



TECHNICAL SERVICES

COMPUTING SERVICES

SIBERCHICOT Aurélie

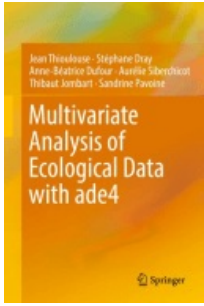
INGÉNIEURE D'ÉTUDE

UCBL

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As a **software engineer**, my work consists in designing, developing, deploying and maintaining biological data analysis tools. As an expert of the **R** language and software, I am in charge of many **R packages** which are available on CRAN, Bioconductor, GitHub and GitLab and of web applications developed with the **shiny** package. I am regularly associated with **training** and teaching modules, and I share, at these occasions, my knowledge and experience regarding the **reproducibility of research** and **good development practices**.

› GitHub:

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› [Google Scholar](#) 

Evolutionary Ecology

- **ade4** (Multivariate data analysis and graphical display):

[CRAN](#) 

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[GitHub](#) 

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[book](#) 

- **ade4TkGUI** (A Tcl/Tk GUI for some basic functions in the ade4 package):

[CRAN](#) 

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[GitHub](#) 

- **adegraphics** (Graphical functionalities for the representation of multivariate data):

[CRAN](#) 

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[GitHub](#) 

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[article](#) 

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[talk](#) 

- **CINID** (Package on the Curculionidae INstar IDentification):

[CRAN](#) 

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[article](#) 

- **Interatrix** (Compute Chi-Square Measures with Corrections):

[CRAN](#) 

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[article](#) 

- **OnAge** (Implements a likelihood ratio test of differential senescence onset between two groups):

[CRAN](#) 

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[web \(https://lbbe.univ-lyon1.fr/fr/onage\)](https://lbbe.univ-lyon1.fr/fr/onage)

- › Analysis of data from the *International Tiger Studbook* and from the *International and North American Regional Studbooks for Ruffed Lemurs* –

[article](#) 

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[article](#) 

- › *AGEX*(ANR-15-CE32-0002-01, 2015-2019) –

[article](#) 

- › *Potenchêne*(GIP-ECOFOR, 2014-2018) –

[article](#) 

- › *CoCoReCo*(ANR JC09-470585, 2009-2012) –

[article](#) 

- › *DL Vitis*(ANR-08-GENM-0002, 2008-2011) –

[article](#) 

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[CRAN](#) 

Ecotoxicology

- › **GUTS-predict** (General Unified Threshold Model of Survival):

[shiny app](#) 

- › **rbioacc** (Inference and Prediction of Toxicokinetic (TK) Models):

[CRAN](#) 

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[GitHub](#) 

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[article](#) 

Bioinformatics

› **DRomics** (Dose Response for Omics):

[CRAN](#) 

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[GitHub](#) 

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[shiny app](#) 

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[web \(https://lbbe.univ-lyon1.fr/fr/dromics\)](https://lbbe.univ-lyon1.fr/fr/dromics)

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[article](#) 

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[IFB cloud appliance](#) 

› **kissDE** (Retrieves Condition-Specific Variants in RNA-Seq Data):

[Bioconductor](#) 

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[GitHub](#) 

› **LDcorSV** (Linkage Disequilibrium Corrected by the Structure and the Relatedness):

[CRAN](#) 

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[article](#) 

› **MareyMap** (Estimation of Meiotic Recombination Rates Using Marey Maps):

[CRAN](#) 

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[GitHub](#) 

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[web \(https://lbbe.univ-lyon1.fr/fr/mareymap\)](https://lbbe.univ-lyon1.fr/fr/mareymap)

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[shiny app](#) 

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[article](#) 

› **phylter** (Detect and Remove Outliers in Phylogenomics Datasets):

[CRAN](#) 

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[GitHub](#) 

Statistics and data analysis

- › **fitdistrplus** (Help to Fit of a Parametric Distribution to Non-Censored or Censored Data):

[CRAN](#) 

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[GitHub](#) 

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[web \(https://lbbe.univ-lyon1.fr/fr/fitdistrplus\)](https://lbbe.univ-lyon1.fr/fr/fitdistrplus)

- › **Mondrian** (A Simple Graphical Representation of the Relative Occurrence and Co-Occurrence of Events):

[CRAN](#) 

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[GitHub](#) 

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[shiny app](#) 

- › **nlsMicrobio** (Nonlinear Regression in Predictive Microbiology):

[CRAN](#) 

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[GitHub](#) 

- › **nlstools** (Tools for Nonlinear Regression Analysis):

[CRAN](#) 

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[GitHub](#) 

IT services

- › **shiny server**:

<http://lbbe-shiny.univ-lyon1.fr> 

- › website of Statistics in Biology:

<http://pbil.univ-lyon1.fr/R/> 

Organization and Program Committee

- *Preditox*, Training school,
[2020](#)
- ,
- [2021](#)
- &
- [2023](#)
- , Lyon (scientific committee)
- [7èmes Rencontres R](#)
- , Conference, juillet 2018, Rennes (programm committee)
- [R pour le calcul](#)
- CNRS National Training Action, octobre 2015, Aussois (co-organizer)
- [2èmes Rencontres R](#)
- , Conference, juin 2013, Lyon (organization committee) –
[article](#)

Trainings and Courses

- *UE Visualization of Biological Data*, M2
[Bio-informatique](#)
- , Lyon
- *Programming with R: from the simplest to the most complex* Groupe Lyon Calcul
- *Build your own package in R*, ANF CNRS

Competition Jury

- Concours externe ENS (2021) – BAP A- IE – Ingénieur-e biologiste en traitement des données
- Concours externe INRA (2019) – Experte – BAP E – AI – Assistant-e statisticien-ne
- Concours externe INRA (2019) – BAP E – IE – Administrateur-trice des systèmes d’information
- Concours externe CNRS (2017) – Experte – BAP E – IE – Ingénieur-e en ingénierie logicielle – 2 postes

Supervision

- Cassandra Bompard, stage M2, Développement d'un package R de visualisation (2023)
- Eliane Schermer, stage M2 et thèse, Modélisation en écologie (2015-2019)
- Luka Matsuda, stage L3, Bioinformatique, Statistique et Modélisation (2018)
- Adrien Bessy, stage M2, Bioinformatique (2015)