

# Simple Tools for Microbial Ecology



Imer Muhovic, Aleix Obiol, Ramiro Logares, Ramon Massana

ICM-CSIC, Barcelona



## Background

Analyzing data is an essential part of microbial ecology. Large datasets require programming skills, which while possessed by an ever increasing number of researchers, are not widespread. By implementing interactive web applications and easier to construct cloud pipelines, we can increase the amount of data exploration a researcher can perform by taking away the need for programming.

## Methods

Websites were developed in Laravel using Vue.js for their front end framework. The SAG assembly pipeline is based on sample code from AWS and previously published pipelines, implemented using AWS specific tools. All project websites are hosted on a custom server at the ICM.

## Contact

Imer Muhovic - imerm@icm.csic.es  
 Aleix Obiol - obiol@icm.csic.es  
 Ramiro Logares - ramiro.logares@icm.csic.es  
 Ramon Massana - ramonm@icm.csic.es

## Interactive Microbial Abundance Analysis

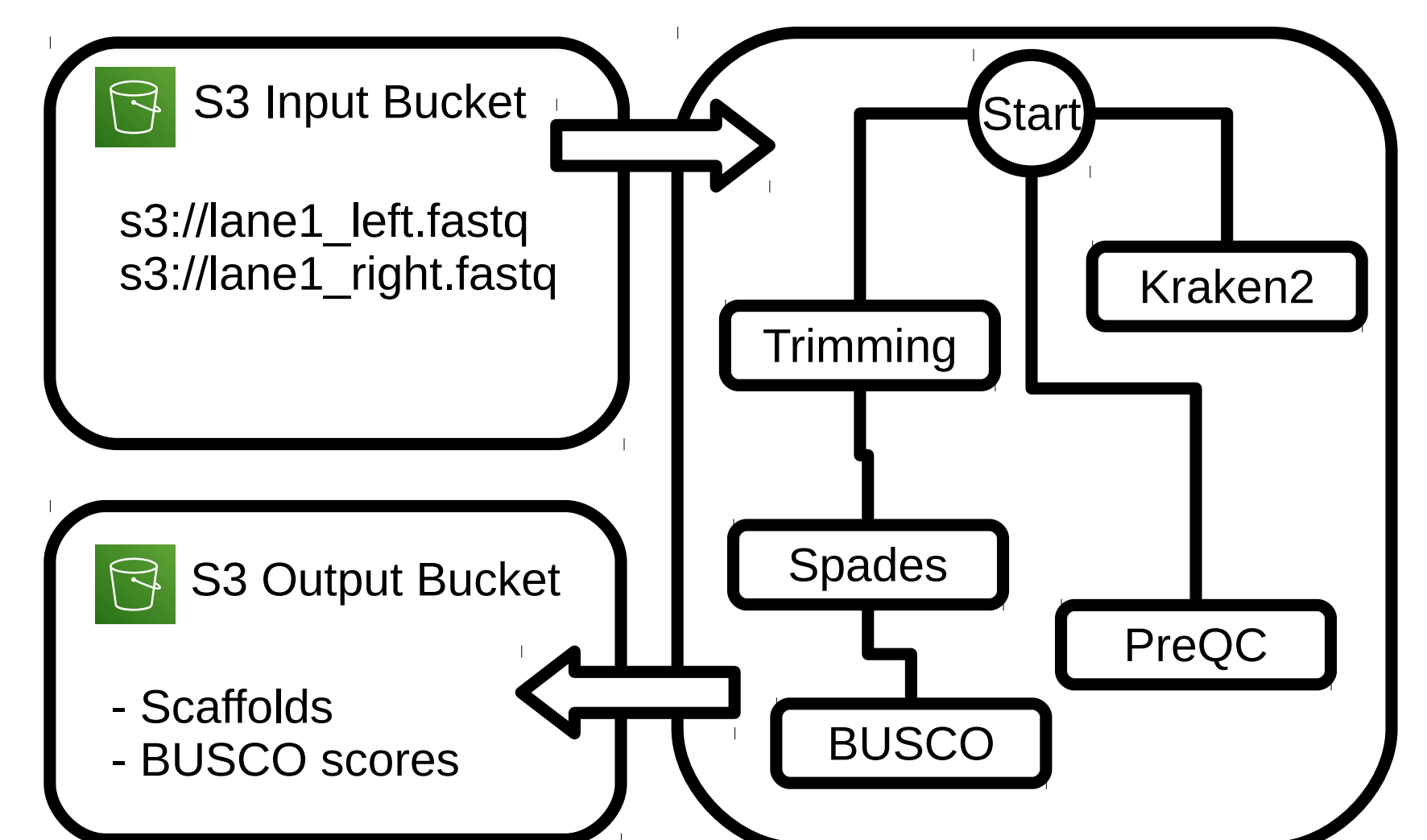
### Geographical sampling <http://micromap.esr15.site>

	A	C	D	E	F
1	sequence_id	sample1	sample2	sample3	sample4
2	ASV_1	7883	4134	7044	1267
3	ASV_10	0	0	0	0
4	ASV_100	78	53	70	61
5	ASV_1000	0	0	0	0
6	ASV_10000	0	0	0	0
7	ASV_10001	0	0	0	0
8	ASV_10002	0	0	0	0
9	ASV_10003	0	0	0	0
10	ASV_10004	0	0	0	0

### Temporal sampling <http://bbs.esr15.site>

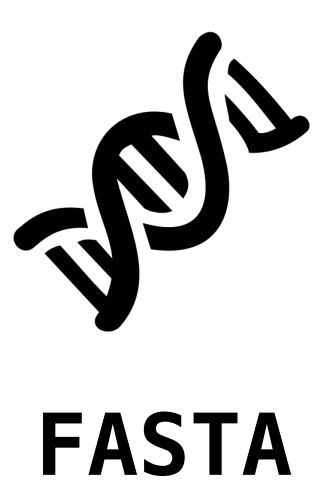
	A	B	C	D	E
1	asv_id	BL040126	BL040223	BL040322	BL040419
2		10.00	0.00	0.00	0.00
3		20.00	0.00	0.00	0.00
4		30.00	0.00	0.00	0.00
5		40.00	0.00	0.00	0.00
6		50.00	0.00	0.00	0.00
7		60.00	0.00	0.00	0.00
8		70.00	0.00	0.00	0.00
9		80.00	0.00	0.00	0.00
10		90.00	0.00	0.00	0.00

## SAG Cloud Assembly Pipeline



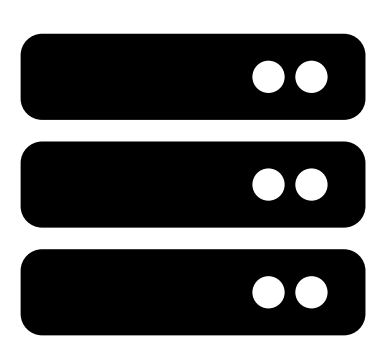
**Total cost:**  
1.6\$

## Inputs

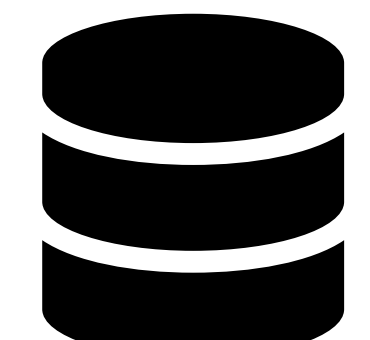


-or- Taxonomy

## Infrastructure



Server



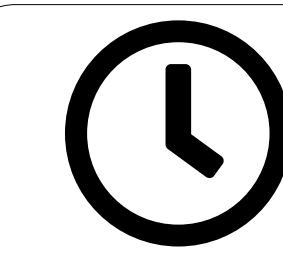
Blast Database



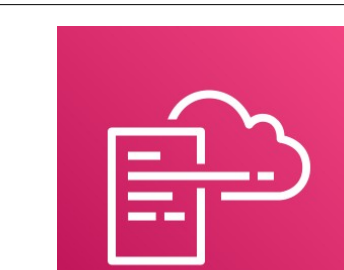
MySQL Database

## Cloud Pipeline Setup

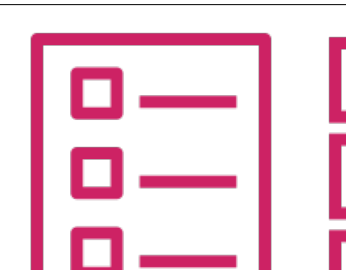
>bash startup.sh



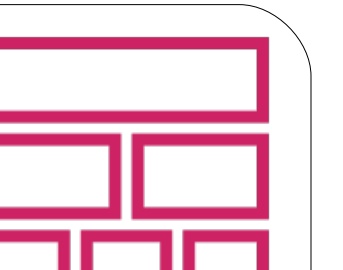
10 minutes



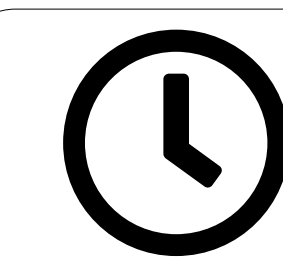
AWS CloudFormation



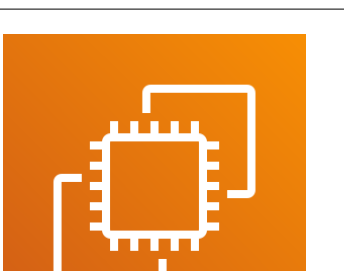
Templates



Stacks



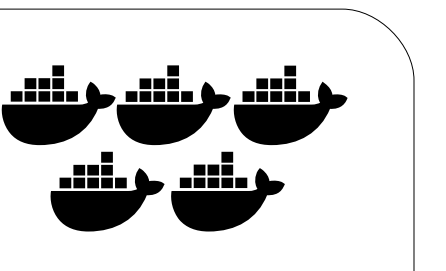
60 minutes



Amazon EC2



AMI



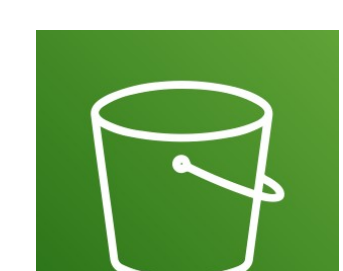
Docker Images



Amazon Elastic Container Registry



AWS Batch



Amazon Simple Storage Service



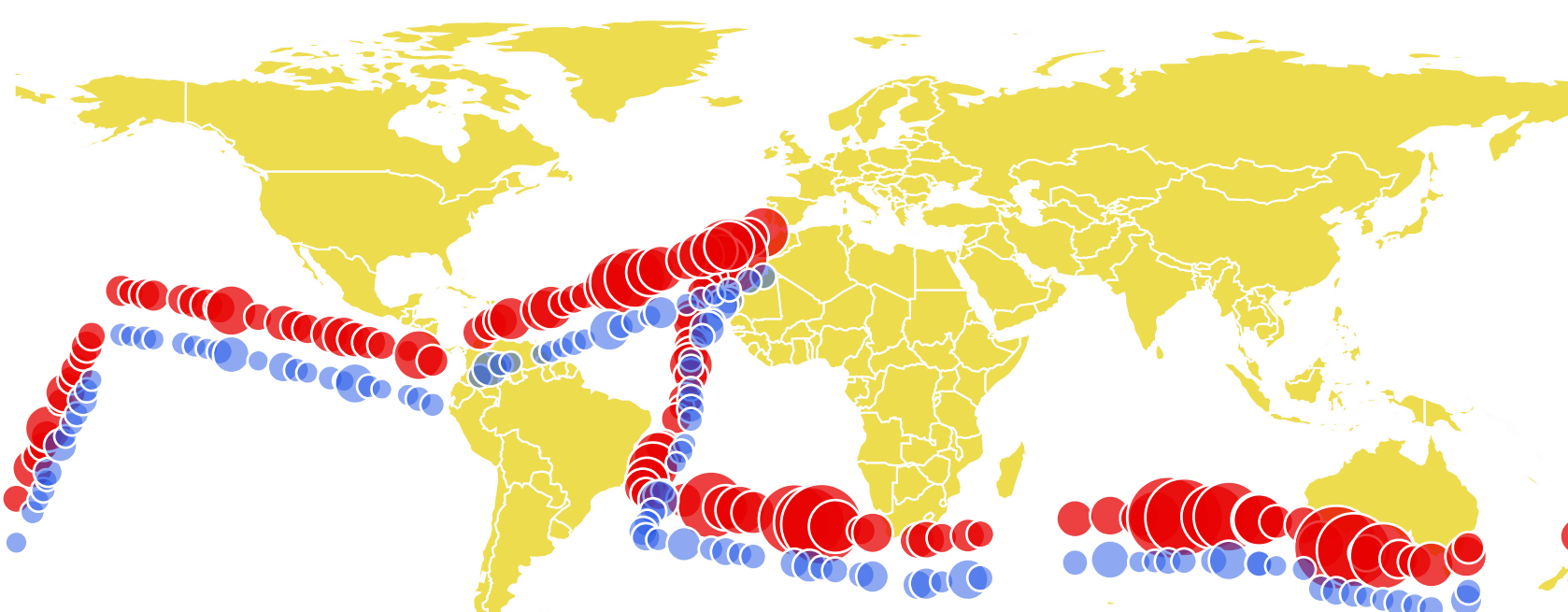
AWS Step Functions

## Interactive Microbial Abundance

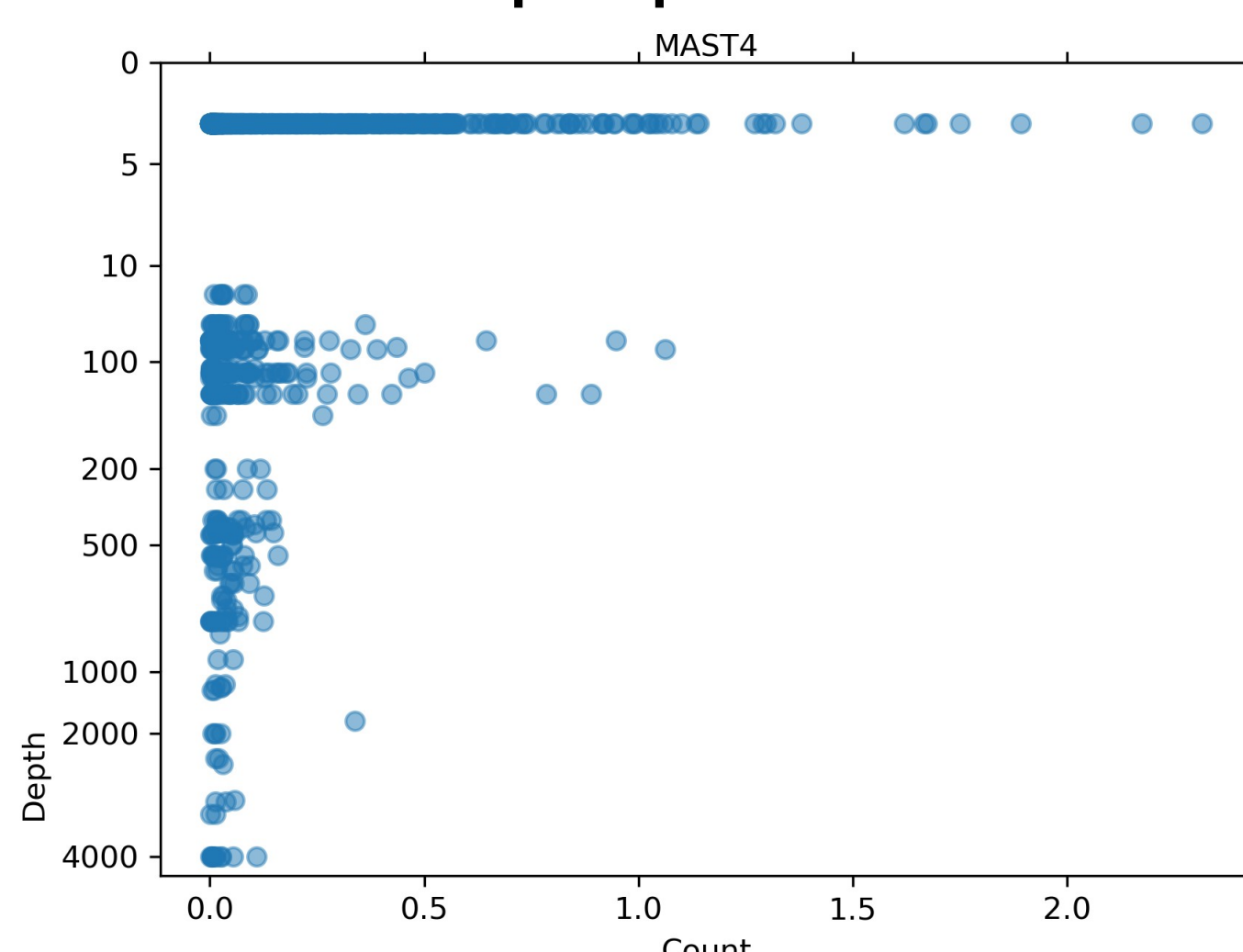
### Interactive map displaying abundances



### Interactive comparisons

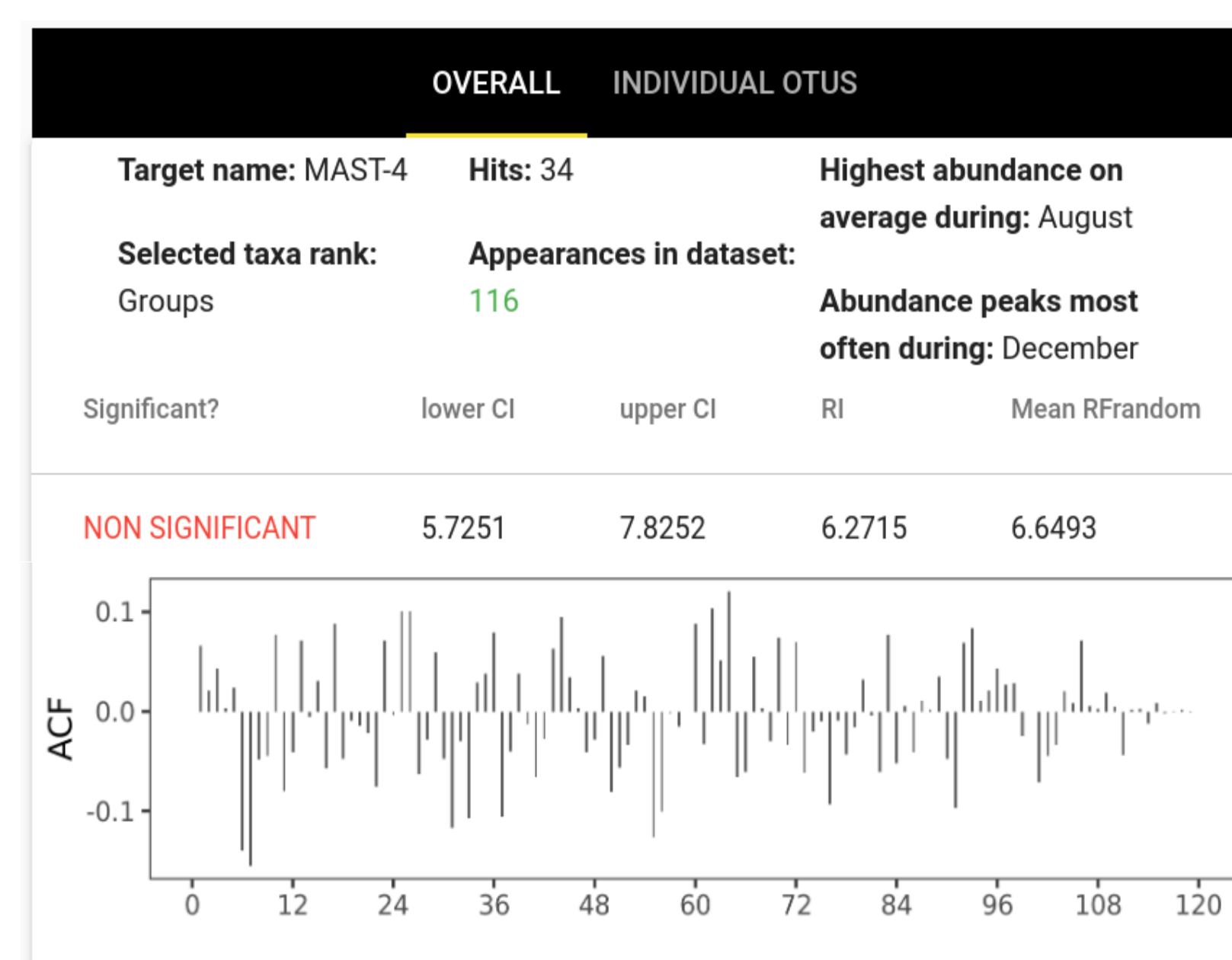


### Depth profiles

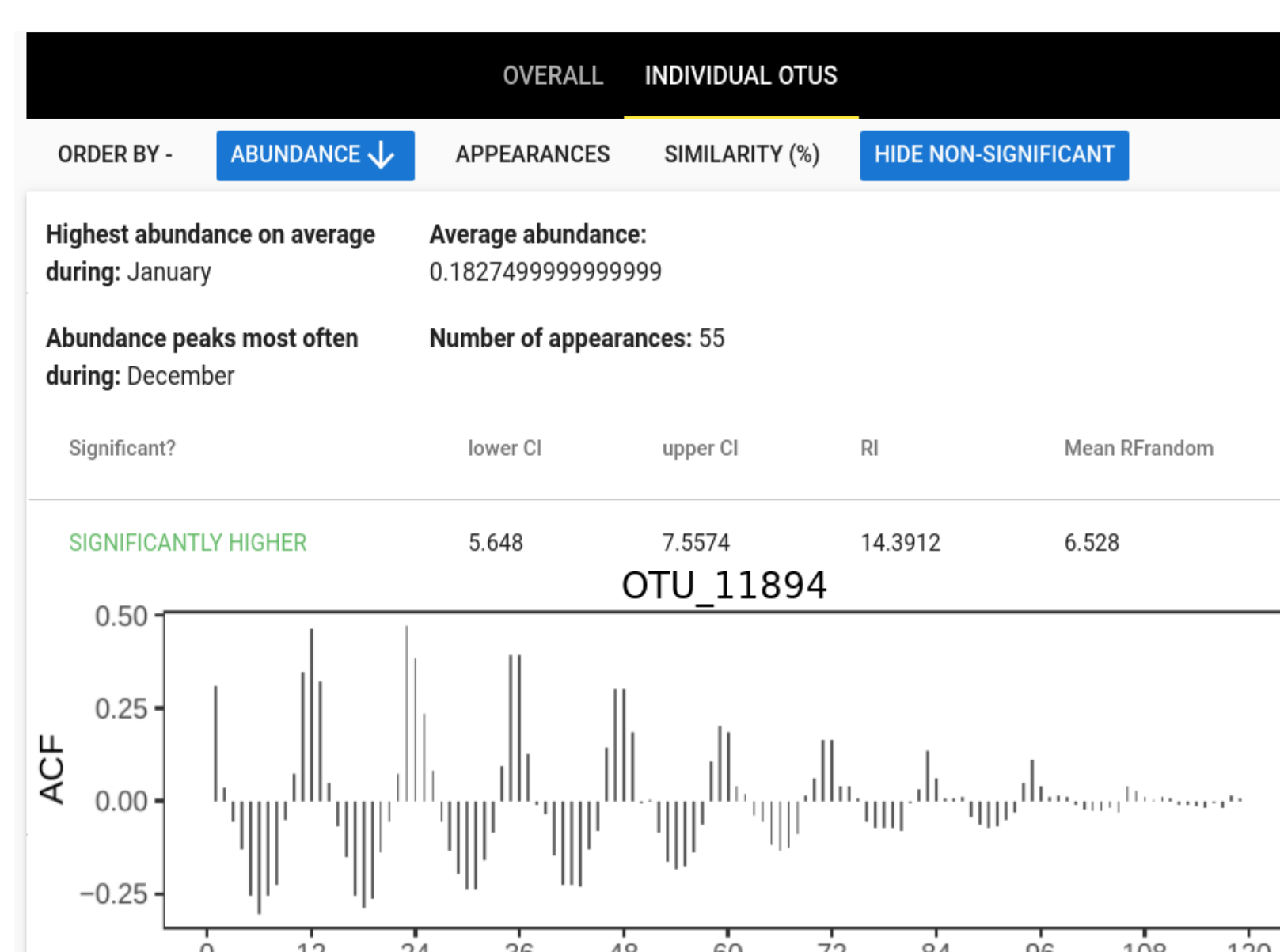


## Blanes Bay Taxa Seasonality

### Overall group seasonality



### Individual OTU seasonality



## References and Funding

Giner, C. R., Balagué, V., Krabberød, A. K., Ferrera, I., Reñé, A., Garcés, E., Gasol, J. M., R. Logares & Massana, R. (2019). Quantifying long-term recurrence in planktonic microbial eukaryotes. *Molecular ecology*, 28(5), 923-935.



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