

Parallel Adaptations to High Temperatures in the Archean Eon

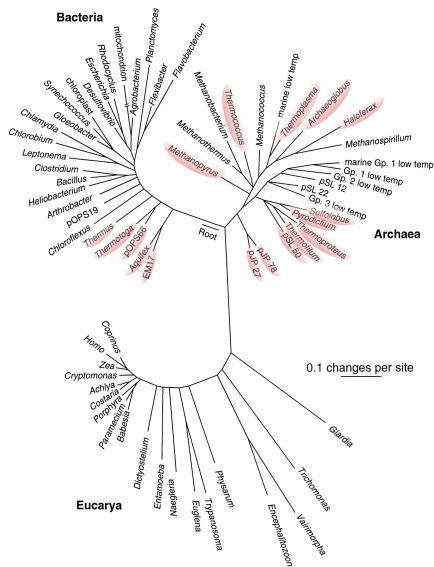
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Nicolas Lartillot², Manolo Gouy¹

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*These authors contributed equally to this work.

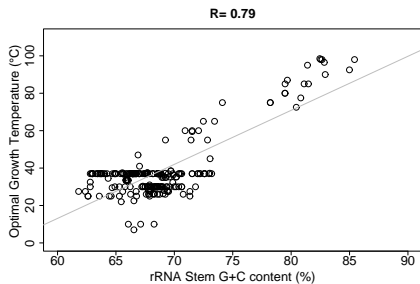
Saturday, June 25th 2008

Thermophiles in the tree of life

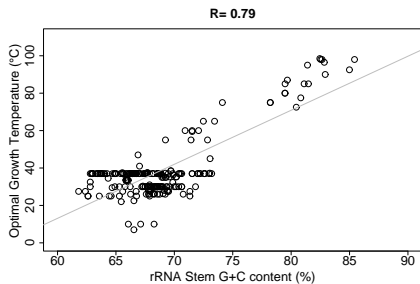


Pace, *Science* 1997.

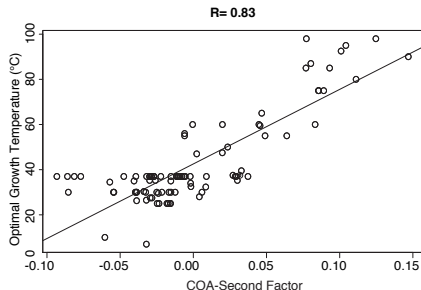
Ribosomal RNA



Ribosomal RNA

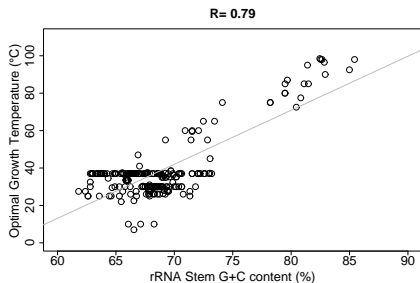


Proteins

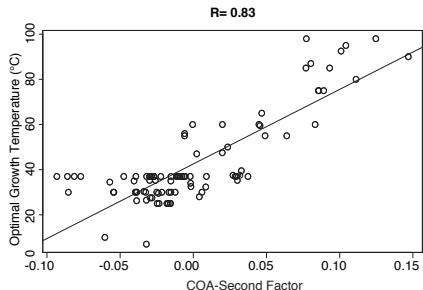


Sequence composition and temperature

Ribosomal RNA



Proteins



rRNA and protein compositions can be used as independent molecular thermometers

Ribosomal RNA

Galtier *et al.*, 1999:

non-hyperthermophilic LUCA

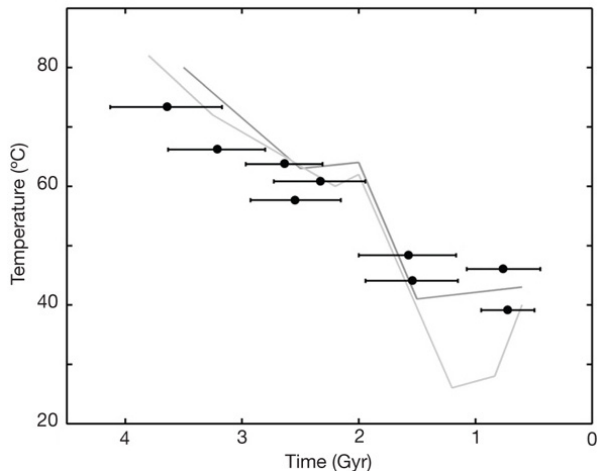
Proteins

Di Giulio 2003, Brooks *et al.* 2004:

hyperthermophilic LUCA

Gaucher *et al.* 2003, 2008:

hyperthermophilic bacterial ancestor



Gaucher *et al.* observe a decrease in optimal growth temperatures from the ancestor of Bacteria to extant organisms.

Ribosomal RNA

Galtier *et al.*, 1999:

non-hyperthermophilic LUCA

Proteins

Di Giulio 2003, Brooks *et al.* 2004:

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Ancestral sequence reconstructions

Ribosomal RNA

Galtier *et al.*, 1999:

non-hyperthermophilic LUCA

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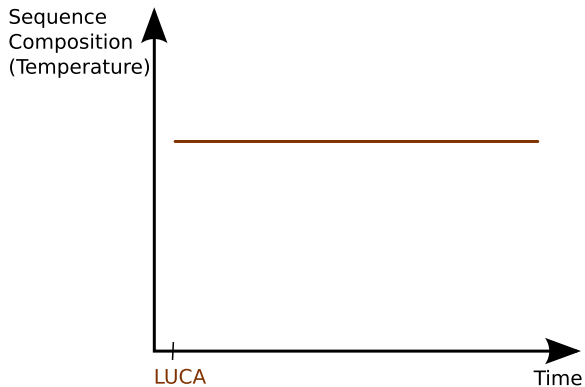
hyperthermophilic bacterial ancestor

Differences

Non-homogeneous model of evolution

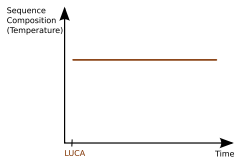
Homogeneous or non-stationary models of evolution

Models of sequence evolution

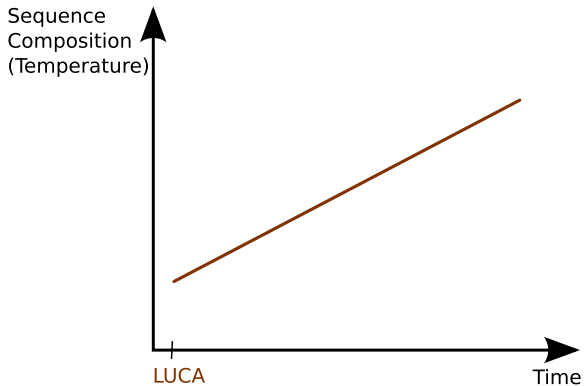


Homogeneous model

Models of sequence evolution

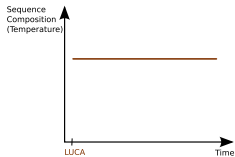


Homogeneous

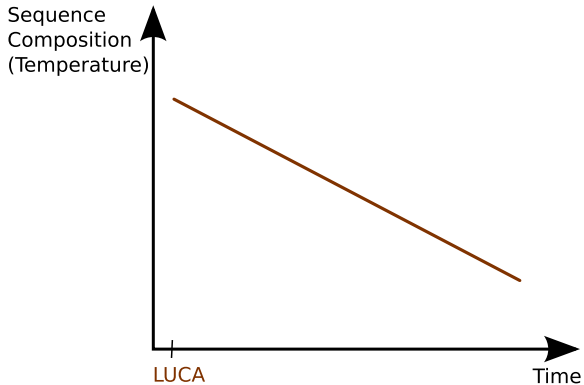


Non-stationary model

Models of sequence evolution

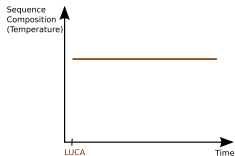


Homogeneous

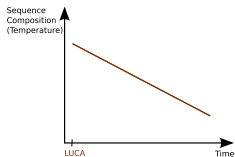


Non-stationary model

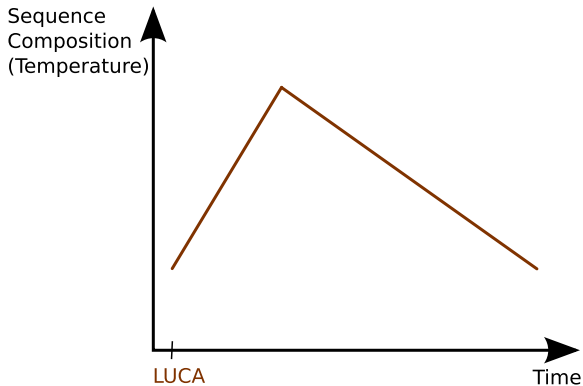
Models of sequence evolution



Homogeneous



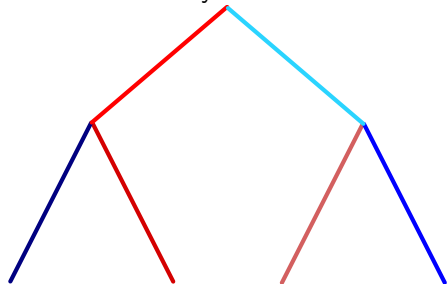
Non-stationary



Non-homogeneous model

Ribosomal RNA

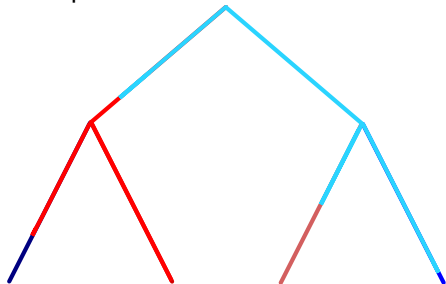
Galtier and Gouy 1998 model



- SSU + LSU genes, stems only
- 456 species
- 1043 sites

Proteins

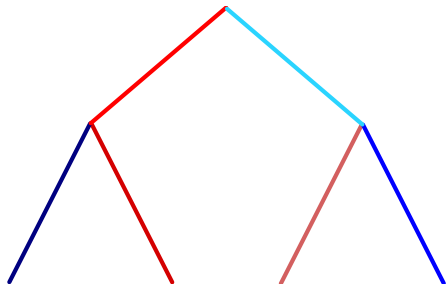
Blanquart and Lartillot 2008 model



- 56 concatenated genes
- 30 species
- 3336 ungapped sites

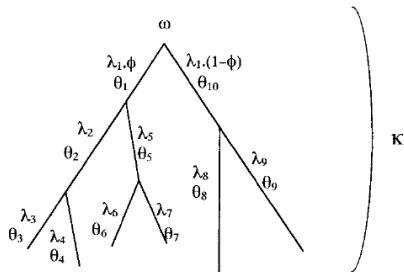
rRNA evolution model: Galtier and Gouy model (1998)

Model

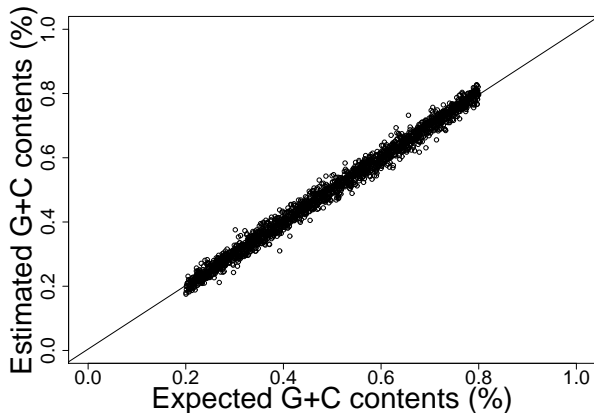


- 1 model per branch
- each model is characterized by an equilibrium G+C content

Parameters



parameters	symbol	number
ancestral G+C %	ω	1
branch lengths	λ_i	$2n - 3$
root location	ϕ	1
Ts/Tv ratio	κ	1
equilibrium G+C %	θ_i	$2n - 2$
		$4n - 2$



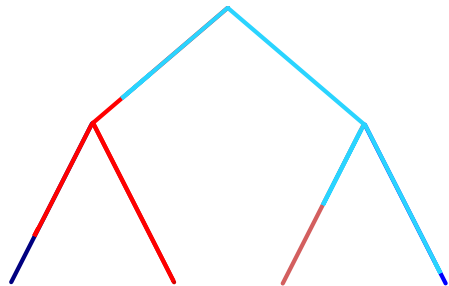
Boussau and Gouy, *Syst. Biol.* 2006.

CAT model



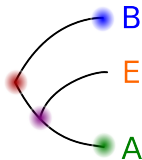
- Gamma model: mixture model over rates of evolution
- CAT model: mixture model over profiles of amino-acids

BP Model

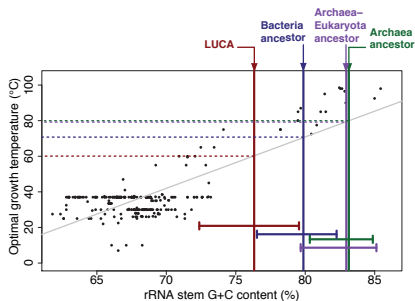


- Breakpoints between profiles are placed along the phylogeny according to a Poisson process.

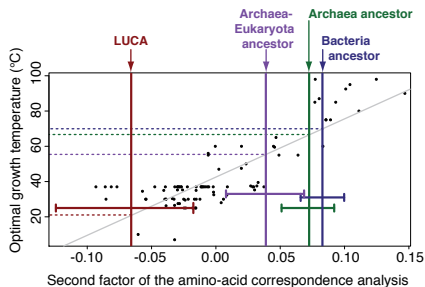
Blanquart and Lartillot, *Mol. Biol. Evol.*, 2008.



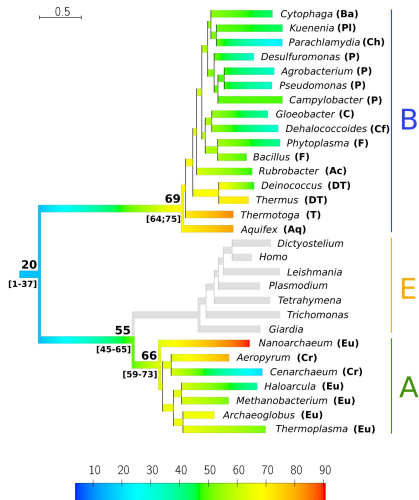
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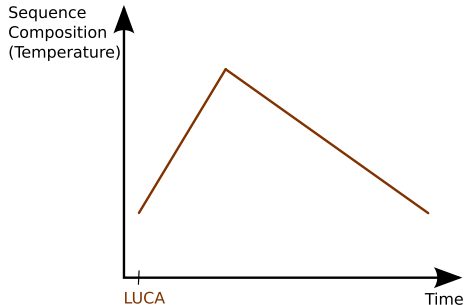
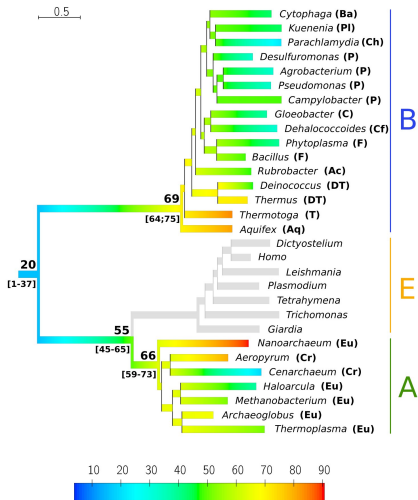
Proteins



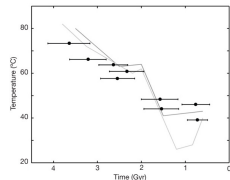
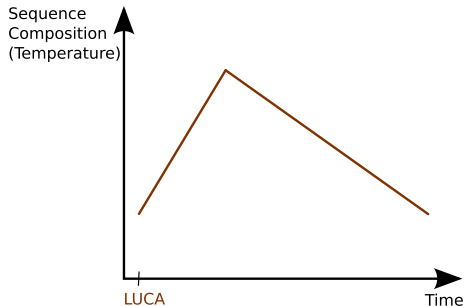
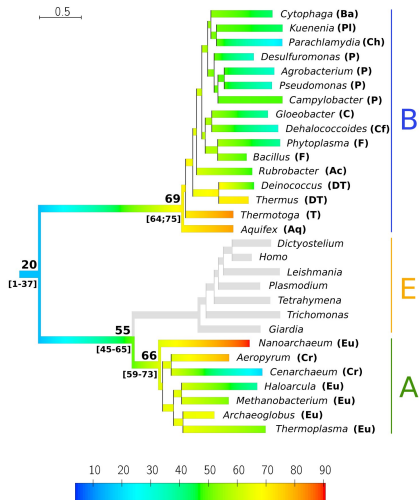
The evolution of Thermophily



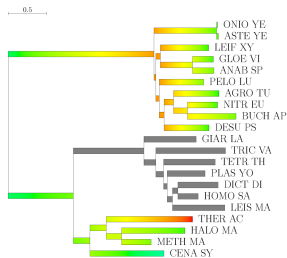
The evolution of Thermophily



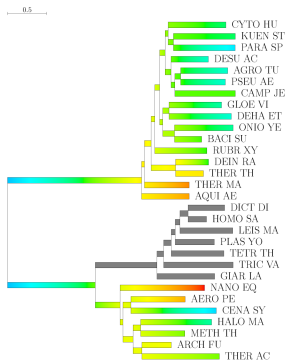
The evolution of Thermophily



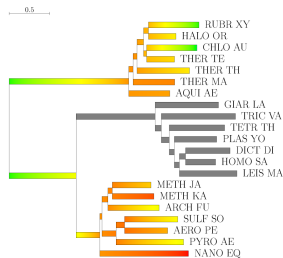
The evidence for parallel adaptations



Mesophilic

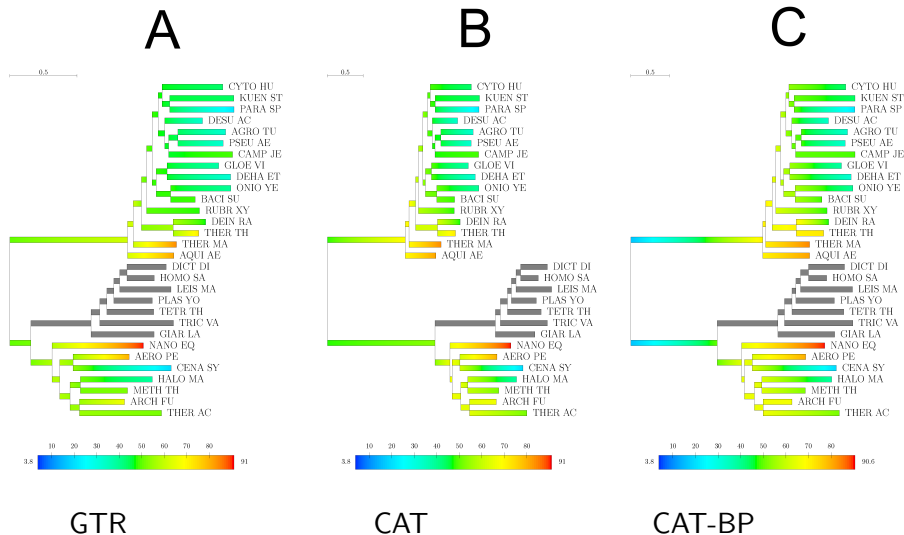


Normal



Thermophilic

The evidence for parallel adaptations: models



The evidence for parallel adaptations

- obtained in the Maximum Likelihood or Bayesian framework

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- obtained in the Maximum Likelihood or Bayesian framework
- obtained with rRNA and proteins

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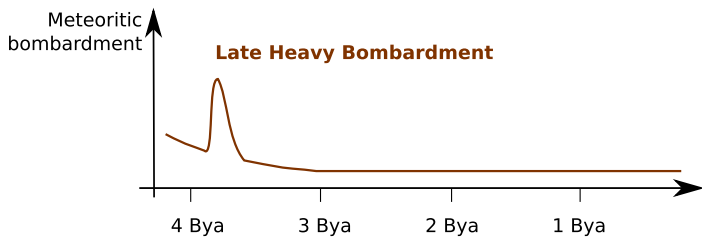
- obtained in the Maximum Likelihood or Bayesian framework
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- robust to changes in the topology
- robust to changes in taxonomic sampling
- robust to changes in prior distributions
- robust to the removal of fast-evolving rRNA sites

The evidence for parallel adaptations

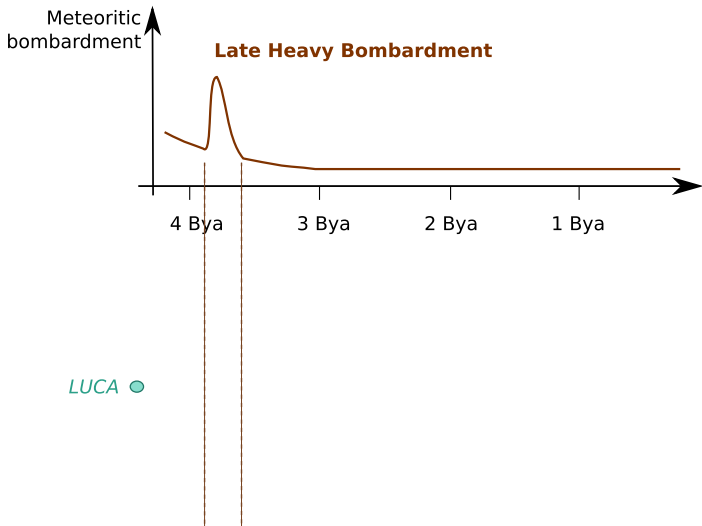
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- robust to changes in the topology
- robust to changes in taxonomic sampling
- robust to changes in prior distributions
- robust to the removal of fast-evolving rRNA sites
- robust to the removal of rare amino-acids

A pressure for parallel adaptations

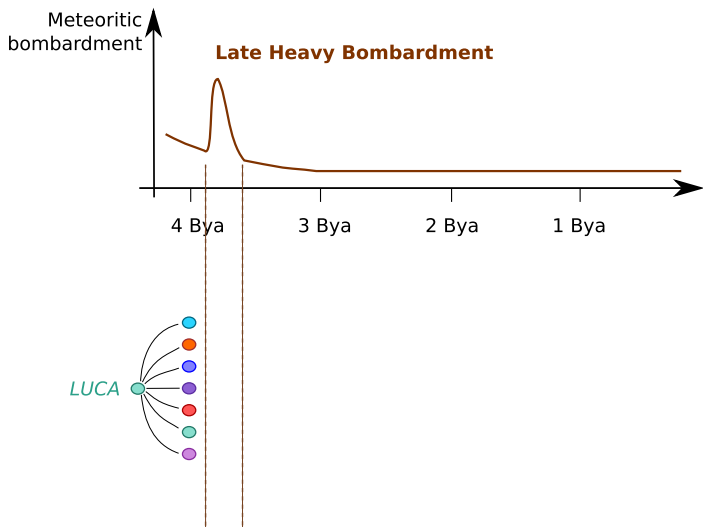
A pressure for parallel adaptations



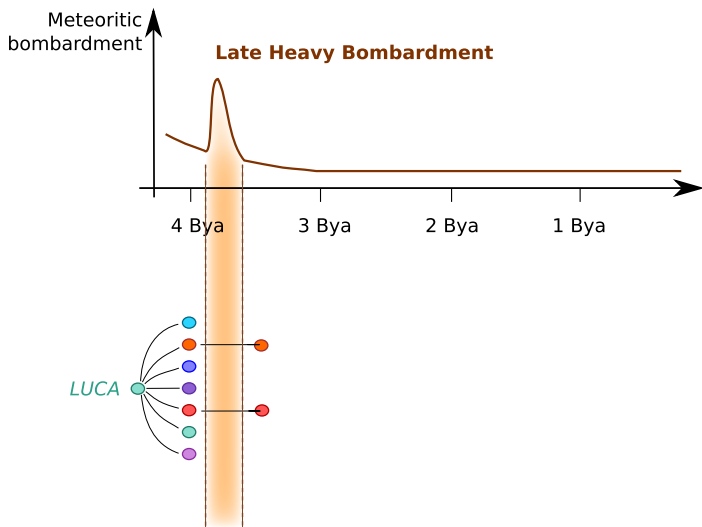
A pressure for parallel adaptations



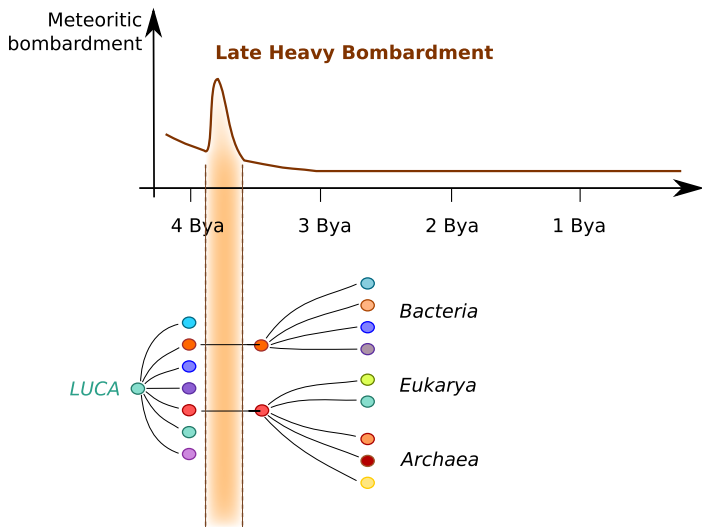
A means for parallel adaptations



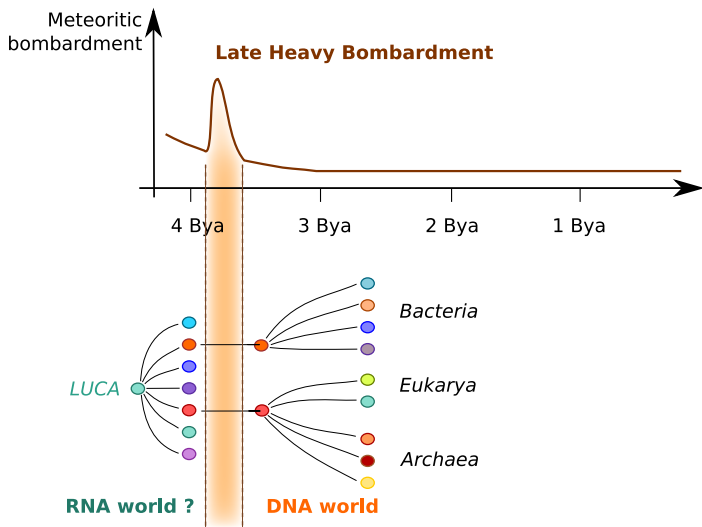
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A means for parallel adaptations



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- Only non-homogeneous models can faithfully reconstruct the evolution of sequence composition
- Non-homogeneous models find evidence for two phases in the history of thermophily:
 - first an increase from LUCA to its direct descendants
 - then a decrease from the bacterial ancestor to extant species
- Such a scenario is in agreement with several hypotheses concerning the early evolution of the Earth and of life

Authors

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Nicolas Lartillot, Manolo Gouy

*These authors contributed equally to this work.

Many thanks to...

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Antonio Lazcano, Mathilde Paris, and members of the BBE Laboratory.

1 Introduction

2 Materials and methods

3 Results

4 Interpretation

5 Conclusions

The evidence for parallel adaptations: roots

