

# Hector Roux de Bézieux

2615 California Avenue – Berkeley, CA 94703

+1 (510) 345-9460 • +33 (0)679215150

✉ hector.rouxdebezieux@gmail.com •   

## Education

### Ph.D in Biostatistics

University of California, Berkeley, USA

Dissertation adviser: Sandrine Dudoit, GPA 4.0

2017 - 2021 (expected)

Degree Emphasis in Computational Biology

- Conceived and implemented machine-learning methods and software for genomic data analyses. Publications include:
  1. **Roux de Bézieux, H.**, Van den Berge, K., Street, K. Dudoit, S. (2021). [Trajectory inference across multiple conditions with condiments: differential topology, progression, differentiation, and expression](#). *BioRxiv*
  2. Van den Berge, K., **Roux de Bézieux, H.**, ... Dudoit, S., Clement, L. (2020). [Trajectory-based differential expression analysis for single-cell sequencing data](#). *Nature Communications*, 11(1), 1201.
- Collaborated with applied biology teams to design experiments and analyze genomic data, including on:
  1. Brann, D. H., ... **Roux de Bézieux, H.**, ... (2020). [Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia](#). *Science Advances*, eabc5801.
  2. Yao, Z., Liu, ... **Roux de Bézieux, H.**, ... (2020). [An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types](#). *BioRxiv*

### Master of Science in Biology & Bioengineering

École polytechnique and UC Berkeley

Fung Institute Fellowship, Outstanding Investment Award, GPA 3.86

2015 - 2017

- Designed and conducted experiments for bacteriophage discovery in the context of antibiotic-resistant bacteria in a year-long project with *SmartPhage*, a UC Berkeley-based start-up.

### Bachelor of Science in Mathematics & Physics

École polytechnique, France

Received with rank 1/4,500 at the national entry exam, GPA 3.94

2011-2015

## Experience

### Pendulum Therapeutics

San Francisco, USA

Computational Biologist

June 2018 - Ongoing

- Analyzed clinical trial data and designed future clinical trial:  
**Roux de Bézieux, H.**, ... , Perraudon, F (2021) [A Pilot Medical Food Study using a Smartphone Application with Continuous Glucose Monitoring Sensors](#) *JMIR Form Res*
- Developed computational methods for the analysis of metagenomic datasets: **Roux de Bézieux, H.**, ... Jacob, L. (2020). [Finding All Significant Closed Connected Subgraphs](#). *Machine Learning in Computational Biology (MLCB)*

### Institut Jacques Monod, Cellular Adhesion and Mechanism Lab

Paris, France

Research Intern, Benoit Ladoux and René-Marc Mège's team

March–July 2016

- Designed and conducted *in vivo* experiments on protein-protein interactions.

### PSA Peugeot Citroën

Shanghai, China

Intern, Strategic Partnership Department

June–August 2015

### French Army, Elite Mountain Troop

France

2<sup>nd</sup> Lieutenant

September 2013– April 2014

- Led a group of 8 professional soldiers during a NATO exercise in great Northern Norway.

Related skills.....

- **Programming:** Python, Bash (Intermediate), Latex (Expert)  
Author of several open-source R packages, with over 5,000 downloads since 2020 on Bioconductor
- **Language:** English (fluent), French (native), German (intermediate)

Interests.....

**First Aid Certification by the Red Cross:** 2011, 2015 **Rowing:** 6 years at national level

**Triathlon:** 1000 miles annually, Ironman 70.3 (Santa Cruz, 2019)

## Publications

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- **Roux de Bézieux, H.**, Van den Berge, K., Street, K. Dudoit, S. (2021). [Trajectory inference across multiple conditions with condiments: differential topology, progression, differentiation, and expression.](#) *BioRxiv*
- **Roux de Bézieux, H.**, . . . , Perraudau, F (2021) [A Pilot Medical Food Study using a Smartphone Application with Continuous Glucose Monitoring Sensors.](#) *JMIR Form Res*
- Van den Berge, K., Chou, H. J., **Roux de Bézieux, H.**, . . . , Dudoit, S. (2021). [Normalization benchmark of ATAC-seq datasets shows the importance of accounting for GC-content effects.](#) *bioRxiv*.
- **Roux de Bézieux, H.**, . . . Jacob, L. (2020). [Finding All Significant Closed Connected Subgraphs.](#) *Machine Learning in Computational Biology (MLCB)*
- Brann, D. H., . . . **Roux de Bézieux, H.**, . . . (2020). [Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia.](#) *Science Advances*, eabc5801.
- Adkins, R. S., . . . **Roux de Bézieux, H.**, . . . (2020). [A multimodal cell census and atlas of the mammalian primary motor cortex.](#) *BioRxiv*.
- **Roux de Bézieux, H.**, Street, K. . . . Dudoit, S. (2020). [Improving replicability in single-cell RNA-Seq cell type discovery with Dune.](#) *BioRxiv*
- Yao, Z., Liu, . . . **Roux de Bézieux, H.**, . . . (2020). [An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types.](#) *BioRxiv*
- Van den Berge, K., **Roux de Bézieux, H.**, . . . Dudoit, S., Clement, L. (2020). [Trajectory-based differential expression analysis for single-cell sequencing data.](#) *Nature Communications*, 11(1), 1201.
- Croizat, G., Kehren, A., **Roux de Bézieux, H.**, Barakat, A. (2018). Influence of pulsatile blood flow on allometry of aortic wall shear stress. *arXiv*

## Talks

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<b>European Bioconductor Meeting 2020</b> <i>90mn workshop</i> Trajectory inference across conditions: differential expression and differential progression.	<b>Europe (Virtual)</b> <i>December 2020</i>
<b>BioC 2020</b> <i>60mn workshop</i> Trajectory inference across conditions: differential expression and differential progression.	<b>USA (Virtual)</b> <i>July 2020</i>
<b>JBIMS Data Sciences Workshop</b> <i>15mn Talk</i> Bacterial and metagenome GWAS	<b>Berkeley, California</b> <i>February 2020</i>
<b>Statistics and Genomics Seminar</b> <i>1h talk</i> Trajectory inference, Differential Expression and clustering along developmental trajectories in single cell RNA-Sequencing.	<b>Berkeley, California</b> <i>May 2019</i>
<b>Berkeley Stem Cell Center Retreat</b> <i>15mn talk</i> Unlocking the power of continuity in single cell RNA-Seq - Differential gene Expression along developmental trajectories.	<b>Monterey, California</b> <i>May 2019</i>
<b>FAST-BIG: Workshop on High-dimensional statistics</b> <i>30mn talk</i> Beyond DBGWAS: exploring assembly graphs in an efficient manner	<b>INRIA, Paris</b> <i>March 2019</i>