

**Master 2e année Biodiversité Ecologie Evolution**  
Parcours Dynamique et modélisation de la biodiversité  
(DynaMo)

this is a very long title to test what happens when i say  
some shit with this title part

Maxime Jaunatre <sup>1</sup>

6 février 2020 | Soutenance : mardi 12 juin 2020

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**Encadrant :**

François Munoz

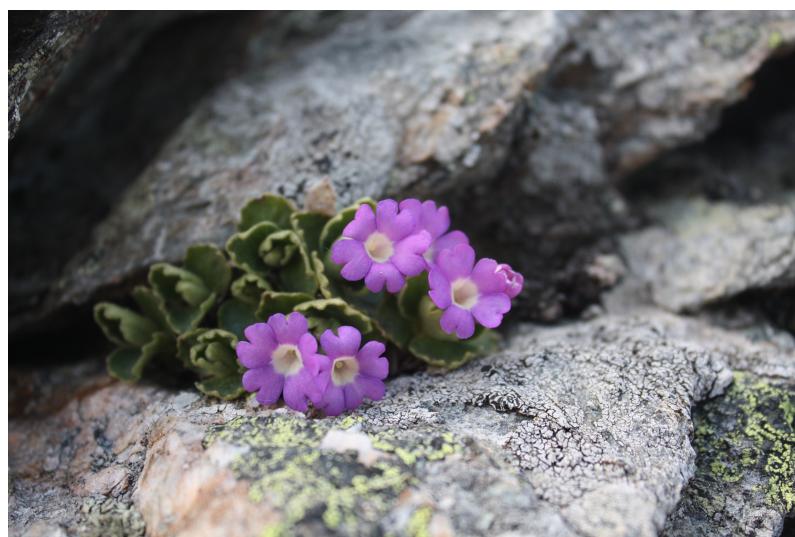
**Laboratoire :**

LECA

**Équipe :**

DivAdapt

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34398 Montpellier cedex 5



## Résumé

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## Abstract

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**Check: this!**

note that this is an example of abstract in 2 language

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note that this page style is 'empty' and have no page number for example

## Todo list

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note that this todo list will disappear if you set notes on false or comment it

This document provide all the command I usually use for my reports. Gray notes are here to explain some stuff, while red ones are here to be a last line limit when I wrote my report too close to the deadline and misread colours. I defined a new todonotes juste for this, to help me manage my work.

### Check: imp command

## 1 Basic command

Here is some memory about basic latex commands. Like putting some text in *italic* for species names. Or **bold** for important parts. This is completed with a possibility to highlight with the **hl** command. The colour is defined at the very beginning of the document, but another command allow to change with **hlc[red]word**. Every colour is possible and you can define them by the xcolor package.

Below is an exemple of a list

- Item A.
- Item B.
  - 1. sub part 1
  - 2. sub part 2
- Item C

## 2 To do notes

To help in long work redaction, the todonotes package is loaded by default, allowing to set inline or marge todonotes . Authors can be specified and the list of to do is loaded at the beginning of the document. Everything is explain in more detail inside this document <http://tug.ctan.org/macros/latex/contrib/todonotes/todonotes.pdf>

### inline

### Gowachin: specifying the author of the todo comment

### 3 Maths

Some packages are also loaded to allow maths equations to be displayed.

$$Y \in B; B = a, c, g, t \quad (1)$$

$$\begin{cases} prey_{t+1} = prey_t + prey_t \cdot r \cdot (1 - prey_t/K) + int_{pred/prey} \cdot pred_t \\ pred_{t+1} = pred_t + pred_t \cdot r \cdot (1 - pred_t/K) + int_{prey/pred} \cdot prey_t \end{cases} \quad (2)$$

with :  $r$  the growth rate and  $K$  the capacity.

### 4 Captions

Multiple captions are possible, like tables, figures and boxes, as display below. To show all the possibilities, there is  **Lorem ipsum** text around.

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  adipiscing elit. Ut purus elit, vestibulum  
  ut, placerat ac, adipiscing vitae, felis. Cu-  
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  vulputate a, magna. Donec vehicula augue  
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  tique senectus et netus et malesuada fames  
  ac turpis egestas. Mauris ut leo. Cras vi-  
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  rat. Integer sapien est, iaculis in, pretium  
  quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi  
  dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec

#### Glossary

**Phylogeny:** Object resuming evolutionary relation between living beings by illustrating distance between them. Mostly represented as a phylogenetic tree.

**Community:** An assemblage of populations from different species, defined by a time and geographic scale restriction. This assemblage can also be represented by interactions between these populations.

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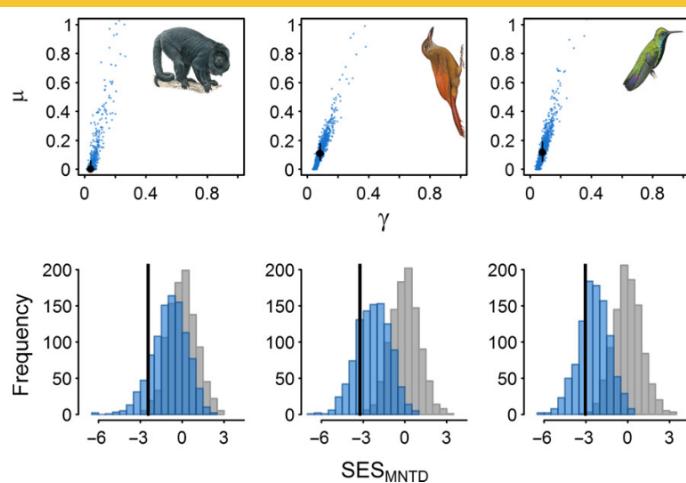
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### Boxe 1: More complex null model, Pigot et al. (2015)

**Context :** To study the assembly processes of a community, ecologist compare metrics (in this example the Mean Nearest Taxon Distance) with random draw species in the community. This null model is easily applicable but build assumption issues. For example, these null models don't take into account the historical aspect of community assembly.

**Results :** Authors found that their null models produce overdispersed community, by just taking into account historical aspect of colonisation and extinction in contrast with just random draw of species. Empirical data shown significantly overdispersed species in the community but fail to reject this null model.

Therefore, overdispersion could just arise from historical processes, independent from traits or biotic interactions. This new null model invite us to rethink more precedent result where overdispersion had been found.



**Figure 5** The dynamics and phylogenetic structure of community assembly for New World primates (left), ovenbirds (middle) and hummingbirds (right) in Manu. Maximum likelihood rate estimates (black points) of colonization ( $\gamma$ ) and local extinction ( $\mu$ ) with uncertainty in estimates (black lines 75% CI) quantified from 1000 bootstrap replicates (blue points). Community phylogenetic structure according to the Mean Nearest Taxon Distance ( $SES_{MNTD}$ ) showing the observed patterns (black lines), the expectation under the random-draw null model (grey) and the expectation under DAMOCLES given estimated rates (from 1000 replicate simulations).

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## 4.1 multicols

Captions are harder to set in twocolumn environnement, but here is an example.

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  gula aliquet magna, vitae ornare odio metus a mi. Morbi ac orci et nisl hendrerit mollis. Suspendisse ut massa. Cras nec ante. Pellentesque a nulla. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Aliquam tincidunt urna. Nulla ullamcorper vestibulum turpis. Pellentesque cursus luctus mauris.

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## 5 Import other documents

This is a subfile, that act exactly like the main file in term of compilation. It means it can be compiled on its own

## 6 Adding R code

As R [1] is commonly used in this master, there is the possibility to paste directly R code and input it inside the document. It is important to note that long lines are broken and it is signaled with line numbers on the left part of the script.

```
1 # this is a random function taken out from a master project. code won't run
2 hudson_lotka <- beepodyna(label = "hudson_lotka", community = hudson,
3   interactions = hudson_int,
4   functions = c(lotka_prey, lotka_pred), verbose = TRUE)
5
5 jpeg("figure/lotka.jpg", width = 802, height = 445)
6 plot(simulate_n_pop_dynamic(hudson_lotka, 10)$community, col = c("tan3",
7   slateblue3),
7   pch = c(1,2), xlim = c(1910,1930), ylim = c(0,100))
8 legend("bottomright", c("hare", "lynx"), col = c("tan3", "slateblue3"),
8   pch = c(1,2))
9 graphics.off()
```

[]

**Check: change bibliography model**

## hello china

[1] R.Team. 2017. R : A language and environment for statistical computing (Version 3.4.2)[Computer software]. *Vienna, Austria : R Foundation for Statistical Computing.*

Web 1 – <https://github.com>

## Ressources

Ce document est disponible en ligne sous format “.Rnw”, contenant tout le code nécessaire à la reproduction de l’analyse, réalisée avec un script en langage R [1], ainsi que le jeu de données de départ. L’ensemble est situé sur Github : <https://github.com/gowachin/Template>

Species	Locality	Code	Morph	Collector	Date	Longitude	Latitude	Altitude	Reads raw	Reads trimmed	Voucher
P. apennina*	Sella del Marmagna, Italy	AMB	Short-styled	F. Boucher/L. Gallien	30/05/14	10.00575	44.3978	1610	6885928	6486849	Photo
P. apennina	Monte Marmagna, Italy	AML	Long-styled	F. Boucher/L. Gallien	30/05/14	9.99731	44.39672	1825	1856867	1663377	Photo
P. apennina	Monte Orsaro, Italy	AOL	Long-styled	F. Boucher/L. Gallien	30/05/14	9.99666	44.39883	1818	3494081	3230296	Photo
P. cottia	Below locus classicus, Italy	CS1	NA	F. Boucher	23/07/14	7.0716	44.9271	1159	5127416	4814386	Photo
P. apennina*	Sella del Marmagna, Italy	AMB	Short-styled	F. Boucher/L. Gallien	30/05/14	10.00575	44.3978	1610	6885928	6486849	Photo
P. apennina	Monte Marmagna, Italy	AML	Long-styled	F. Boucher/L. Gallien	30/05/14	9.99731	44.39672	1825	1856867	1663377	Photo
P. apennina	Monte Orsaro, Italy	AOL	Long-styled	F. Boucher/L. Gallien	30/05/14	9.99666	44.39883	1818	3494081	3230296	Photo
P. cottia	Below locus classicus, Italy	CS1	NA	F. Boucher	23/07/14	7.0716	44.9271	1159	5127416	4814386	Photo

Annexe 1 – Exemple d’annexe