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Two postdoctoral positions on comparative transcriptomics to study the evolution of new genes

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We are looking to recruit two highly motivated researchers at the postdoctoral level to perform research on comparative genomics, transcriptomics and translomics with the goal to better understand the molecular basis of the evolution of new genes. The positions are funded by an ERC Advanced Grant (NovoGenePop) and will have an initial duration of three years.

Postdoc 1. The first position is to study transcriptome diversity in **wild and domesticated populations of yeast**. The researcher will develop computational approaches to analyze a large amount of RNA-seq and Ribo-seq data from different yeast strains and *Saccharomyces* species. She/he will characterize the transcriptomic diversity in different populations and identify recently evolved genes. Mutations and selective signatures associated with *de novo* gene birth will be identified using genomics data from a large number of strains.

Postdoc 2. The second position is to study transcriptome and protein diversity in **human and primate cells**. The researcher will develop methods to integrate and analyze RNA-seq and Ribo-seq data from lymphoblastoid cell lines (LCLs) and other cell types. Data from related mammalian species, including several primates, will also be generated and compared. The main goal of the project is to better understand the molecular processes underlying the formation of new genes in humans and primates.

Requirements (for both positions)

- Research experience in comparative genomics and transcriptomics
- Expertise in at least one programming language
- Expertise in a programmatic statistics language (ideally R)
- Sound knowledge of population genetics and molecular evolution
- Excellent verbal and written communication skills in English

Representative Publications:

Blevins, W.R., Ruiz-Orera, J., Messeguer, X., Blasco-Moreno, B., Villanueva-Cañas, J.L., Espinar, L., Díez, J., Carey, L.B., Albà, M.M. (2021). Uncovering de novo gene birth in yeast using deep transcriptomics. *Nature Communications*, vol. 12: 604.

Reixachs-Solé, M., Ruiz-Orera, J., Albà, M.M., Eyraçs, E. (2020) Ribosome profiling at isoform level reveals evolutionary conserved impacts of differential splicing on the proteome. *Nature Communications*, vol. 11: 1768.

Ruiz-Orera, J., Grau-Verdaguer, P., Villanueva-Cañas, J-L., Messeguer, X., Albà, M.M. (2018) Translation of neutrally evolving peptides provides a basis for *de novo* gene evolution. *Nature Ecology and Evolution*, vol. 2: 890 - 896.

Ruiz-Orera, J., Hernández-Rodríguez, J., Chiva, C., Sabidó, E., Kondova, I., Bontrop, R., Marqués-Bonet, T., Albà, M.M. (2015). Origins of de novo genes in human and chimpanzee. *Plos Genetics*, vol 11: e1005721.

Location: We are located at the Barcelona Biomedical Research Park (PRBB), one of the most vibrant interdisciplinary research centers in Southern Europe with more than 1000 scientists in the building alone, including a large bioinformatics and evolutionary biology community. The researchers will have access to state-of-the-art computational resources and a wide range of training opportunities.

Starting date and salary: Flexible starting date but ideally between Oct 1st 2022 and February 1st 2023. Salary 34,636-40,531 Eur per year depending on experience.

Contact: Please send an email to Mar Albà (malba@imim.es) with subject "PostdocERC" including a CV and a motivation letter, together with the name of two contacts for references. The deadline for the first round of applications is the 15th of July 2022.