm for division"

\*By algorithm, we simply mean to represent that a few things must be happening for evolution to happen. We do not mean to imply any higher purpose to the process.

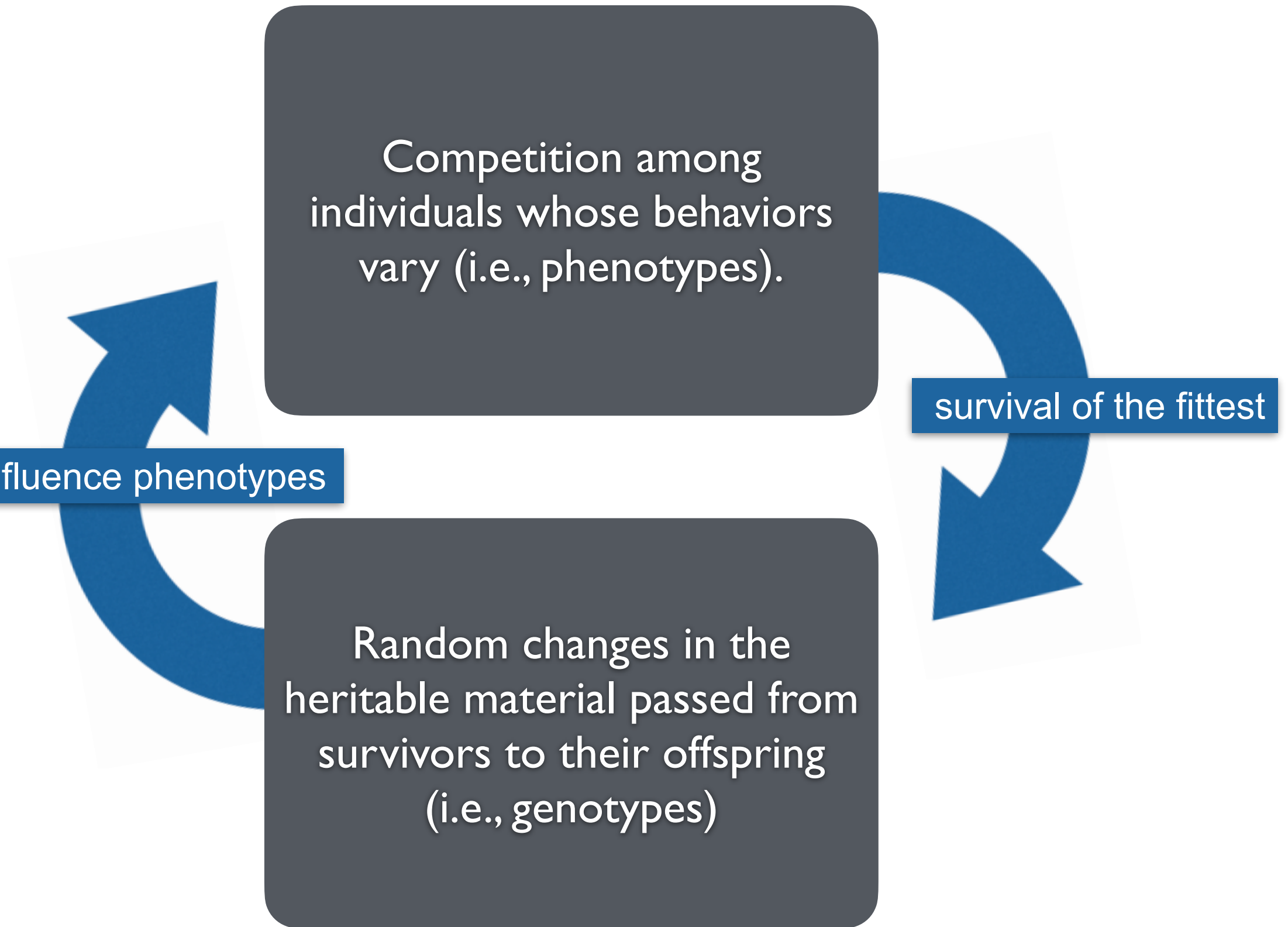
# Evolution as algorithm

Competition among individuals whose behaviors vary (i.e., phenotypes).

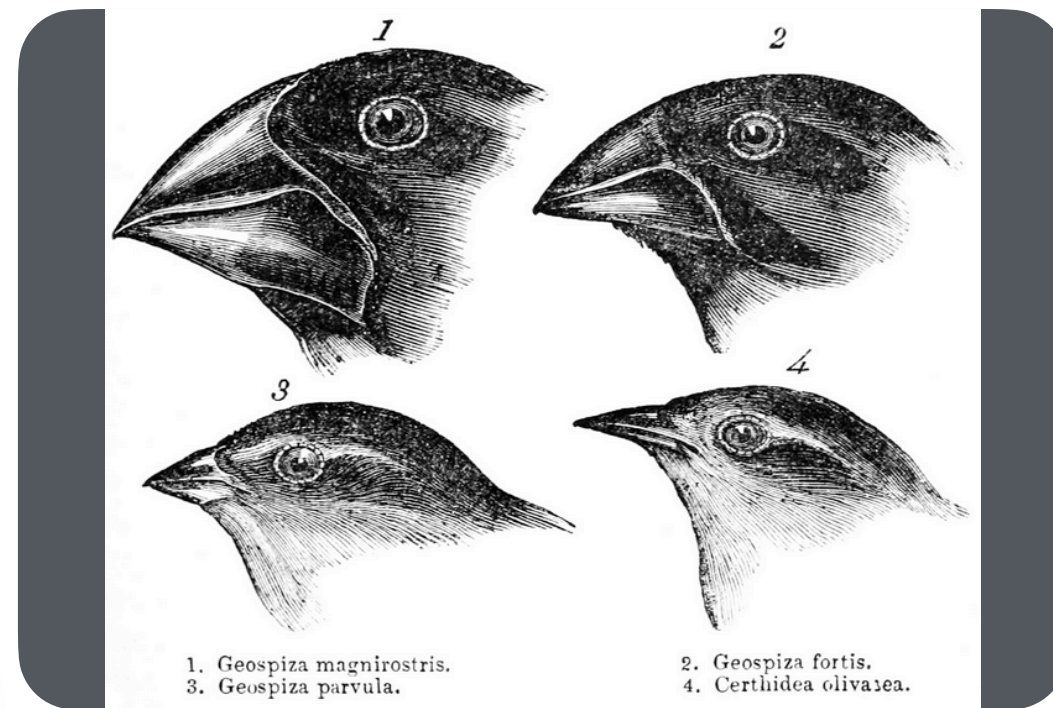
survival of the fittest

genotypes influence phenotypes

Random changes in the heritable material passed from survivors to their offspring (i.e., genotypes)



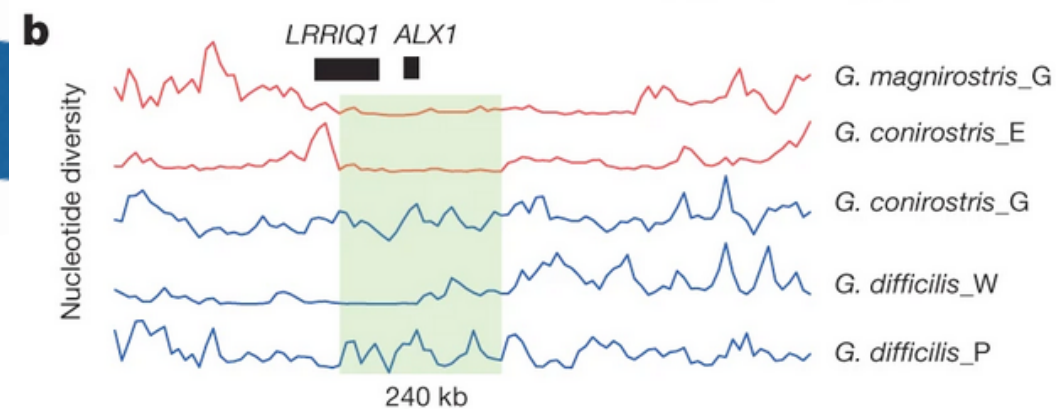
# Evolution as algorithm



[https://en.wikipedia.org/wiki/Darwin%27s\\_finches](https://en.wikipedia.org/wiki/Darwin%27s_finches)

genotypes influence phenotypes

survival of the fittest



<https://www.nature.com/articles/nature14181>

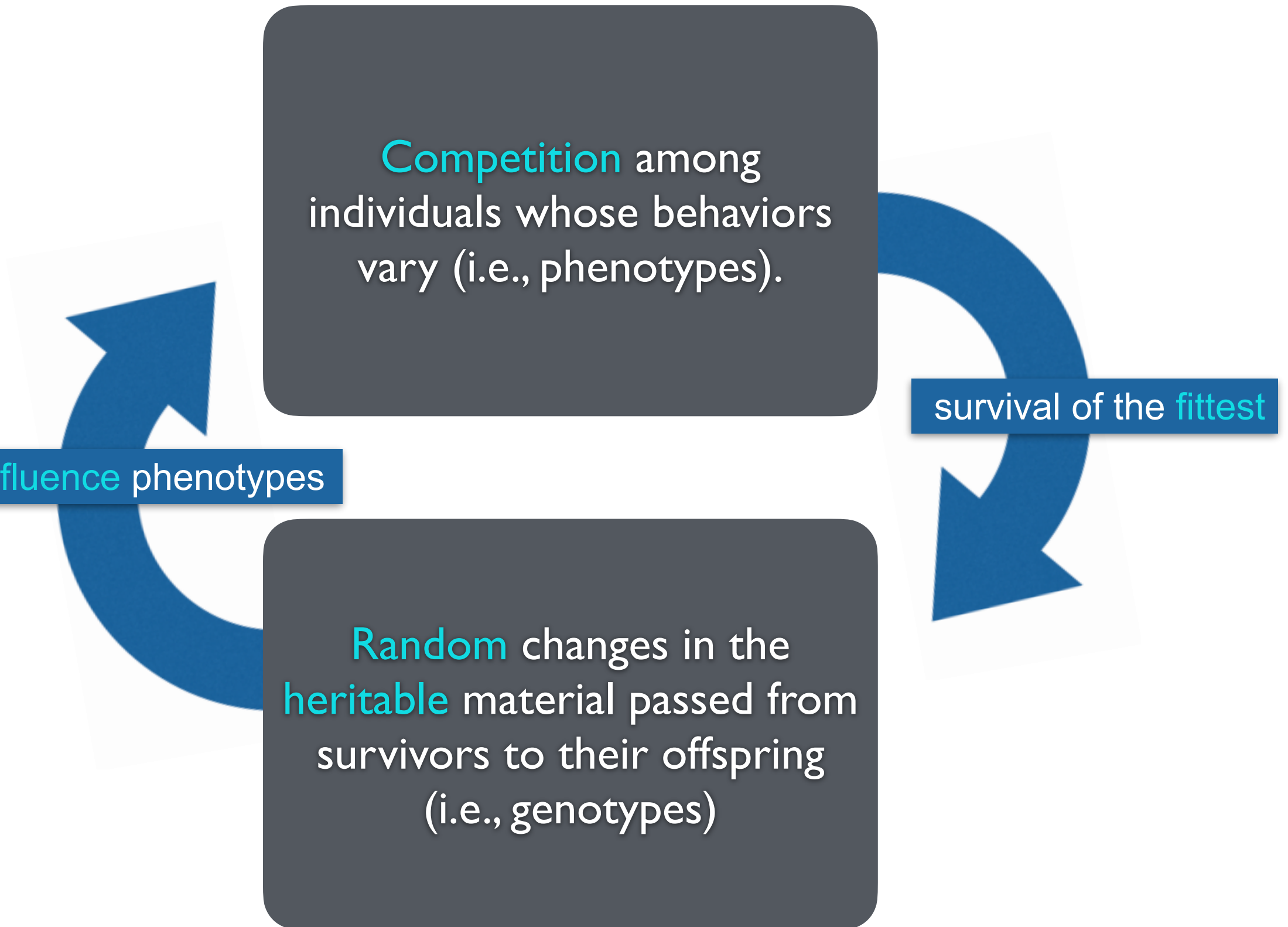
# Evolution as algorithm

**Competition** among individuals whose behaviors vary (i.e., phenotypes).

survival of the **fittest**

genotypes **influence** phenotypes

**Random** changes in the **heritable** material passed from survivors to their offspring (i.e., genotypes)





# Evolution as substrate agnostic algorithm

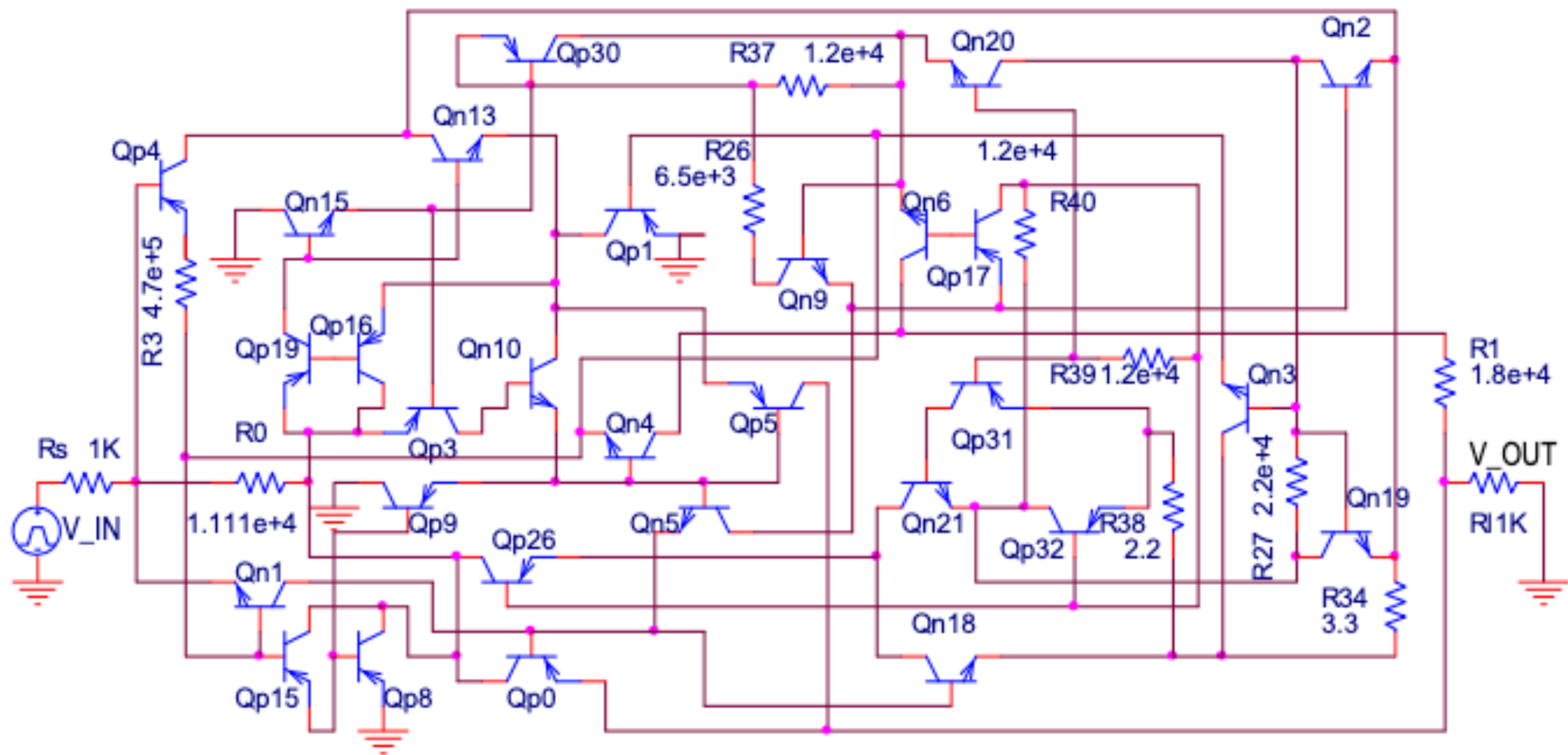


Figure 6. The evolved cube root circuit.

Q. how to evolve electrical circuits?

Q. what else can be evolved?



# Factors influencing evolution

Competition among individuals whose behaviors vary (i.e., phenotypes).

details of the competition?

survival of the fittest

Random changes in the heritable material passed from survivors to their offspring (i.e., genotypes)

how many survivors?

to what extent?

genotypes influence phenotypes

what sorts of changes?  
how many changes per individual per generation?

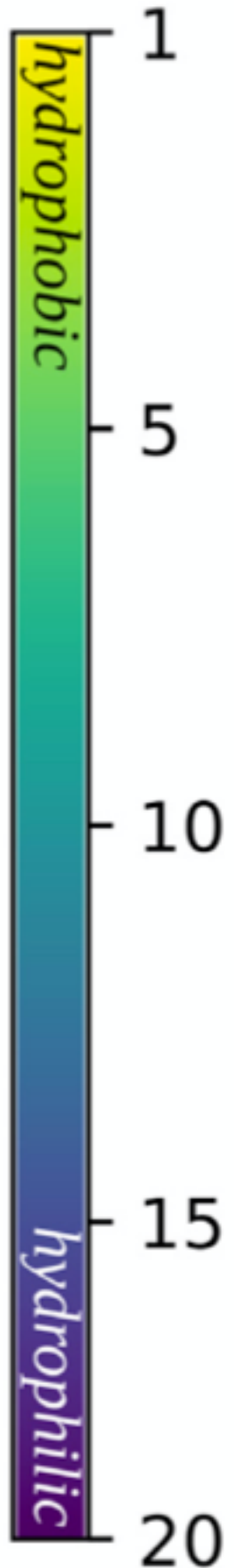
E.g., to what extent  
(do changes in genotypes  
result in changes in  
phenotypes)?

# Standard Code

## Second Position

		Second Position				
		U	C	A	G	
First Position	U	UUU : F	UCU : S	UAU : Y	UGU : C	U
		UUC : F	UCC : S	UAC : Y	UGC : C	C
		UUA : L	UCA : S	UAA : *	UGA : *	A
		UUG : L	UCG : S	UAG : *	UGG : W	G
	C	CUU : L	CCU : P	CAU : H	CGU : R	U
		CUC : L	CCC : P	CAC : H	CGC : R	C
		CUA : L	CCA : P	CAA : Q	CGA : R	A
		CUG : L	CCG : P	CAG : Q	CGG : R	G
	A	AUU : I	ACU : T	AAU : N	AGU : S	U
		AUC : I	ACC : T	AAC : N	AGC : S	C
		AUA : I	ACA : T	AAA : K	AGA : R	A
		AUG : M	ACG : T	AAG : K	AGG : R	G
	G	GUU : V	GCU : A	GAU : D	GGU : G	U
		GUC : V	GCC : A	GAC : D	GGC : G	C
		GUA : V	GCA : A	GAA : E	GGA : G	A
		GUG : V	GCG : A	GAG : E	GGG : G	G

Third Position

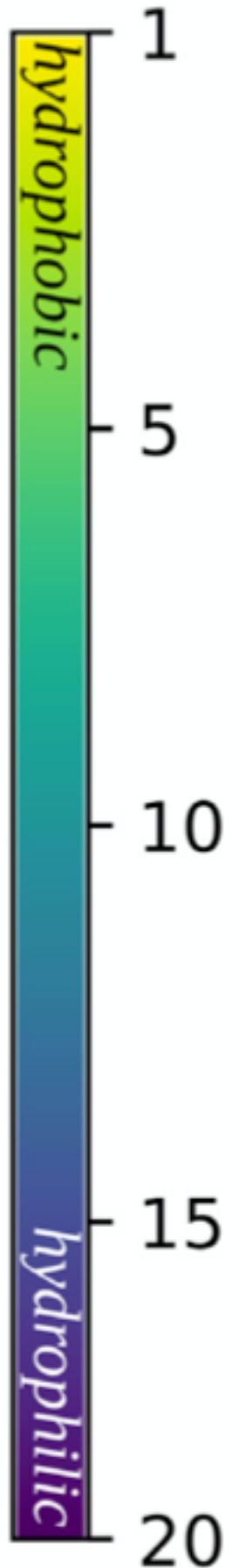




# Random Code

## Second Position

		Second Position					
		U	C	A	G		
First Position	U	UUU : V	UCU : V	UAU : L	UGU : S	U	Third Position
		UUC : D	UCC : G	UAC : E	UGC : C	C	
		UUA : R	UCA : A	UAA : Q	UGA : T	A	
		UUG : M	UCG : I	UAG : F	UGG : P	G	
	C	CUU : H	CCU : H	CAU : N	CGU : A	U	
		CUC : M	CCC : *	CAC : E	CGC : A	C	
		CUA : H	CCA : V	CAA : M	CGA : H	A	
		CUG : M	CCG : F	CAG : G	CGG : L	G	
	A	AUU : I	ACU : H	AAU : K	AGU : G	U	
		AUC : Q	ACC : D	AAC : S	AGC : M	C	
		AUA : S	ACA : Y	AAA : E	AGA : V	A	
		AUG : K	ACG : C	AAG : *	AGG : L	G	
	G	GUU : M	GCU : E	GAU : I	GGU : Q	U	
		GUC : C	GCC : W	GAC : I	GGC : D	C	
		GUA : W	GCA : P	GAA : E	GGA : Y	A	
		GUG : G	GCG : *	GAG : C	GGG : M	G	



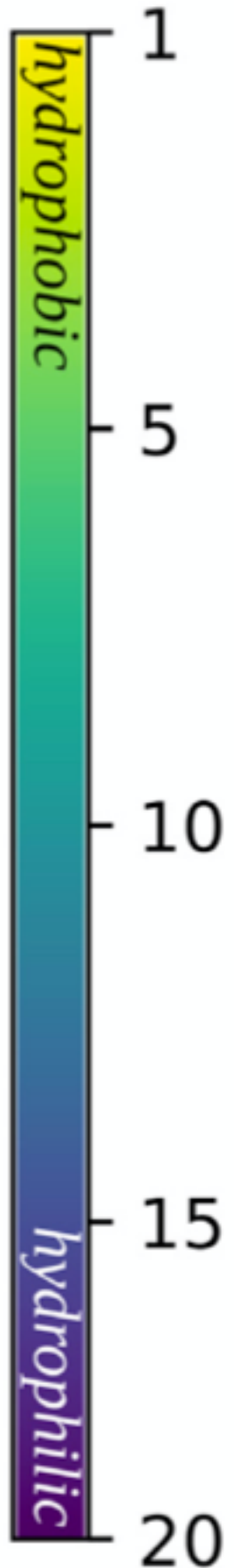
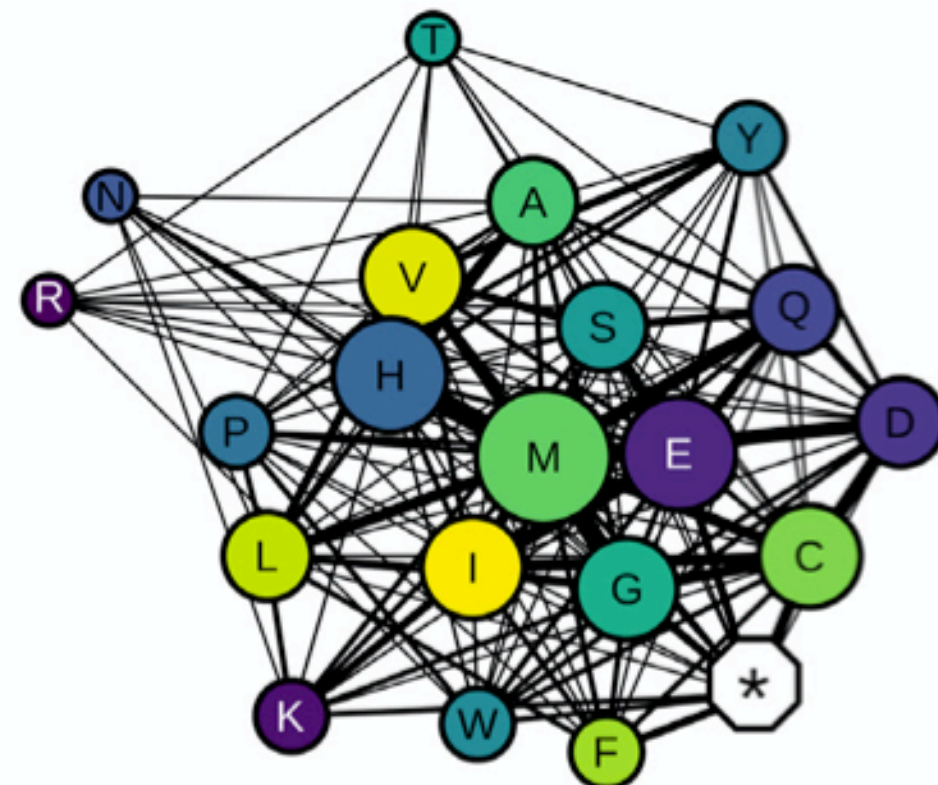
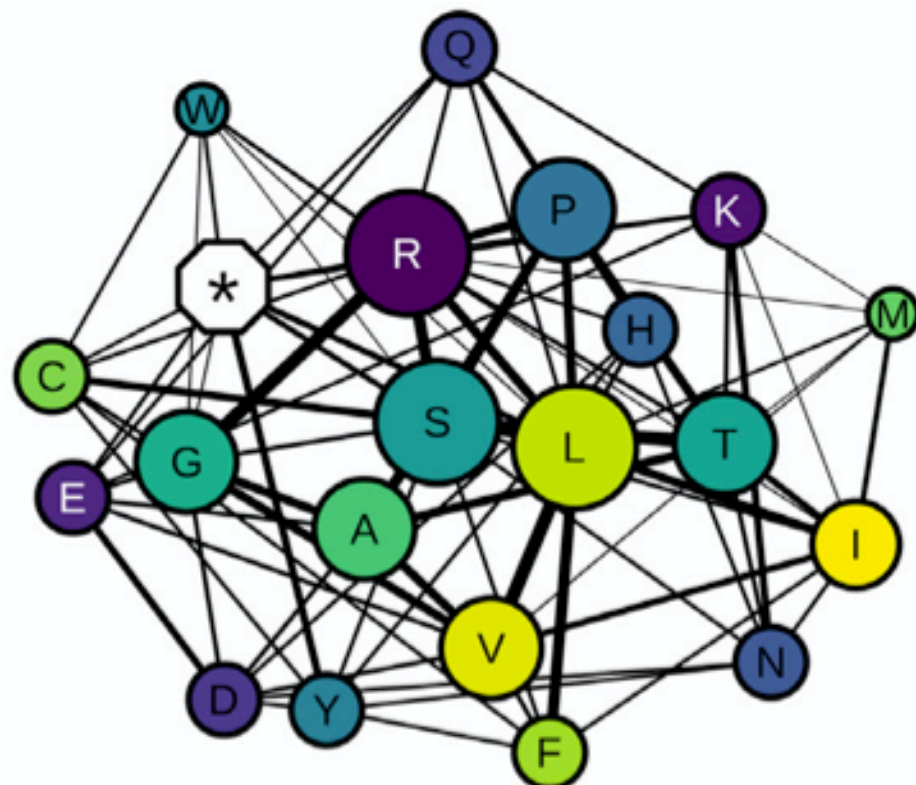


# Standard Code

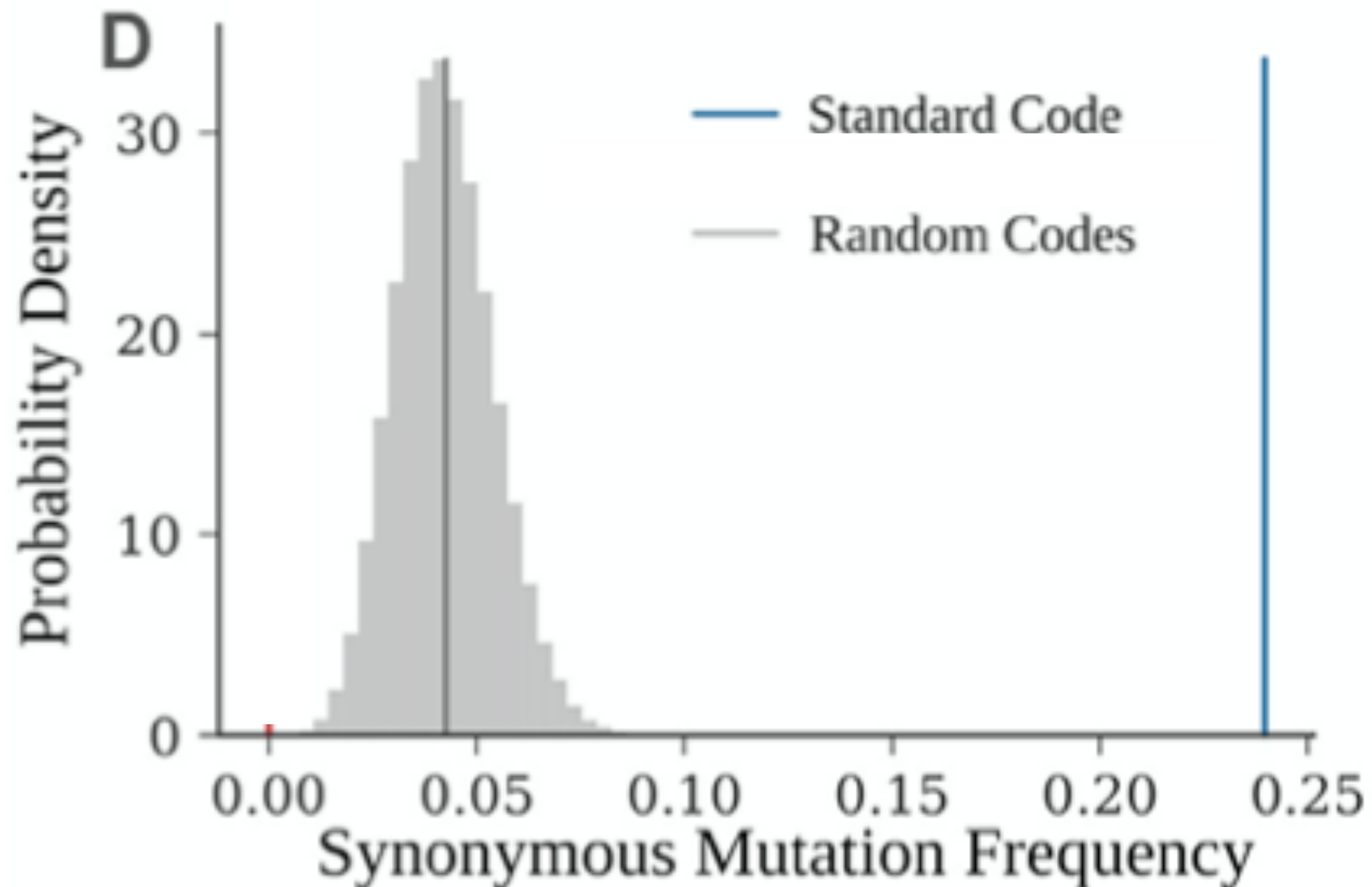
		Second Position				
		U	C	A	G	
First Position	U	UUU : F	UCU : S	UAU : Y	UGU : C	U
		UUC : F	UCC : S	UAC : Y	UGC : C	C
		UUA : L	UCA : S	UAA : *	UGA : *	A
		UUG : L	UCG : S	UAG : *	UGG : W	G
	C	CUU : L	CCU : P	CAU : H	CGU : R	U
		CUC : L	CCC : P	CAC : H	CGC : R	C
		CUA : L	CCA : P	CAA : Q	CGA : R	A
		CUG : L	CCG : P	CAG : Q	CGG : R	G
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		AUC : I	ACC : T	AAC : N	AGC : S	C
		AUA : I	ACA : T	AAA : K	AGA : R	A
		AUG : M	ACG : T	AAG : K	AGG : R	G
	G	GUU : V	GCU : A	GAU : D	GGU : G	U
		GUC : V	GCC : A	GAC : D	GGC : G	C
		GUA : V	GCA : A	GAA : E	GGA : G	A
		GUG : V	GCG : A	GAG : E	GGG : G	G
						Third Position

# Random Code

		Second Position				Third Position
First Position		U	C	A	G	
U	UUU : V	UCU : V	UAU : L	UGU : S	U	
	UUC : D	UCC : G	UAC : E	UGC : C	C	
	UUA : R	UCA : A	UAA : Q	UGA : T	A	
	UUG : M	UCG : I	UAG : F	UGG : P	G	
C	CUU : H	CCU : H	CAU : N	CGU : A	U	
	CUC : M	CCC : *	CAC : E	CGC : A	C	
	CUA : H	CCA : V	CAA : M	CGA : H	A	
	CUG : M	CCG : F	CAG : G	CGG : L	G	
A	AUU : I	ACU : H	AAU : K	AGU : G	U	
	AUC : Q	ACC : D	AAC : S	AGC : M	C	
	AUA : S	ACA : Y	AAA : E	AGA : V	A	
	AUG : K	ACG : C	AAG : *	AGG : L	G	
G	GUU : M	GCU : E	GAU : I	GGU : Q	U	
	GUC : C	GCC : W	GAC : I	GGC : D	C	
	GUA : W	GCA : P	GAA : E	GGA : Y	A	
	GUG : G	GCG : *	GAG : C	GGG : M	G	



Q. why is the standard genetic code six-fold less likely to change an amino acid given any point mutation in an open reading frame?

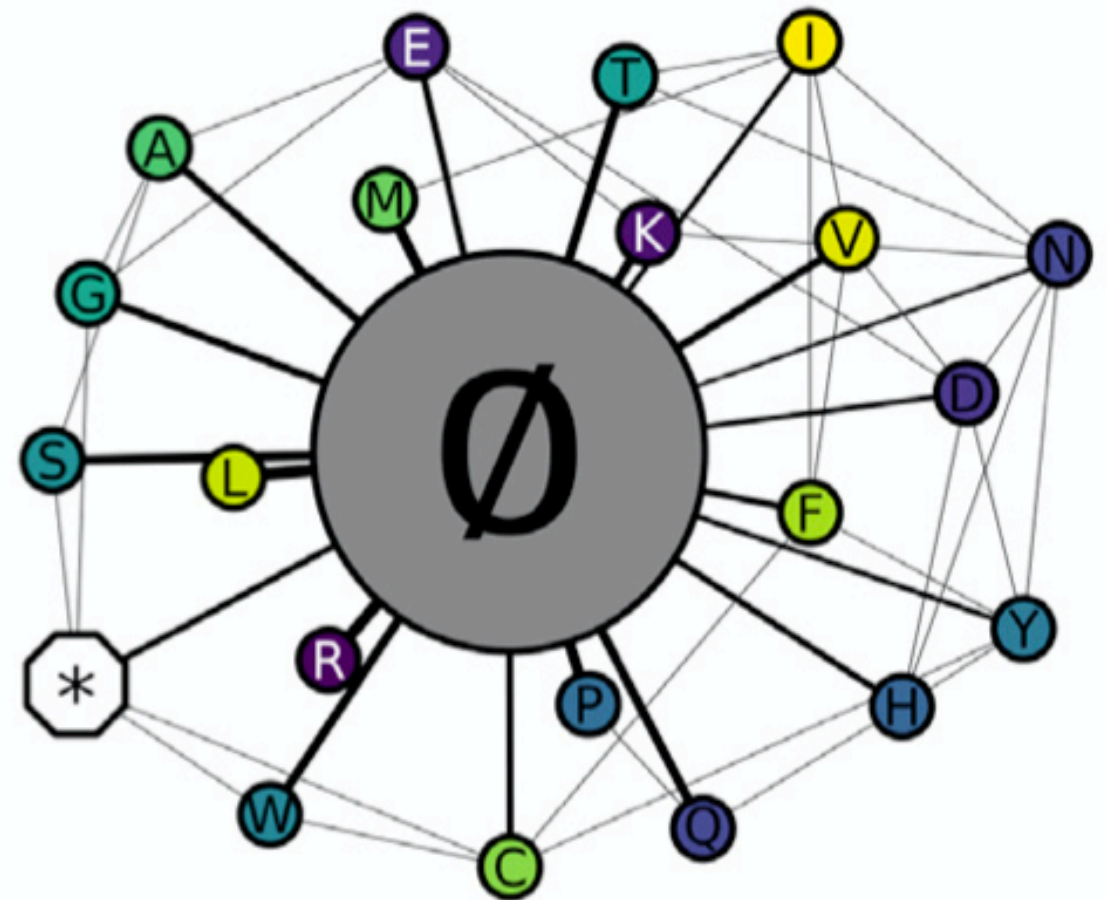




Q. what would be the expected impact on evolution for organisms in which most point mutations land on codons that cannot be decoded?

RED20

		Second Position				
		U	C	A	G	
First Position	U	UUU : 0	UCU : 0	UAU : 0	UGU : 0	U
		UUC : F	UCC : 0	UAC : Y	UGC : C	C
		UUA : 0	UCA : S	UAA : *	UGA : *	A
		UUG : 0	UCG : 0	UAG : *	UGG : W	G
C	C	CUU : 0	CCU : 0	CAU : 0	CGU : R	U
		CUC : 0	CCC : 0	CAC : H	CGC : 0	C
		CUA : L	CCA : 0	CAA : 0	CGA : 0	A
		CUG : 0	CCG : P	CAG : Q	CGG : 0	G
A	A	AUU : 0	ACU : 0	AAU : 0	AGU : 0	U
		AUC : I	ACC : T	AAC : N	AGC : 0	C
		AUA : 0	ACA : 0	AAA : K	AGA : 0	A
		AUG : M	ACG : 0	AAG : 0	AGG : 0	G
G	G	GUU : 0	GCU : 0	GAU : 0	GGU : 0	U
		GUC : V	GCC : 0	GAC : D	GGC : 0	C
		GUA : 0	GCA : A	GAA : E	GGA : G	A
		GUG : 0	GCG : 0	GAG : 0	GGG : 0	G





# The origin of mutants

**John Cairns, Julie Overbaugh & Stephan Miller**

Department of Cancer Biology, Harvard School of Public Health, 665 Huntington Avenue, Boston, Massachusetts 02115, USA

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*Nucleic acids are replicated with conspicuous fidelity. Infrequently, however, they undergo changes in sequence, and this process of change (mutation) generates the variability that allows evolution. As the result of studies of bacterial variation, it is now widely believed that mutations arise continuously and without any consideration for their utility. In this paper, we briefly review the source of this idea and then describe some experiments suggesting that cells may have mechanisms for choosing which mutations will occur.*

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**Claim — mutations are not random in occurrence, rather genes whose mutating would be most beneficial for fitness in a given environment are somehow preferentially mutated...**

**Q. How would this work?**

# A. Evolution is cleverer than we are\*

## **Evidence That Selected Amplification of a Bacterial *lac* Frameshift Allele Stimulates Lac<sup>+</sup> Reversion (Adaptive Mutation) With or Without General Hypermutability**

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*\*Department of Biology, University of Utah, Salt Lake City, Utah 84112 and*

*<sup>†</sup>Swedish Institute for Infectious Disease Control, Solna, S 17182, Sweden*

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Accepted for publication May 2, 2002

### ABSTRACT

In the genetic system of Cairns and Foster, a nongrowing population of an *E. coli lac* frameshift mutant appears to specifically accumulate Lac<sup>+</sup> revertants when starved on medium including lactose (adaptive mutation). This behavior has been attributed to stress-induced general mutagenesis in a subpopulation of starved cells (the hypermutable state model). We have suggested that, on the contrary, stress has no direct effect on mutability but favors only growth of cells that amplify their leaky mutant *lac* region (the amplification mutagenesis model). Selection enhances reversion primarily by increasing the mutant *lac* copy number within each developing clone on the selection plate. The observed general mutagenesis is attributed to a side effect of growth with an amplification—induction of SOS by DNA fragments released from a tandem array of *lac* copies. Here we show that the *S. enterica* version of the Cairns system shows SOS-dependent general mutagenesis and behaves in every way like the original *E. coli* system. In both systems, *lac* revertants are mutagenized during selection. Eliminating the 35-fold increase in mutation rate reduces revertant number only 2- to 4-fold. This discrepancy is due to continued growth of amplification cells until some clones manage to revert without mutagenesis solely by increasing their *lac* copy number. Reversion in the absence of mutagenesis is still dependent on RecA function, as expected if it depends on *lac* amplification (a recombination-dependent process). These observations support the amplification mutagenesis model.

\*see Orgel's rules...

[https://en.wikipedia.org/wiki/Orgel%27s\\_rules](https://en.wikipedia.org/wiki/Orgel%27s_rules)

# In-progress project assessments

Group-1	Green
Group-2	Yellow - Red
Group-3	Red
Group-4	Yellow - Red
Group-5	Yellow - Red
Group-6	Yellow-Green
Group-7	Red
Group-8	Green
Group-9	Yellow - Red
Group-10	Yellow-Green
Group-11	Yellow-Green
Group-12	Yellow-Green
Group-13	Yellow - Red
Group-14	Yellow - Red
Group-15	Yellow-Green
Group-16	Yellow-Green
Group-17	Yellow
Bioe Baddies	Yellow