

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-platform and graphical user interface for bioinformatics.
- Integration and improvements 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 Grenoble Alpes

Grenoble, France

PHD IN COMPUTER SCIENCE

2020-

- Programming • Machine learning • 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 Sequence Alignment, 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.

2020

STAMATAKIS, E. TANNIER, D.P. PARSONS

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.

2018

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

Bioinformatics