Workshop: Phylogenetic approaches to diversification

Inferring evolutionary past from phylogenetic tree shapes

Center for interdisciplinary research in biology (CIRB) – Collège de France, Paris

October 22-23, 2012

Organizers: Amaury Lambert (CIRB and UPMC), Hélène Morlon (CNRS and Ecole Polytechnique)

Sponsors: SMILE, College de France, CNRS, CIRB

Conference venue: Collège de France, 11 place Marcelin Berthelot (see map below) – Salle 5

In the past few years, phylogenies have played an increasing role in our understanding of the way ecological and evolutionary processes generate biological diversity. The goal of the workshop is to foster interactions between theoreticians working on the development of phylogenetic inference methods and empiricists applying these methods to large datasets.

The workshop will consist in 15 invited talks of 40 minutes (including questions), starting at 8:30 on Monday, October 22, and finishing at 13:00 on Tuesday, October 23. There will also be a poster session on Monday (see list and abstracts below)

List of speakers

- Alexandre Antonelli (U. Gothenburg)
- Folmer Bokma (U. Umeå)
- Jérôme Chave (CNRS, U. Toulouse)
- Fabien Condamine (Ecole Polytechnique, Palaiseau)
- Emmanuel Douzery (U. Montpellier)
- Rampal S. Etienne (U. Groningen)
- Susanne Fritz (Bik-F, Francfort)
- Amaury Lambert (CIRB and UPMC Univ Paris 06)
- Alexander Pigot (EGI, U. Oxford)
- Susanne Renner (U. Munich)
- James Rosindell (Imperial College)
- Daniele Silvestro (U. Lausanne)
- Tanja Stadler (ETH Zürich)
- Mike Steel (U. Canterbury)
- Chris Venditti (U. Hull)
Tentative schedule and titles

Monday 22, morning

• 8:30 Registration
• 8:50 Introduction
• 9:00 Mike Steel  
  *What can the 'shape' of phylogenetic trees tell us about the processes of macro-evolution?*
• 9:40 Susanne Renner  
  *Ecological neutral theory and phylogenetics*
• 10:20 Rampal S. Etienne  
  *A conceptual and statistical framework for adaptive radiations*
• 11:00 Coffee break
• 11:30 Alexandre Antonelli  
  *An integrated framework for inferring the evolution of species-rich biomes*
• 12:10 Amaury Lambert  
  *Coalescent point processes for stochastic models of phylogenies*

Monday 22, afternoon

• 14:30 Folmer Bokma  
  *Null models of lineage diversification*
• 15:10 Jérôme Chave  
  *Some random thoughts on ecology, phylogenies and tropical forests*
• 15:50 Daniele Silvestro  
  *Bayesian inference of macroevolutionary processes using the fossil record*
• 16:30 Poster session
• 17:10 Emmanuel Douzery  
  *From genomes to time-calibrated trees: The case of mammalian phylogenetics*
• 17:50 Chris Venditti  
  *The evolutionary sources of organismic diversity*

Tuesday 23, morning

• 9:00 Tanja Stadler  
  *Phylogenetics in action: Uncovering population dynamics based on molecular sequence data*
• 9:40 Susanne Fritz  
  *Macroevolution and macroecology of birds, mammals and amphibians – investigating biodiversity patterns in space and time*
• 10:20 Alexander Pigot  
  *The geography of species diversification*
• 11:00 Coffee break
• 11:30 Fabien Condamine  
  *How does temperature influence diversification? Testing the effect of Cenozoic paleotemperatures on the diversification of plants and animals*
• 12:10 James Rosindell  
  *A new way to visualise the tree of life*
• 13:00 Lunch with Paris views
Posters

Authors and titles

- **Krzysztof Bartoszek** (Chalmers U., Gothenburg)
  *Conditioned branching processes and phenotype evolution*

- **Florian Boucher** (U. Grenoble)
  *Neutral biogeography and the evolution of climatic niches*

- **Kyle G. Dexter** (U. Leeds)
  *Correlates of diversification in South American trees*

- **Karolina Doan** (U. Warsaw)
  *Phylogenetic analyses of the Pleistocene red deer (Cervus elaphus)*

- **Alvaro Dugo Cota** (CSIC, Seville)
  *Correlates of the molecular evolution in glass‐frogs: A comparative study*

- **Fanny Gascuel** (ENS, SMILE)
  *The effects of archipelago spatial structure on the biodiversity patterns predicted by neutral models*

- **Magdalena Gonciarz** (U. Warsaw)
  *Genetic analyses of northern pike (Esox lucius), pike perch (Sander lucioperca) and eelgrass (Zostera marina) populations in order to perform their conservation*

- **Renske Gudde** (U. Hull)
  *Exploring sexual size dimorphism in mammals*

- **Matthew Helmus** (Vrije U.)
  *Anole Anthropocene island biogeography*

- **Arnaud Le Rouzic** (CNRS)
  *Inferring the dynamics of genome evolution from phylogenies of repeated sequences*

- **Öncü Maracı** (Bogaziçi U.)
  *Genetic structure of harbour porpoise (Phocoena phocoena) in the Turkish seas*

- **Matt Pennell**
  *TBA*

- **Elisabeth Reyes** (U. Paris-Sud)
  *Presence in Mediterranean hostspots but not floral symmetry affect speciation and extinction rates in Proteaceae*

- **Jonathan Rolland** (Ecole Polytechnique)
  *The latitudinal gradient of diversification rates in mammals*

- **Cristina Roquet** (U. Grenoble)
  *Endemic alpine plants: An evolutionary perspective*

- **Martin Ryberg** (Uppsala U.)
  *Two software packages for estimating and comparing species diversification rates and the diversification rates of ectomycorrhizal Agaricales (Basidiomycetes)*

- **Jeanne Tonnabel** (U. Montpellier)
  *Relationship between life-history traits and environmental niche optima in the Leucadendron genus*

- **Eugenia Zarza** (Bik-Francfort)
  *Prior information as a tool for biogeographical and paleoclimatic hypothesis comparison in a Bayesian framework*
Abstracts of posters

- **Krzysztof Bartoszek** (Chalmers U., Gothenburg)
  
  *Conditioned branching processes and phenotype evolution*

  **Abstract.** Conditioned branching processes have recently received a lot of attention in the biomathematical literature. They are useful for modelling and developing software in the field of phylogenetic tree inference. However on top of this they can also be combined with continuous stochastic processes to describe the evolution of character traits without the need to use a fixed phylogeny. This makes them an appealing tool for the field of phylogenetic comparative methods where often there can be great uncertainty attached to the underlying evolutionary relationships. By using them we can predict how much we expect species to diverge (in the trait of interest) and include uncertainty due to phylogeny in our conclusions. Morphological characteristics are an important factor in the field of systematics, for example for the delimitation of species, and therefore the framework of phylogenetic comparative models on top of branching processes offers an attractive application of stochastics in biology.

- **Florian Boucher** (U. Grenoble)
  
  *Neutral biogeography and the evolution of climatic niches*

  **Abstract.** Climatic niche evolution has turned into an important issue in biogeography for addressing many questions related to past, present and future species distributions. To date, most macroevolutionary studies have used Brownian Motion (BM) as a null model for climatic niche evolution, either explicitly or implicitly. BM has been brought to phylogenetics in order to model macroevolutionary drift in continuous traits but might not be suited for climatic niches since they are not individual traits and are tightly linked to geography. In contrast, neutral biodiversity theory (NBT) could provide valuable insights into the study of climatic niche evolution since it explicitly takes into account the spatial structure of species ranges. Here, we compare neutral models of macroevolution (BM) to neutral models of biogeography (NBT) and show that they produce very different outcomes. In particular, gradual evolution should not be the null expectation for the evolution climatic niches. Furthermore, our model shows that the inherent geographic boundaries of continents can generate apparent signatures of phylogenetic niche conservatism, as depicted by macroevolutionary models of stabilizing selection. We thus suggest that testing the fit of alternative macroevolutionary models on an entire clade may constitute a poor test of climatic niche conservatism. Biological traits should rather be included in macroevolutionary studies of climatic niche evolution in order to properly identify the drivers of climatic niche evolution.

- **Kyle G. Dexter** (U. Leeds)
  
  *Correlates of diversification in South American trees*

  **Abstract.** This poster describes a project just getting underway that has, among its principal goals, an assessment of the correlates of diversification in South American trees. We are using tree plot and environmental data to quantify the ecological niche of most woody angiosperm genera and woody legume species in lowland tropical South America for diverse niche axes, primarily edaphic and climatic. We are uniting this data with DNA-sequence-based, temporally calibrated molecular phylogenies that are sampled at the genus level for all woody angiosperms and at the species level for Leguminosae. Using this data, we will be able to assess variation in diversification rates across the angiosperm phylogeny and how they relate to rates of evolution and niche disparification within clades. The analyses of Leguminosae will allow us to assess if results from the broader genus-level work are consistent with those obtained at lower phylogenetic levels. The aim of this poster is to obtain feedback on the project in its beginning phases.

- **Karolina Doan** (U. Warsaw)
  
  *Phylogenetic analyses of the Pleistocene red deer (Cervus elaphus)*

  **Abstract.** Analyses of mitochondrial DNA sequences of contemporary red deer populations show that this species can be divided into two major geographically separated groups (Western and Eastern). Western red deer group inhabits Europe, Middle East and Africa while Eastern group is present in Asia and North America. This observed phylogeographic pattern is probably caused by climatic and environmental changes during Pleistocene. Analyses of ancient DNA from Crimean
red deer samples, dated to the late Pleistocene were performed. The aim of this study was to investigate phylogenetic position and the migration routes of the Pleistocene red deer. The whole mitochondrial cytochrome b sequence of 16 individuals was amplified by multiplex PCR. Obtained sequences were used to build phylogenetic tree by Bayesian MCMC analysis implemented in BEAST software. Phylogenetic analyses show that during Late Pleistocene Crimean Peninsula was inhabited by specimens belonging to both Western and Eastern red deer group. Obtained results suggest that Crimea served as a Pleistocene refugium for European and Asian red deer’s populations.

- **Alvaro Dugo Cota** (CSIC, Seville)
  
  *Correlates of the molecular evolution in glass-frogs: A comparative study*

**Abstract.** Understanding the factors that affect the rate of molecular evolution is essential for evolutionary biology. Recent studies reject the “molecular clock” hypothesis and suggest that body size, population size or environmental factors (e.g. climate) are associated with the rate of molecular evolution. In this study we analyzed the influence of body size, altitude, latitude, temperature, range size and speciation events on the rate of molecular evolution, estimated by the substitution rate and the ratio of non-synonymous to synonymous substitutions ($\omega$) in mitochondrial and nuclear genes using a “whole-tree” approach. We focused on glass-frogs (Centrolenidae), which present high diversity in habitat, range size and body size. The results do not support an association between body size or latitude and the rate of molecular evolution. In contrast, altitude is significantly negatively associated with substitution rate in mitochondrial non-coding genes and positively with $\omega$ in nuclear genes. Moreover, the number of speciation events and temperature were positively correlated with substitution rate in mitochondrial genes. Finally, range size was positively correlated with substitution rate of nuclear genes. We propose that metabolic rate and species’ demographic histories are potential explanations for these associations. Smaller population sizes, fluctuations in population size and higher metabolic rate promote evolutionary change, although the effect differs between mitochondrial and nuclear genes, being greater in the former probably due to its reduced effective population size and/or higher mutation rate.

- **Fanny Gascuel** (ENS, SMILE)
  
  *The effects of archipelago spatial structure on the biodiversity patterns predicted by neutral models*

**Abstract.** MacArthur and Wilson’s Theory of Island Biogeography (1967) and Hubbell’s Neutral Theory (2001) revolutionized ecology with their ability to predict, through assumptions of ecological equivalence and processes of stochastic demography, speciation and dispersion, a certain number of insular biodiversity patterns. These theories, and some more recent developments, have highlighted the role of geographic configuration, particularly of island area and distance to the mainland, in structuring insular communities. However, despite a new emphasis on spatially-explicit neutral models, the complex spatial arrangements of real archipelagos have received little attention, with island systems typically modeled as simple one-dimension systems of a single island and one mainland. Here, we investigate whether modeling the spatial structure of archipelagos modifies the predictions of biodiversity patterns made by a classical spatially-explicit neutral model. First, and building on recent methods for simulating communities (coalescence algorithms, protracted speciation), we propose a methodology for generating more realistic spatially-explicit models. Secondly, we demonstrate that accounting for different components of spatial structure (including intra-archipelago connectivity, island internal structure, island shape, and archipelago structure) substantially changes the predictions of species richness and endemism on islands, both quantitatively and qualitatively. This reflects the effect of spatial structure on the processes of colonization, extinction and speciation (due to stepping-stone effects, fragmentation effects and to differentiation between and within islands). This study therefore demonstrates the importance of better accounting for the spatial structure of communities for understanding biodiversity patterns.

- **Magdalena Gonciarz** (U. Warsaw)
  
  *Genetic analyses of northern pike (Esox lucius), pike perch (Sander lucioperca) and eelgrass (Zostera marina) populations in order to perform their conservation*

**Abstract.** During the 1960s the ecological condition of the Polish Baltic Sea coast– the interior
Puck Bay – remained in equilibrium. This reservoir was an important habitat for plants - macrofits, forming underwater meadows, which represent a spawning and feeding grounds of many fish species. Among them, the most important ecologically as well as economically are predator fish – northern pike (Esox lucius) and pike perch (Sander lucioperca). However, the increasing economic and turistic exploitation of this area in the 1990s, brought highly negative effects: devastation of the underwater meadows and reduction of the ichtiofauna population size. In the same time, invasive fish species such as round goby (Neogobius melanostomus; foreign origin) and stickleback (Gasterosteus aculeatus; native) went through a demographic expansion. Therefore a necessity for a complex ecosystem reconstruction arose. One of the major elements of this process is the restoration of northern pike, pike perch as well as eelgrass (Zostera marina) populations. Previous ecological and genetic studies, indicated the existence of tree reproductively isolated groups in both the fish species: fresh water, migrative and brackish water. The main idea of the research are genetic analyses of northern pike and pike perch populations from the Puck Bay, adapted to live in brackish water. Later genetic studies are crucial for the identification of the most appropriate source population for the stocking purposes. Genetic analyses are based on neutral variation of microsatellite loci and sequences of mitochondrial DNA obtained from contemporary and historical samples from the 1960s. In case of eelgrass microsatellite and AFLP markers variation will be obtained. The results should reveal which European population of this plant is genetically the closest to the Polish population. In practice, this knowledge will be used as a base for selecting an optimal method for restoration of the Polish eelgrass. To evaluate the success of the restoration program, a continuous genetic monitoring will be performed.

- **Renske Gudde** (U. Hull)
  *Exploring sexual size dimorphism in mammals*

**Abstract.** The drive for sexual size dimorphism has puzzled evolutionary biologists for decades. Previous studies suggest that male-male competition for mating opportunities and the possession of resources drives towards bigger males. Females have to keep up with this growth, in order to give birth to larger offspring. The reason that females are often smaller than males is thought to be caused by fecundity selection: the trade-off between growth and reproduction. A new method to study the pattern of life history trait evolution can explain how male and female body mass have evolved over time. Preliminary results suggest this is a valuable method to explore sexual size dimorphism.

- **Matthew Helmus** (Vrije U.)
  *Anole Anthropocene island biogeography*

**Abstract.** The number of species on oceanic islands is hypothesized to be dependent on island area and isolation. Isolated islands have fewer species than proximate islands and large islands have more species than small islands. Genetic patterns among species of island organisms thus reflect the influence of area and isolation on speciation. However, with human spread of exotic species, it is unknown how well area and isolation still determine island biogeography. Here we compile an exhaustive list of past and present Anolis lizard diversity across Caribbean islands and show that the processes that determine natural anole island biogeography are intact, but exist in an altered state. Island area and isolation strongly affected natural colonization and speciation—larger islands received more colonists, had higher in situ speciation, and sent more colonists than smaller islands; and proximate islands exchanged more colonists than isolated islands. However, opposite to native richness, exotic richness positively correlated with isolation. This decreased the importance of isolation in determining present-day biogeography by 70% compared to the past. In contrast, the overall effect of area increased by 30%. Similar to global-scale anthropogenic impacts, the number of established exotic anoles in the Caribbean follows a temporal trend of an initially slow rise up to WWII, and then a great acceleration in the rate of establishment. Establishment success of colonizing exotics was higher when exotic and native anoles were ecologically distinct, but as important was an ability to thrive in anthropogenic habitats like tourist resorts. While humans are leaving a lasting impact on the biological record of oceanic islands, this impact can be understood in the context of natural biogeographic and ecological principles that govern organism dispersal, population growth, and speciation.
**Arnaud Le Rouzic** (CNRS)

*Inferring the dynamics of genome evolution from phylogenies of repeated sequences*

**Abstract.** The genome of most eukaryotes contains a large amount of repeated sequences. DNA repetitions arise through various processes (including segmental duplications, recombination, polyploidization, or transposition), which generate two or more identical copies of an original DNA sequence. The resulting sequences evolve independently, accumulating mutations with time. It thus becomes possible to align and reconstruct the phylogeny of a family of homologous repeated sequences from a single fully sequenced genome. The branching pattern of this tree reflects the evolutionary dynamics of the genome, and can be analyzed with the methodological tools developed for understanding diversification patterns from species trees, speciations and extinctions being interpreted as duplications and deletions. We focused on transposable elements, a widespread, virtually universal class of repeated sequences. Transposable elements are parasitic, selfish DNA sequences, and their copy number depends on a complex transposition - deletion balance which evolutionary pattern is not well understood. From the genome of *Fusarium oxysporum*, a recently sequenced filamentous fungus, we analyzed four sub-families of transposable elements. Our results highlight important differences in the evolutionary histories of these four elements: two of them appear to be compatible with a constant birth-death process, one shows an increase in the transposition rate, and the last one a drop in transposition activity. Hence, phylogenetic inference methods combined to new-generation sequence data provide powerful tools for a better understanding of the evolutionary dynamics of genome structure.

**Öncü Maracı** (Bogaziçi U.)

*Genetic structure of harbour porpoise (Phocoena phocoena) in the Turkish seas*

**Abstract.** Mitochondrial DNA sequences of three individuals of the harbour porpoise (Phocoena phocoena) sampled in the Black Sea, Marmara Sea and Aegean Sea, revealed three polymorphic sites, resulting in three different haplotypes. None of the haplotypes obtained in this study clustered with those in the Atlantic populations, consistent with previous findings. The Black Sea and the Aegean haplotypes sequenced in this study had been previously detected from the Ukraine coast of the Black Sea, supporting the idea that harbour porpoises from the Black Sea dispersed into the northern Aegean through the Istanbul and Çanakkale Straits. The third sample from the Marmara Sea had the same unique haplotype as the one found in three individuals from the same sea in an earlier study. This structuring supports the possibility of an isolated population in the Marmara Sea. It should also be noted that this is the first genetic study of the harbour porpoise, in which a sample from the Turkish coast of the Northern Aegean Sea was studied.

**Matt Pennell**

*TBA*

**Abstract.**

**Elisabeth Reyes** (U. Paris-Sud)

*Presence in Mediterranean hostspots but not floral symmetry affect speciation and extinction rates in Proteaceae*

**Abstract.** Proteaceae is a large angiosperm family with both species-rich and species-poor genera. This study aimed at testing if differences in speciation and/or extinction rates explain these variations in species richness across the family and, if they do, whether these differences are linked to the presence in biodiversity hotspots and floral symmetry. We investigated shifts in diversification rates in a dated phylogenetic tree establishing the relationships among all Proteaceae genera. Then, using character state dependent models of diversification ,we tested whether diversification rates depend on : 1) the biogeographical zones in which species were located, specifically biodiversity hotspots with a Mediterranean climate in which Proteaceae are more diverse than in the rest of their range ; and 2) floral symmetry (actinomorphy vs. zygomorphy). We detected 10 diversification rate shifts within Proteaceae, confirming that the tempo of diversification has not remained homogeneous across lineages. Speciation rates were inferred to be higher and extinction rates lower inside than outside Mediterranean hotspots, suggesting that the specific environmental conditions found in Mediterranean regions had a significant impact on
diversification in Proteaceae. Conversely, floral symmetry does not seem to have influenced
diversification in the family.

- **Jonathan Rolland** (Ecole Polytechnique)
  *The latitudinal gradient of diversification rates in mammals*

Abstract. The increase in species richness from the poles to the tropics, often referred to as the
latitudinal diversity gradient, is one of the most ubiquitous biodiversity patterns in the natural
world. While understanding how rates of speciation and extinction vary with latitude is central to
explaining this pattern, such analyses have been impeded by the difficulty of estimating
diversification rates associated with specific geographic locations. Here, we use biogeographical
models of diversification and a nearly complete phylogeny of mammals to estimate speciation and
extinction rates associated with the tropical and temperate biomes. Overall, we found that speciation
rates are higher, and extinction rates lower, in the tropics than temperate regions. The diversity of
the eight most specious mammalian orders (covering 92% of all mammals) peaks in the tropics,
except that of the Lagomorpha (hares, rabbits and pikas), which peaks in northern-temperate
regions. These peaks of diversity are explained by low extinction rates (Artiodactyla, Primates,
Lagomorpha and Carnivora), high speciation rates (Diprodontia and Soricomorpha), or both
(Chiroptera and Rodentia). On the whole, our results suggest that differences in diversification
rates, in particular extinction rates, have played a major role in shaping the striking latitudinal
diversity gradient of mammals we observe today.

- **Cristina Roquet** (U. Grenoble)
  *Endemic alpine plants: An evolutionary perspective*

Abstract. The European Alps are a rich mountain-biome with ca. 4500 vascular plant species, of
which about 350 are endemic. A vast number of these endemics are high mountain species living in
extremely harsh environmental conditions, constituting a sort of terrestrial island system. These
conditions have likely provided a repeated stimulus for local (and sometimes rapid) species
diversification; indeed, the proportion of endemic species increases with the altitudinal zonation in
the Alps. In this study, we aim to study the evolutionary origins of alpine endemic species to
enhance our understanding on how the alpine biome diversified. Using a dated genus-level
phylogeny for the entire plant taxa of the Alps, we show that endemics are phylogenetically
clustered and evolved rather recently; thus, diversification was probably enhanced by Pleistocene
climatic oscillations in the highly structured landscape of the Alps. Next step analyses will be
focused on delimitating which trait innovations have likely fueled possible repeated ecological
radiations in high alpine ecosystems of the Alpine Arc.

- **Martin Ryberg** (Uppsala U.)
  *Two software packages for estimating and comparing species diversification rates and the
diversification rates of ectomycorrhizal Agaricales (Basidiomycetes)*

Abstract. Two software packages are presented. DivBayes is a program to estimate diversification
rates from species richness and ages of a set of clades. SubT estimates diversification rates from
node heights within a clade. Both programs implement Bayesian statistics and provide the ability to
account for uncertainty in the ages of taxa in the underlying data. The utility of the programs are
demonstrated by comparing the diversification rates of ten lineages of ectomycorrhizal fungi within
the largest order of mushroom-forming fungi, the Agaricales. It is shown that both types of data
yield similar results and that diversification rates differ between clades.

- **Jeanne Tonnabel** (U. Montpellier)
  *Relationship between life-history traits and environmental niche optima in the
Leucadendron genus*

Abstract. In fire-prone environments, perennial plant species have developed a range of specific
adaptations to fire, which differ in the source of new recruits following fire events. Resprouting
species are characterized by the persistence of adult plants, which regenerate vegetatively from
protected buds. In contrast, other species that do not exhibit this capacity, called ‘obligate seeders’
are killed by fire. Populations of these ‘obligate seeders’ will only persist through seeds stored
either in the soil or in the canopy (serotiny). More specifically, serotiny refers to the retention of
seeds in closed fruits or cones within the crown for more than 1 year. Environmental conditions, and especially fire regime, (i.e. mean and variance of fire intervals) are supposed to have shaped these different adaptations to fire through evolutionary history. We investigate whether these life-history traits have played a role in the evolution of environmental niche optimas. Using robust methods that account for phylogenetic uncertainty, intraspecific variability of environmental requirements and different life-history evolution scenarios, we compare different models of niche evolution using the newly reconstructed phylogeny of the Leucadendron genus (Proteaceae). We show that both seed storage strategies and post-fire survival strategies were very labile across the evolutionary history of the Leucadendron genus. Models of quantitative trait evolution show that serotinous species have evolved niches with lower variances of fire intervals than species bearing underground seed banks.

- **Eugenia Zarza** (Bik-Francfort)

  *Prior information as a tool for biogeographical and paleoclimatic hypothesis comparison in a Bayesian framework*

**Abstract.** Inferring the impact of biogeographical and paleoclimatic events on diversification has been a central question in evolutionary biology. Here we offer a Bayesian approach for hypothesis comparison that takes advantage of prior information and that serves as an alternative to the traditional null-hypothesis testing method. The aim of this study is to explore if assigning constrained-age priors to nodes of interest in a time calibrated phylogeny would serve as a means for hypothesis comparison. These priors would be equivalent to scenarios for lineage origin under different hypotheses. From comparing the likelihood values of the competing hypotheses, modeled under different priors, we would be able to select the hypothesis that explains best the data and thus assign a level of confidence to evolutionary inferences. A simulation approach was taken to evaluate the performance of the proposed method and the power of indices for hypothesis selection (Akaike Information Criterion; Bayes Factors based on Harmonic Mean, Path Sampling and Stepping Stone). With our approach the correct hypothesis is selected at least 85% times. For a best performance, data sets with 3500-10000 bp sequences are required. The method is most reliable when competing hypothesis are not temporally too close. Indices for hypothesis comparison have similar performance.
A = place Marcelin Berthelot (dead end street, just walk a little further for main entrance of Collège de France)

Access by RER line B (St-Michel Notre-Dame or Luxembourg), by RER line C (St-Michel Notre-Dame), by metro line 10 (Cluny-La Sorbonne) or by metro line 4 (Odéon).
Restaurants

...Recommended by Amaury and Hélène:

<table>
<thead>
<tr>
<th>No.</th>
<th>Restaurant Name</th>
<th>Cuisine</th>
<th>Lunch Menu</th>
<th>Dinner Menu</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Le Prè Verre</td>
<td>French</td>
<td>Menu (lunch) 13,5€</td>
<td>Menu (dinner) 30€</td>
</tr>
<tr>
<td>1</td>
<td>La Rose du Sommerard</td>
<td>Asian</td>
<td>Menu from 8€</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Le Grenier de Notre-Dame</td>
<td>Vegetarian</td>
<td>Menu (lunch) 15,5€</td>
<td>Menu (dinner) 17,5€</td>
</tr>
<tr>
<td>4</td>
<td>Les fontaines</td>
<td>High-standard</td>
<td>Menu (dinner) 31€</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Tugalik</td>
<td>World healthy food</td>
<td>Menu (lunch) 15€</td>
<td>Menu (dinner) 27€</td>
</tr>
<tr>
<td>5</td>
<td>La Fourmi Ailée</td>
<td>French</td>
<td>15-20€</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>La Montagne sans Geneviève</td>
<td>French</td>
<td>15-20€</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>L'arbre à Cannelle</td>
<td>French (pies)</td>
<td>10-20€</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>La Petite Périgourdine</td>
<td>French</td>
<td>Menu (lunch) 13,5€</td>
<td>Menu (dinner) 18€</td>
</tr>
</tbody>
</table>

...Other suggestions close to Collège de France:

<table>
<thead>
<tr>
<th>No.</th>
<th>Restaurant Name</th>
<th>Cuisine</th>
<th>Lunch Menu</th>
<th>Dinner Menu</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Sumo</td>
<td>Japanese</td>
<td>Menu (lunch) 9-12€</td>
<td>Menu (dinner) 13-20€</td>
</tr>
<tr>
<td>8</td>
<td>Il Pescatore</td>
<td>Italian</td>
<td>15-30€</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>La petite Cún</td>
<td>Vietnamese</td>
<td>Menu (lunch) 11,5€</td>
<td>Menu (dinner) 15€</td>
</tr>
<tr>
<td>9</td>
<td>Bagdad Café</td>
<td>Lebanese</td>
<td>Menu 18-20€</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>La Méthode</td>
<td>Bistrot- French</td>
<td>Menu (lunch) 13,5€</td>
<td>Menu (dinner) 15€</td>
</tr>
<tr>
<td>9</td>
<td>Chez Jafaar</td>
<td>Tunisian</td>
<td>Menu (lunch) 12€</td>
<td>Menu (dinner) 15-18€</td>
</tr>
<tr>
<td>9</td>
<td>Café Cantante</td>
<td>Spanish</td>
<td>Menu (lunch) 14-16€</td>
<td>Menu (dinner) 31€</td>
</tr>
<tr>
<td>11</td>
<td>Bouillon des Colonies</td>
<td>World food</td>
<td>Menu (lunch) 14,5€</td>
<td>Menu (dinner) 24,5€</td>
</tr>
</tbody>
</table>

... And also:
Plenty of other restaurants in the colored zones on the map! (see overleaf)
5 Sandwiches...

1 Restaurants
(see list overleaf)

Lots of other restaurants...