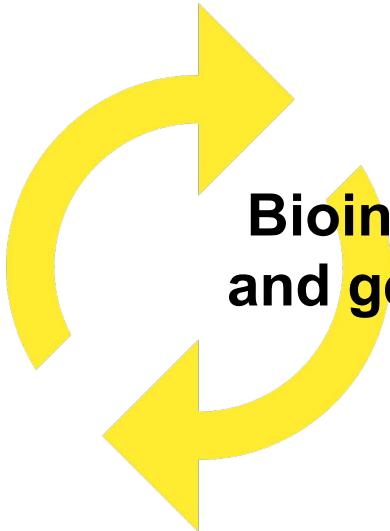




Session de formation 2019





Bioinformatics platform dedicated to the genetics
and genomics of tropical and Mediterranean plants
and their pathogens

comparative genomics
phylogeny
GWAS
population genetics
polyploidy

genome assembly
transcriptome assembly
metagenomics

SNP detection
structural variation
differential expression



Rice



Banana



Palm



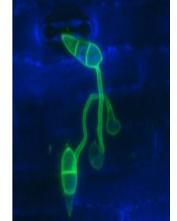
Sorghum



Coffee



Cassava



Magnaporthe

South Green

bioinformatics platform



Larmande Pierre
Sabot François
Tando Ndomassi
**Tranchant-Dubreuil
Christine**



Comte Aurore
Dereeper Alexis



Orjuela-Bouniol Julie



Bocs Stephanie
De Lamotte Fredéric
Droc Gaetan
Dufayard Jean-François
Hamelin Chantal
Martin Guillaume
Pitollat Bertrand
Ruiz Manuel
Sarah Gautier
Summo Marilyne



Rouard Mathieu
Guignon Valentin
Catherine Breton



Mahé Frédéric
Ravel Sébastien



Sempere Guilhem



South Green bioinformatics platform

Workflow manager

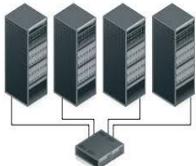
TOGGLE

Toolbox for generic NGS analyses

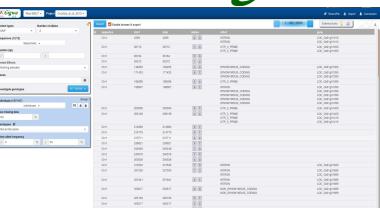


SNAKEMAKE

HPC and trainings....



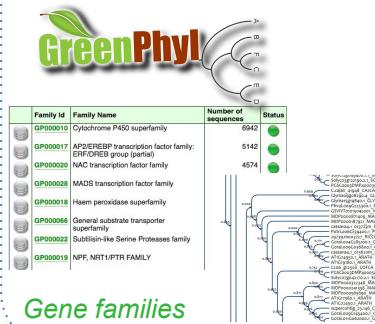
Genome Hubs & Information System



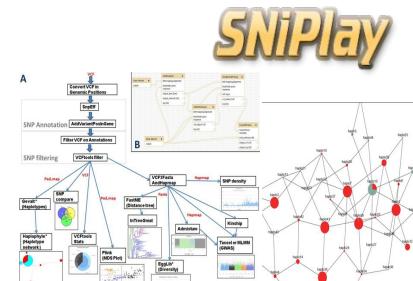
SNPs and Indels



Family Id	Family Name
GP000010	Cytochrome P450 superfamily
GP000017	AP2/EGRBP transcription factor superfamily
GP000020	ERF/DREB group (partial)
GP000022	NAC transcription factor family
GP000024	MADS transcription factor family
GP000018	Heim peroxidase superfamily
GP000066	General substrate transporter superfamily
GP000022	Subtilisin-like Serine Protease superfamily
GP000019	NPF, NRT1/PTR FAMILY



Gene families



<https://github.com/SouthGreenPlatform>



@green_bioinfo

The South Green portal: a comprehensive resource for tropical and Mediterranean crop genomics, Current Plant Biology, 2016



Erwan Corre



Marie Simonin
Sébastien Cunnac



Etienne Loire
Julie Reveillaud



Florentin Constancias



Valentin Klein



Valérie Noël



Emmanuelle Beyne



[@ItropBioinfo](https://twitter.com/ItropBioinfo)

And more collaborators !

18-19/03	Guide de survie à Linux - IRD
21/03	Initiation à l'utilisation du cluster CIRAD – CIRAD
22/03	Initiation à l'utilisation du cluster itrop - IRD
15-16/04	Initiation au gestionnaires de workflow SG & Gigwa – IRD
18-19/04	Guide du Jedi en Linux & bash - CIRAD
13-16/05	Python - IRD
17/05	Initiation aux analyses de données transcriptomiques – IRD
21/05	Utilisation avancée du cluster IRD – IRD
23-24/05	Initiation aux analyses de données métagénomiques – IRD
6/06	Manipulation de données et figures sous R – CIRAD
25-27/09	Assemblage et annotation de transcriptomes - IRD



Modules de formation 2019

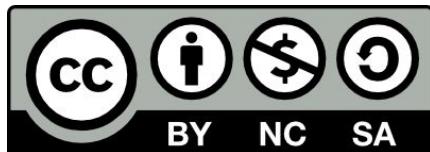
- Toutes nos formations :
<https://southgreenplatform.github.io/trainings/>
- Topo & TP : [Linux For Dummies](#)
- Environnement de travail : [Logiciels à installer](#)

Assembling and functionally annotating a de-novo transcriptome from RNA-seq data



www.southgreen.fr

<https://southgreenplatform.github.io/trainings>



Introduction

[survival] Basic commands in SLURM : [see](#)

Reads quality checking

- Practice 1. Checking Reads Quality [see](#)

Assembly with Trinity

- Practice 2. Assembling transcriptome from RNA-seq [see](#)
- Practice 3. Assessing transcriptome assembly quality [see](#)

Annotation with Trinotate

- Practice 5 : Functional annotation [see](#)

Differential Expression

- Practice 4 : Differential Expression Analysis (DE) [see](#)

Conclusions



Erwan Corre 



Julie Orjuela-Bouniol



Christine Tranchant-Dubreuil



Stéphanie Bocs-Sidibe 



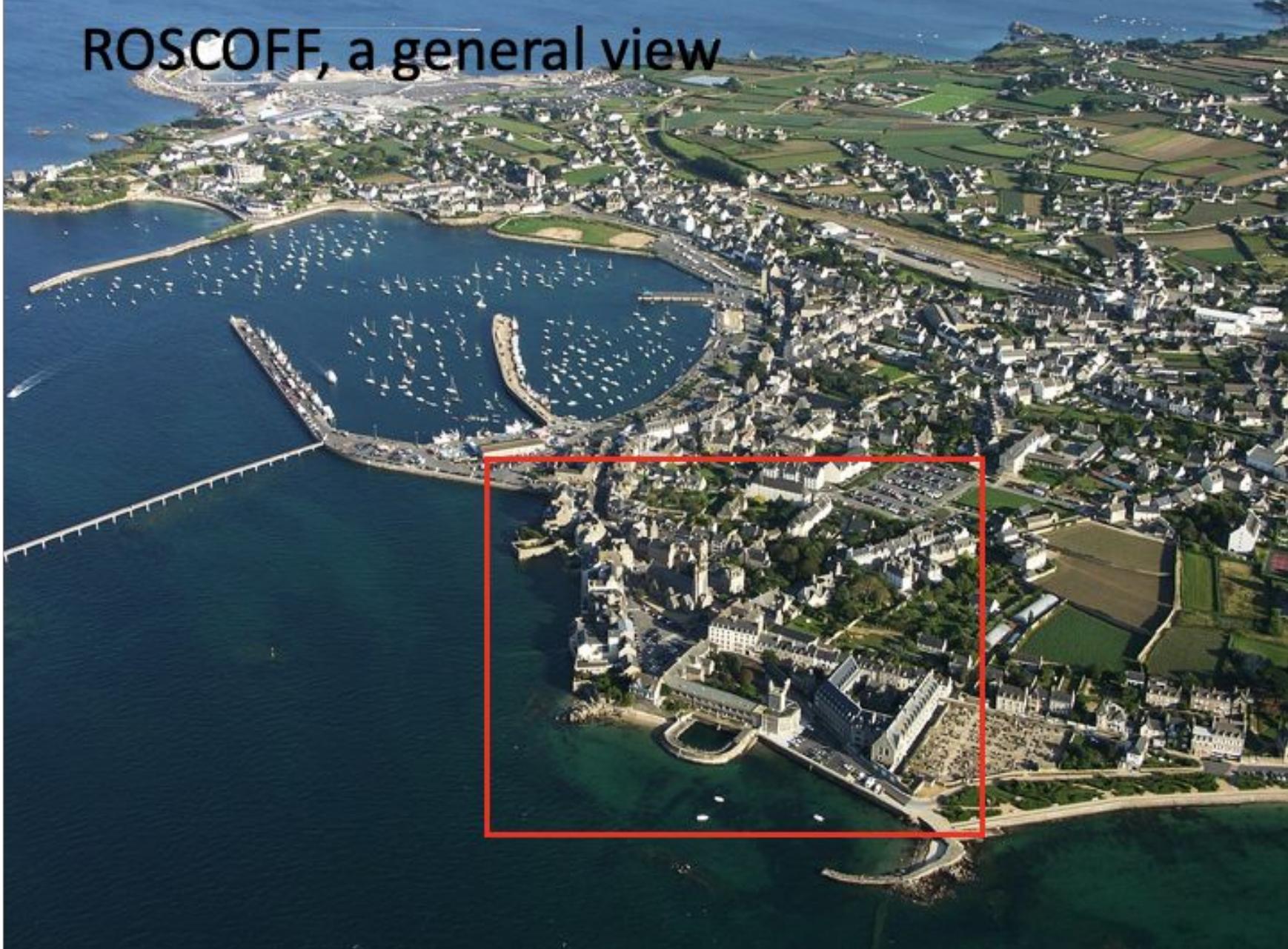
David Lopez 



Aurore Comte 

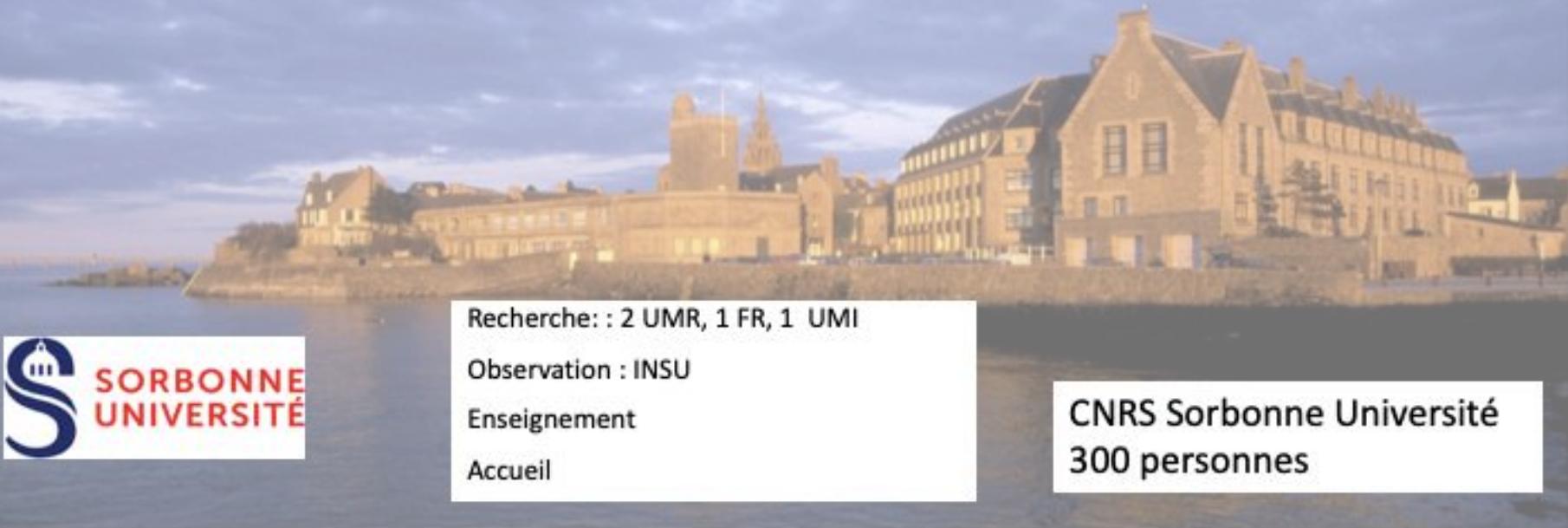


ROSCOFF, a general view





La Station Biologique de Roscoff



Recherche: : 2 UMR, 1 FR, 1 UMI

Observation : INSU

Enseignement

Accueil

CNRS Sorbonne Université
300 personnes

Recherche:

- la biochimie et le développement des algues brunes et rouges,
- l'écophysiologie de la faune hydrothermale et l'adaptation aux milieux extrêmes,
- la diversité du phytoplancton et du zooplancton,
- l'évolution et la génétique des populations,
- l'écologie benthique.
- chimie marine, phénomènes de circulation océanique des masses d'eau.

ABIMS : Analysis and Bioinformatics for Marine Science

Activities

Infrastructure



E-infrastructure

Expertise

Software Engineering

Bio-analysis

Data management

Training

Support

User Communities

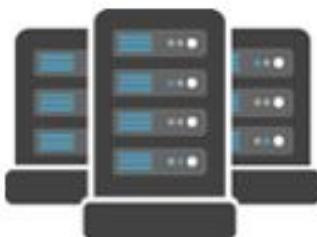


ABIMS : Analysis and Bioinformatics for Marine Science

2019



Storage : 3 PB

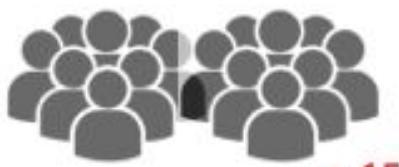


Cluster : 1,900 CPU
(3rd largest french open infrastructure)

900 support tickets/year



Int. Bandwidth : 1 Gb/s
Ext. Bandwidth : 10 Gb/s



100 internal accounts
500 external accounts

Transcriptome analysis:

Arctic Krill

Red abd Brown algae

Marine Pico Eukaryotes

Radiolaires

Artemia

Sepia, Pterois, Heterotis , Saculine

Sabellaria alveolata

Habalone

Mucor

Vertebrates Jaws

Quercus.

Canard Foie gras.

Mouse



Practice

1

Aller sur la practice 1 [Checking Reads Quality](#) du github



Practice

2

Aller sur la practice 2 [Assembling transcriptome from RNA-seq](#) du [github](#)



Practice

3

Aller sur la practice 3 [Assessing transcriptome assembly quality](#) du [github](#)



Practice

5

Aller sur la practice 5 [Functional annotation](#) du [github](#).

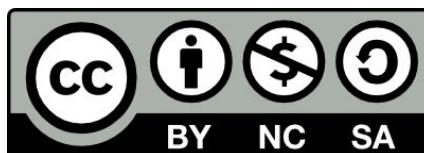


Practice

4

Aller sur la practice 4 [Differential Expression Analysis \(DE\)](#) du [github](#)

Merci pour votre attention !

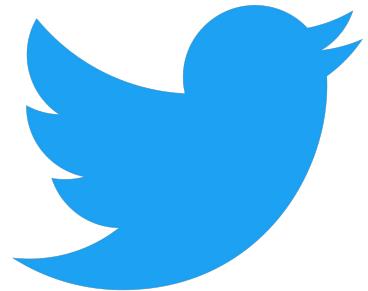


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SUIVEZ NOUS SUR TWITTER !



South Green : [@green_bioinfo](https://twitter.com/@green_bioinfo)



i-Trop : [@ItropBioinfo](https://twitter.com/@ItropBioinfo)



N'oubliez pas de nous citer !

Comment citer les clusters?

"The authors acknowledge the IRD i-Trop HPC at IRD Montpellier for providing HPC resources that have contributed to the research results reported within this paper. URL: <http://bioinfo.ird.fr/> "

"The authors acknowledge the CIRAD UMR-AGAP HPC (South Green Platform) at CIRAD montpellier for providing HPC resources that have contributed to the research results reported within this paper. URL:
<http://www.southgreen.fr>"