

Nicolas Comte

PHD STUDENT - R&D ENGINEER · COMPUTER SCIENCE AND MODELING

☎ +33 675835060 | ✉ nicolas.comte1@gmail.com | 🏠 cometicon.github.io | 📄 nicolascomte

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).

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

Lyon, France

END-OF-STUDIES INTERNSHIP

February- July 2016 (6 months)

- Design and implementation of a new model of artificial life at Inria (team Beagle). More realistic and for Aevol, an open-source digital genetics platform that captures the evolutionary process using genetic algorithms and individual based modeling.

Soladis

Lyon, France

STATISTICAL PROGRAMMING, INTERNSHIP

April - July 2015 (4 months)

- Design and programming of an R *package* which allows the building of statistical reports.
- Wrote a manual for R programming (180 pages).

Extracurricular Activity

Team INSA-Lyon, IGEN 2014 competition

Lyon, France ; Boston, USA

BIOINFORMATICIAN R&D

2014

- The IGEN (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	TEX, 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.

2020

STAMATAKIS, E. TANNIER, D.P. PARSONS

Bioinformatics

RecPhyloXML: a format for reconciled gene trees

W. DUCHEMIN, G. GENGE, 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