Nicolas **Comte**

PhD student – R&D engineer · Computer Science and modeling

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Experience

Inria (Grenoble-Alpes, team Morpheo), Anatoscope, Université Grenoble-Alpes

Grenoble, France

PhD student-R&D engineer — *2019 -*

- Collaboration between Inria (Grenoble-Alpes, team Morpheo), Anatoscope and Grenoble Hospitals
- PhD subject: Learning Scoliosis Patterns using Anatomical Models and Motion Capture
- Design of models, registration and analysis tools from imaging and motion capture data.

Inria (French Institute for Research in Computer Science and Automation)

Lyon, France

R&D engineer — *2016 - 2018 (2 years)*

- Creation of a new bioinformatics tool: Treerecs and contribution to existing softwares, especially Seaview, a multi-plateform and graphical user interface for bioinformatics.
- Integration and improvments of existing algorithms.
- Create tests, continuous integration.
- Co-supervision of interns on software design.
- Teaching programming at INSA Lyon (48 cumulated hours), Bioinformatics and modelling studies (third year).

INSA de Lyon • Inria • Soladis

Lyon, France

Internships — *2015-2016*

- 2016 (6 months): creation of a model for the artificial evolution platform Aevol at the Inria team Beagle.
- 2015 (4 months): design of a R package and writing of a book about R programming (180 pages) at Soladis.

Extracurricular Activity

Team INSA-Lyon, IGEM 2014 competition

Lyon, France ; Boston, USA

Bioinformatician R&D — *2014*

- The IGEM (for *International Genetically Engineered Machine*) is an international competition of synthetic biology organized in Boston. With our project Curly'on, we designed a bio-filter heavy-metals-specific which is created by genetically modified bacterias.
- Creation of simulation softwares, data analysis and modelling.
- Awards : *Gold Medal* and *Best Composite Part*

Formation

Université Grenobles Alpes

Grenoble, France

PhD in Computer Science — *2020-*

- Programming • Data sciences • Medical imaging • Anatomy • Biomechanics • Computer graphics

INSA Lyon

Lyon, France

INSA Engineer, Bioinformatics and modeling studies — *2013-2016*

- Programming • Data mining • Bioinformatics • Image processing • Statistics • Biomathematics (ODE, PDE, *etc.*) • Biology • Molecular biology

University of Lyon

Lyon, France

Bachelor in Biology, Mathematics and Computer Sciences for Life Sciences studies — *2010-2013*

- Bioinformatics • Programming • Statistics • Biomathematics • Biology • Molecular biology

Skills

languages	French (mother tongue), English (academic, toeic 895), Italian (notions)
Programming	C++, Python, Cython, SQL, Git
Scientific computing	Python, R, Matlab, SAS, ImageJ, Sofa
Communication	LaTeX, Beamer, HTML, Markdown, Inkscape, Gimp, Krita, Blender
Miscellaneous	Driving licence category B

Interests

Médiation scientifique chez DéMesures *Lyon, France*

Laboratory of young researchers for scientific popularization and communication. *October 2017 -*

- Projects of communication between scientists and artists: ArtScience 2018-2019 (Lyon, France)
- Scientific popularization events: "Fête de la Science" 2017 and 2018 (Villeurbanne, France) ; Geek Touch 2018 (Lyon, France)

Staff Scientific events *Lyon, France*

• R Meeting, 2013

• ECAL (*European Conference in Artificial Life*), 2017 *2013, 2017*

Other

Drawing, Digital Painting, photography, classical music

Honors

International

2014 **Gold Medal and Best Composite Part**, IGEM (for *International Genetically Engineered Machine competition*) *Boston, U.S.A*

Scientific contribution

Conferences

Aevol-4b: Toward a new simulation platform to benchmark phylogenetic tools

N. Comte, V. Liard, C. Knibbe & G. Beslon *2017*

ALPHY (ALignments and PHYlogeny)

A 4-base model for the Aevol in-silico experimental evolution platform

V. Liard, J. Rouzaud-Cornabas, N. Comte & G. Beslon *2017*

European Conference on Artificial Life

Publications

Seaview Version 5: A Multiplatform Software for Multiple SequenceAlignment, Molecular Phylogenetic Analyses, and Tree Reconciliation

M. Gouy, E. Tannier, N. Comte, D.P. Parsons *2021*

Multiple Sequence Alignment: Methods and Protocols, Springer Protocols

Treerecs: an integrated phylogenetic tool, from sequences to reconciliations

N. Comte, B. Morel, D. Hasic, L. Guéguen, B. Boussau, V. Daubin, S. Penel, C. Scornavacca, M. Gouy, A. Stamatakis, E. Tannier, D.P. Parsons *2020*

Bioinformatics

RecPhyloXML: a format for reconciled gene trees

W. Duchemin, G. Gence, A.-M. Arigon Chifolleau, L. Arvestad, M. S. Bansal, V. Berry, B. Boussau, F. Chevenet, N. Comte, A. A. Davín, C. Dessimoz, D. Dylus, D. Hasic, D. Mallo, R. Planel, D. Posada, C. Scornavacca, G. Szöllősi, L. Zhang, E. Tannier, V. Daubin *2018*

Bioinformatics