

Nicolas Maillet

PhD in Bioinformatics

About **Interests**

8, rue de Bretagne
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(Comparative) metagenomics analysis, NGS technology, algorithms, interdisciplinary work

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February 22 1986
Driver licence: A, B

Languages

French – Mother tongue
English – Fluent written
and spoken
Spanish, Portugese &
Italian - notions

Programming

♥ Python, C, Bash
C++, Java, SQL, R
PHP, CSS3 & HTML5
Everyday use of Unix
environments

Education

- Since 2014 **Postdoctoral position in Bioinformatics** Stazione Zoologica Anton Dohrn, Naples, Italy
Inside the *Laboratory of Ecology and Evolution of Plankton*, developing new ways for a global comparison of the Tara Oceans samples.
- 2010 – 2013 **PhD in Bioinformatics** INRIA/IRISA, Université de Rennes 1, Rennes, France
Algorithms for de novo comparisons of huge metagenomic experiments. Application on Tara Oceans project.
Advisors: Dominique Lavenier and Pierre Peterlongo
PDF version: http://tel.archives-ouvertes.fr/docs/00/94/19/22/PDF/Maillet_Nicolas.pdf
- 2008 – 2010 **Research Master's Degree of Science** Université de Rennes 1, Rennes, France
Majoring in Modelisation of Biological Systems
Specialization in Bioinformatics
- 2007 – 2008 **Bachelor's Degree in Computer Science** Université de Bretagne Sud (UBS), Vannes, France
Specialization in Mathematics, Informatics & Statistics
- 2004 – 2006 **Higher National Diploma of Computer Science** IUT Informatique, UBS, Vannes, France
Specialization in Computer Engineering
- 2004 **French Scientific Baccalauréat** Lycée Joubert, Ancenis, France
Specialization in Earth and Life Sciences

Experience

- 2010 – 2013 **INRIA/IRISA, Rennes, France** PhD position
Creating a new data structure called *BDS* and a software using the *BDS*, *Compareads*, with the goal of finding similarity between huge metagenomic samples.
- 2010 (01 – 06) **Louis Bernatchez laboratory, Université Laval, Quebec** Research Internship
Meta-analysis of Whitefish (*Coregonus clupeaformis*) transcriptome studies with the goal of finding correlations between phenotypes and gene expression.
- 2009 (04 – 06) **INRIA/IRISA, Rennes, France** Research Internship
Creating a program for the detection of conserved protein regions, integrating five different programming languages.

Software

- 2015 **METEOR** In progress
METEOR (“METagenome: Each One of Reads”) is design to remove duplicate reads from huge metagenomes. Combined with COMMET, it will provide informations about α and β -diversity.
- 2014 **COMMET** <https://colibread.inria.fr/software/commet>
COMMET (“COMpare Multiple METagenomes”) provides a global similarity overview between all datasets of a large metagenomic project, directly from non-assembled reads.
- 2013 **Compareads** <https://colibread.inria.fr/software/compareads>
Compareads was designed to extract similar reads between potentially huge metagenomic datasets (i.e., hundreds of millions reads per dataset).

Publications

Article in peer-reviewed journal

Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species

K. R. Bradnam, J. N. Fass, A. Alexandrov, P. Baranay, M. Bechner et al.

Gigascience 2.1 (Jan. 2013) p. 10. 2013

Compareads: comparing huge metagenomic experiments

N. Maillat, C. Lemaitre, R. Chikhi, D. Lavenier, P. Peterlongo

BMC Bioinformatics 13 Suppl 19 (Dec. 2012) S10. 2012

Genome-wide patterns of divergence during speciation: the lake whitefish case study

S. Renaut, N. Maillat, E. Normandeau, C. Sauvage, N. Derome, S. M. Rogers, L. Bernatchez

Philos. Trans. R. Soc. Lond., B, Biol. Sci. 367.1587 (Feb. 2012) pp. 354–363. 2012

Assemblathon 1: a competitive assessment of de novo short read assembly methods

D. Earl, K. Bradnam, J. St John, A. Darling, D. Lin et al.

Genome Res. 21.12 (Dec. 2011) pp. 2224–2241. 2011

International peer-reviewed conferences/proceedings

COMMET: comparing and combining multiple metagenomic datasets

N. Maillat, G. Collet, T. Vannier, D. Lavenier, P. Peterlongo

Bioinformatics and Biomedicine (BIBM) (Acceptance ratio: 19%), IEEE International Conference, Belfast. 2014

Award

2012 **Best poster among 112 in JOBIM conference.**

Poster session

Compareads: comparing huge metagenomic experiments

N. Maillat, C. Lemaitre, R. Chikhi, D. Lavenier, P. Peterlongo

JOBIM, Rennes. Poster session, 2012

Mobility

Since 2014 **Laboratory of Ecology and Evolution of Plankton at SZN (Italy)**

<http://www.szn.it>

Dr. Daniele Iudicone

Metagenomics analyses of Tara Oceans data.

2012 (03 – 06) **Bioinformatics Laboratory at LNCC (Brazil)**

<http://www.lncc.br>

Dr. Ana Tereza Ribeiro de Vasconcelos

Metagenomics analyses and development of algorithms.

2010 (01 – 06) **Louis Bernatchez laboratory (Canada)**

<http://www.bio.ulaval.ca/louisbernatchez>

Dr. Louis Bernatchez

Meta-analysis of Whitefish (*Coregonus clupeaformis*) transcriptome.

Miscellaneous

2013 **Scientific popularization event**

<http://www.sciences-en-courts.fr>

Organisation of a short-movie festival dedicated to PhD students.

Since 2012 **Scientific popularization writing**

<http://bioinfo-fr.net/author/nico-m>

Author for the francophone website: <http://bioinfo-fr.net>

2011 **Scientific popularization by movie**

http://www.sciences-en-courts.fr/?page_id=836

Realisation of a science popularization short-movie.

Sport **Paragliding – Climbing – Scuba Diving – Running – eSport**

Hobbies

Paragliding: IPPI IV // Scuba Diving: PADI OWD / CMAS ★ (in progress)