Nicolas **Comte**

PhD – 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 - 2023*

- Research and industrial collaboration between Inria (Grenoble-Alpes, team Morpheo), Anatoscope and Grenoble Hospitals
- Thesis title: *Learning Scoliosis Patterns using Anatomical Models and Motion Capture*
- Development of new methods for analyzing spinal deformations through 3D imaging and motion capture.
- Involvement in industrial projects in anatomical simulations and reconstructions.

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

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

- Creation of Treerecs and contribution to Seaview, a multi-plateform and graphical user interface for bioinformatics.
- Integration and improvments of existing algorithms.
- Implementation of 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 Lyon • Inria • Soladis   *Lyon (France)*

Internships   *2015-2016*

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

Team INSA-Lyon, IGEM 2014 competition   *Lyon (France) ; Boston (USA)*

Computational biologist   *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 generated by genetically modified bacteria.
- Creation of simulation tools, data analysis and modelling of molecular interactions. See our project Curly'On.
- Awards : *Gold Medal* and *Best Composite Part*

Formation

Université Grenobles Alpes   *Grenoble (France)*

Ph.D in Computer Science   *2020-2023*

- Programming • Machine learning • Medical imaging • Anatomical simulation • Biomechanics • Computer vision and graphics

INSA Lyon   *Lyon (France)*

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

- Programming • Data mining • Computational biology • Image processing • Statistics • Biology

University de Lyon   *Lyon (France)*

Bachelor in Computational Biology   *2010-2013*

- Bioinformatics • Programming • Statistics • Mathematical modeling • Biology

Skills

Programming	C++, Python, Cython, Sofa, R, SAS, SQL, Git
Computer sciences	Deep learning, Computer vision, Computer graphics, Statistics, Anatomical simulation, Computational biology
Communication	LaTeX, HTML, Markdown, Inkscape, Gimp, Krita, Blender
Miscellaneous	Driving licence category B
Languages	French (mother tongue), English

Interests

Science communication in DéMesures (association)   *Lyon (France)*
LABORATORY OF YOUNG RESEARCHERS FOR SCIENTIFIC POPULARIZATION AND COMMUNICATION.   *2017-2019*
- Projects of communication between scientists and artists: ArtScience 2018 (Lyon, France)
- Scientific popularization events: "Fête de la Science" 2017 and 2018 (Villeurbanne, France) ; Geek Touch 2018 (Lyon, France)

Staff in scientific events   *Lyon, France*
- R MEETING, 2013
- ECAL (*European Conference in Artificial Life*), 2017   *2013, 2017*

Others
DRAWING, DIGITAL PAINTING, WILDLIFE PHOTOGRAPHY, PROGRAMMING

Awards

| 2023 | **Best Poster in medical imaging**, IABM - *French symposium in Artificial Intelligence in Biomedical Imaging* | *Paris (France)* |
| 2014 | **Gold Medal and Best Composite Part**, IGEM - *International Genetically Engineered Machine competition* | *Boston (USA)* |

Scientific contribution

ABSTRACTS IN CONFERENCES (ORALS AND POSTERS)

3D inference of the scoliotic spine from depth maps of the back
N. COMTE, S. PUJADES, A. COURVOISIER, O. DANIEL, J.-S. FRANCO, F. FAURE, E. BOYER   *2023*
CMBBE - International Symposium on Computer Methods in Biomechanics and Biomedical Engineering

Multi-modal registration for Adolescent Idiopathic Scoliosis subject specific avatar creation
N. COMTE, S. PUJADES, A. COURVOISIER, O. DANIEL, J.-S. FRANCO, F. FAURE, E. BOYER   *2023*
CMBBE - International Symposium on Computer Methods in Biomechanics and Biomedical Engineering

Inference 3D du rachis depuis une carte de profondeur du dos
N. COMTE, S. PUJADES, A. COURVOISIER, O. DANIEL, J.-S. FRANCO, F. FAURE, E. BOYER   *2023*
IABM - Colloque Français en Intelligence Artificielle en Imagerie Médicale

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

3D inference of the scoliotic spine from depth maps of the back
N. COMTE, S. PUJADES, A. COURVOISIER, O. DANIEL, J.-S. FRANCO, F. FAURE, E. BOYER   *2023*
HAL, preprint

Multi-Modal Data Correspondence for the 4D Analysis of the Spine with Adolescent Idiopathic Scoliosis
N. COMTE, S. PUJADES, A. COURVOISIER, O. DANIEL, J.-S. FRANCO, F. FAURE, E. BOYER   *2023*
Bioengineering, MDPI

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