

**Elucidating the proximal origin of SARS-CoV-2  
using molecular evolution**  
*Open Research Engineer position, Paris*

We are recruiting a “Research Engineer” (with a scientific PhD) in bioinformatics and molecular evolution for 1 year, with possible renewal of 1 year.

The last intermediate step between a non-human animal virus and the current human SARS-CoV-2 is still a major enigma. More precisely, i) the evolution from the ancestral (very likely bat) virus to the human strain, ii) the transport from tropical Yunnan bat caves to Wuhan more than 1000 km away, and iii) the contamination of the first human, are three distinct aspects of the proximal origin on which we have little to no information. Each aspect could, in various proportions, result from contributions due to natural, accidental or intentional mechanisms. Determining these contributions requires an observation-based scientific approach free of a priori.

We propose a state-of-the-art analysis of the available sequences of SARS-CoV-2 and related viruses, to examine whether the identity of the virus (bat-adapted/human-adapted, natural/artificial) has changed across generations. The expected outputs of this work are not only scientific publication(s), but more importantly scientific insights on the origin of the ongoing pandemic and therefore hints on how to prevent a future pandemic.

The work will be organized in order to develop open science bioinformatic tools in order to allow the inclusion of new sequence data in the analysis when available. We will investigate both small-scale and large-scale changes: synonymous and non-synonymous mutations, insertions/deletions of small or large sequence pieces, and finally recombinations of fragments from different viruses, as recombination is a key mechanism of coronavirus evolution.

The recruited engineer will share her/his working time between the Université de Paris main Campus (V. Courtier; IJM and F. Graner, MSC) and the Collège de France (G. Achaz, CIRB). She/he will benefit from further expertise through the regular inputs of a larger group of scientists discussing this question in weekly meetings. She/he will develop and apply bioinformatics tools to perform an in-depth molecular evolution analysis of the relevant accessible SARS viral genomes.

The ideal candidate (1) will be familiar with concepts of molecular evolution (*i.e.* phylogeny, detection of recombination, ratio of non-synonymous/synonymous mutations, codon usage, etc.) and (2) will have skills in computer programming (e.g. python 3, R and/or C language).

Salary: around 2 500€ /month with taxes (~1 925 € after taxes). The exact salary will depend on the candidate’s experience.

Starting date: September 2021.

Application deadline: May 23<sup>th</sup> 2021. Later applications might be considered.

To apply, send a letter of motivation and a scientific CV to [virginie.courtier@ijm.fr](mailto:virginie.courtier@ijm.fr) and [guillaume.achaz@mnhn.fr](mailto:guillaume.achaz@mnhn.fr). Furthermore, at least one mentor of the candidate should send a letter of recommendation directly to the same addresses.