



# Exploration of neighbourhoods for inductive reasoning



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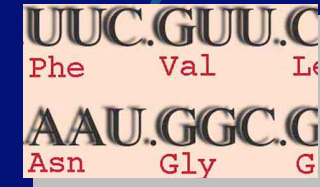


# A Chinese view for ....



# a virtuous circle

- Context
- Data
- Hypotheses => Today's presentation



# « Bombardment of the Chinese Embassy in Belgrade »





# Data vs Hypotheses

**What biological  
question are you  
asking?**



**Empedocle / Maupertuis / Malthus / Darwin**



**Variation / Selection / Amplification**

**Evolution**



*creates*

**Function**



*recruits*

**Structure**



*coding process*

**Sequence**



# What is Life?



➔ **Physics: *matter, energy, time***

➔ **Biology: Physics + *information, coding, control...***



# What functions for Life? An extension of Cuvier's view....



- Physical stability ([cyto]skeleton)
- Reproduction
- Respiration
- Locomotion
- Perception
- Transport (import / export)
- Circulation (internal fluxes)
- Digestion and recycling
- Assimilation
- Accommodation (regulation)
- Maintenance (repair)
- Etc...



# What is Life?



**Three processes are needed for Life:**

→ **Information transfer (Living Turing Machines)**

Driving force for a coupling between the genome structure and the structure of the cell:

→ **Metabolism (Internal organisation)**

→ **Compartmentalization (General structure)**

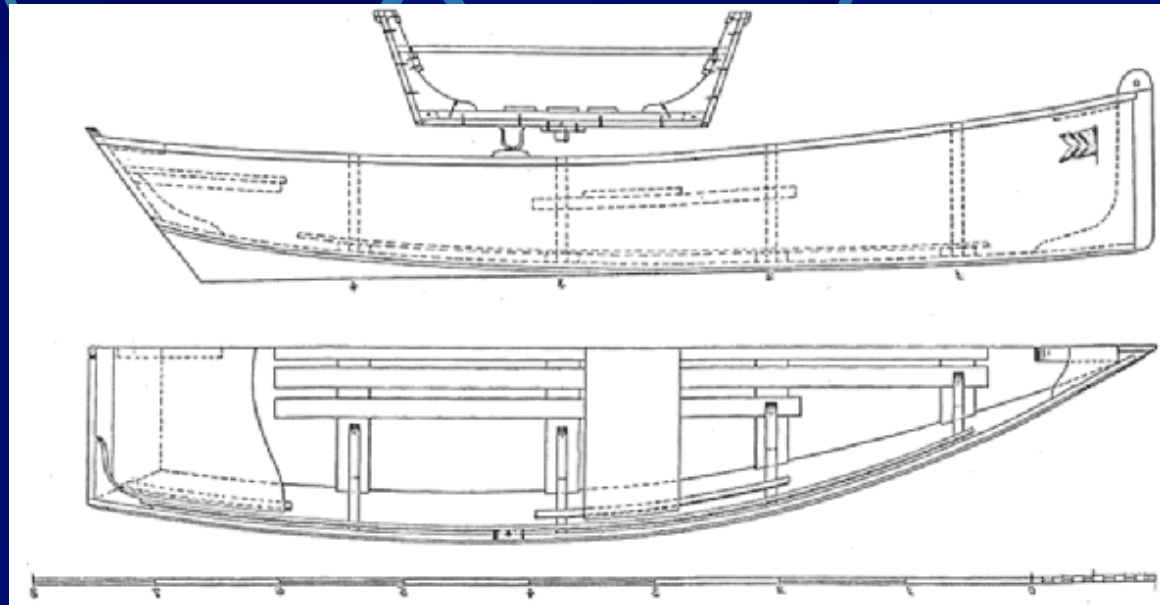
Because of these two processes, note that “concentration” usually does not have a meaning inside a cell



# Inductive strategy: exploring “neighborhoods”

UUC.GUU.C  
Phe Val Le  
AAU.GGC.G  
Asn Gly G

- Genes do not operate in isolation
- Proteins are part of complexes, as are parts in an engine
- It is important to understand their relationships, as those in the planks which make a boat



*The Delphic Boat*: Harvard University  
Press, february 2003



# Induction: exploring neighborhoods



To make discoveries we explore the general « neighborhoods » of genes of interest: proximity in the chromosome, in evolution, **in the literature**, in biochemical complexes, in metabolism etc.

Comparative genomics is essential, hence the use of « subtractive » genomics (comparison of pairs or larger sets of similar genomes)



# From sequence to function



Combining genome sequence data and *in silico* prediction (bioinformatics) we test our hypotheses using large scale genomics techniques (transcriptome and proteome analysis) as well as other types of neighborhoods, such as common electric charge or codon usage bias.

✳ Note that **regulation evolves much faster** than all other processes