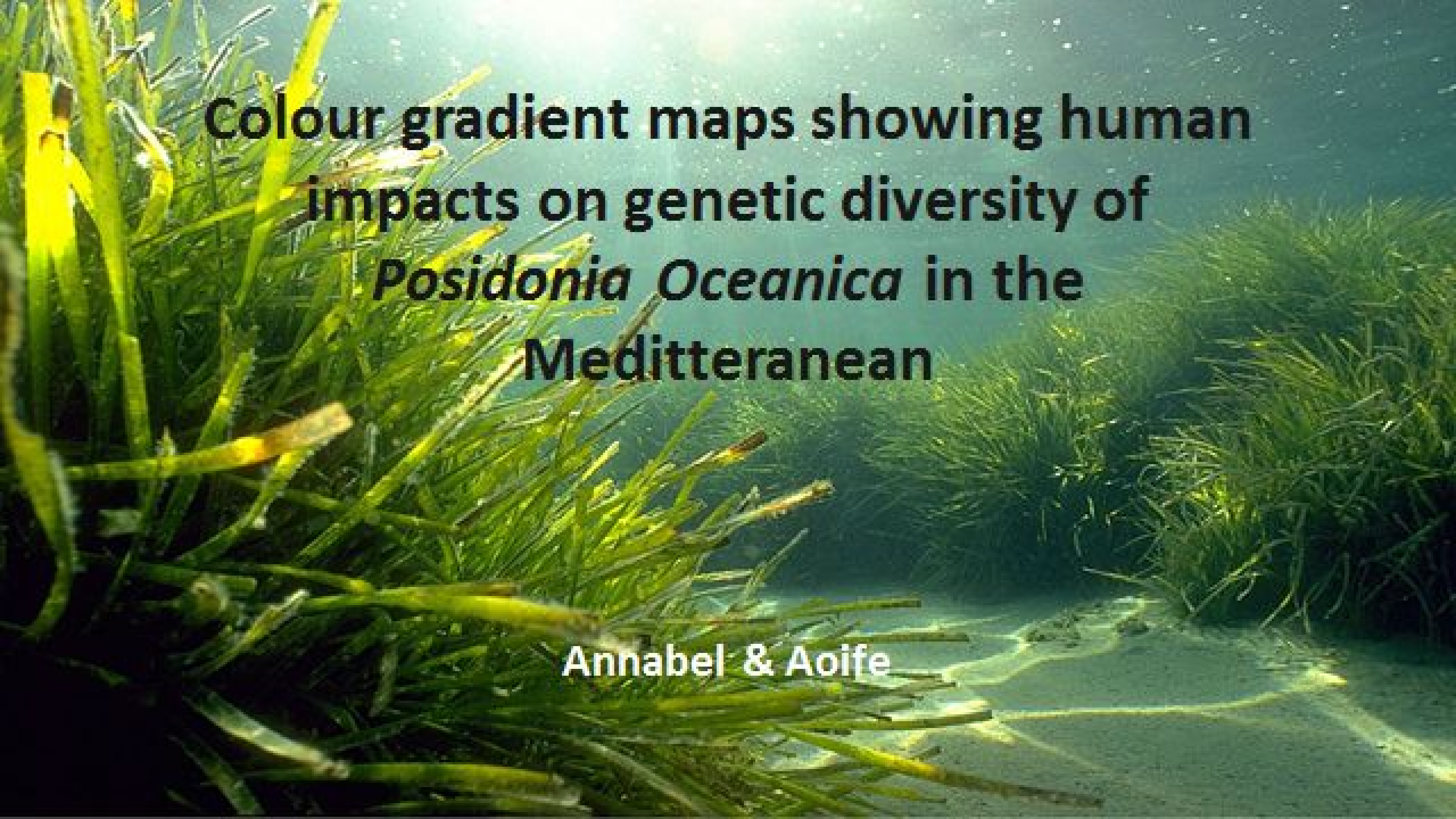


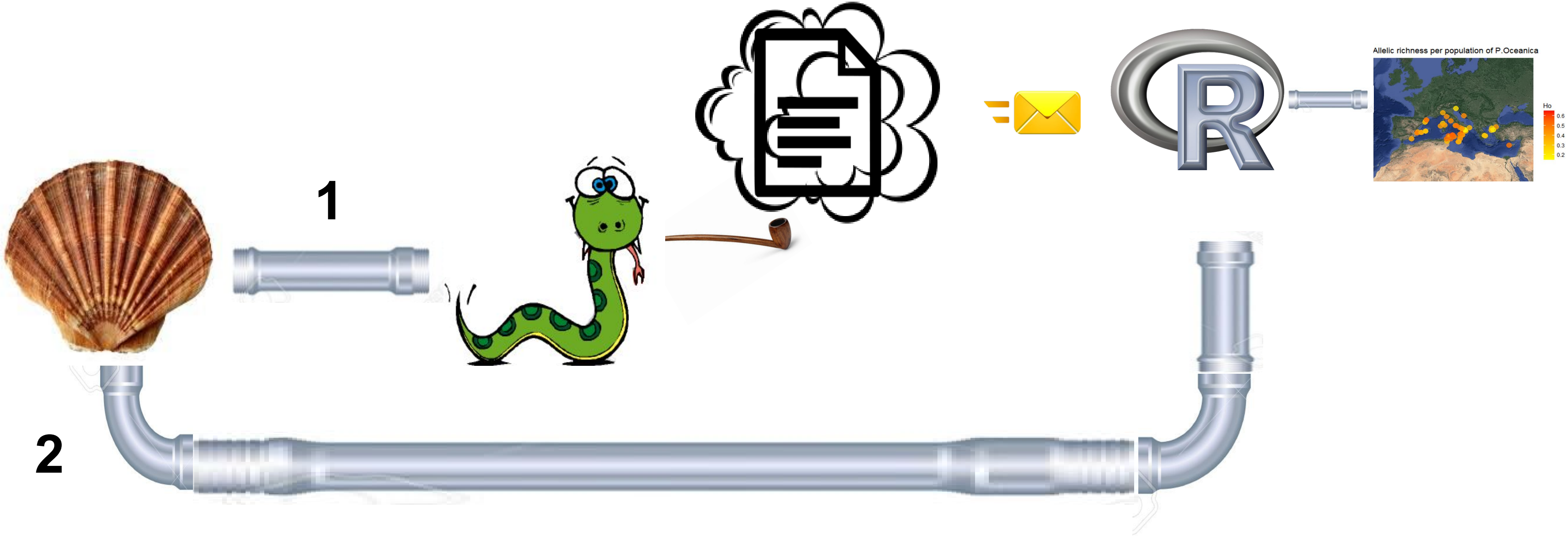
Colour gradient maps showing human impacts on genetic diversity of *Posidonia Oceanica* in the Meditteranean

Annabel & Aoife

Aim

Create a colour-scaled map showing the level of genetic diversity of different populations of *Posidonia oceanica* (Jahnke et al., 2015)

Work Flow


1
2
Allelic richness per population of P.Oceanica
Ho
0.6
0.5
0.4
0.3
0.2

Part 1: Genetic Data

Country	Location	Long	Lat	No. in Fig. 1	Sampling design	N	R original paper	Na original paper	Ho original paper	R (N=14)	Na (N=14)	A_{20} (MLG =20)	Ho (N=14)	Ref	Cum. threat in questionnaire
	Skerki	11.08	37.70	1	Randomly, every 8–10 m or as in Arnaud-Haond *et al.* (2007b).	21	0.35	1.77	*0.52*	0.23	1.7		0.53	Serra *et al.* 2010	
	Talbot	11.59	37.49	2	Randomly, every 8–10 m or as in Arnaud-Haond *et al.* (2007b).	23	0.59	1.85	*0.36*	0.69	1.85		0.37	Serra *et al.* 2010	
Croatia	Split	16.42	43.50	3	At randomly drawn coordinates in a 20 m x 80 m area (for 16 meadows). Every 7–8 m following a linear transect (for 16 meadows).	22	0	1.38	0.5	0	1.46		0.46	Arnaud-Haond *et al.* 2007	

Jahnke et al., 2015

Reformat Data (Gedit)

Step 1: Remove excessive tabs and replace with nothing:

Find: \t\t\t\t\t
Replace: <nothing>

Step 2: Replace all missing values with 'NA' so that R can read it in:

Find: \t \t
Replace: \tNA\t

Step 3: Replace extra lines with a single carraige return:

Find: \n\n
Replace: \n

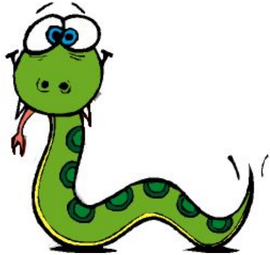
Result

Long	Lat	NInd	R14	Na14	A20	Ho14
11.08	37.7	21	0.23	1.7	NA	0.53
11.59	37.49	23	0.69	1.85	NA	0.37
16.42	43.5	22	0	1.46	NA	0.46
32.44	34.73	38	0.92	2.61	2.9	0.51
9.09	41.42	20	0.85	2.2	NA	0.3
23.93	37.72	40	0.69	2.3	NA	0.31
26.22	39.39	18	0.77	1.7	NA	0.31
23.73	37.86	29	0.38	1.6	NA	0.3
15.77	39.85	24	0.77	2.85	NA	0.39
16.05	39.15	25	0.77	2.77	NA	0.45
15.64	38.12	29	0.15	2.08	NA	0.47
15.57	38.21	39	0.23	2.08	NA	0.61
15.19	37.29	40	1	3.39	3.72	0.5
12.33	37.91	41	1	3	3.32	0.65
12.43	37.81	41	1	2.92	3.25	0.52
13.08	37.5	40	0.46	2.85	NA	0.48
11.92	36.83	38	1	4.23	4.15	0.51
15.98	37.91	40	0.77	2.85	NA	0.4
17.15	39.09	25	0.69	2.31	NA	0.34
16.96	39.5	36	0.46	1.54	NA	0.15

Shell

- Run Python
- Run R

Python



Goal: make a subset of a complete data set according to what the user would like to use

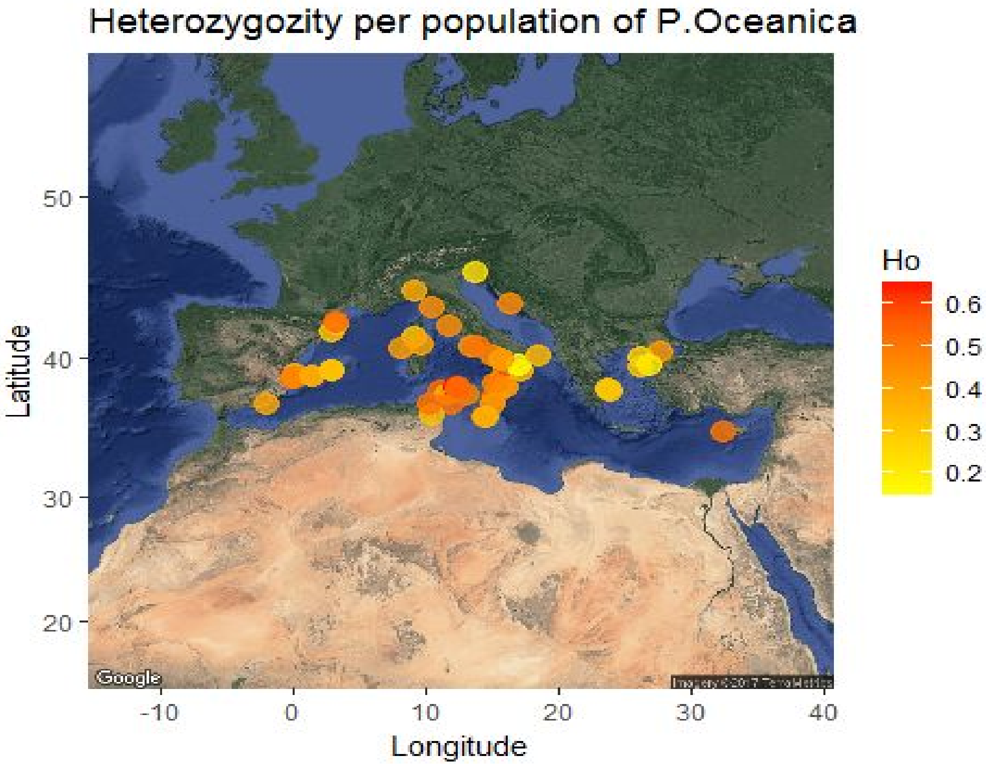
- choice of possible data with associated code
  "Make a map of: "
  "AllelicRichness(MLG=20): A20"
  "Observed Heterozygozity (N=14): Ho14"
- Ask user to input choice (raw input) "Enter the code of the desired data: "
- Translate the code to its associated column name Trans={'NInd':2, 'R14':3,...}
- Make subset of complete data for the map, with Long, Lat and chosen data
  OutFile.write(ElementList[a])

R

Goal: make a map of the data generated from the python file

- Import the data made in python and saved on the current directory
- Make a map of mediterranean using coordinates
- Put the data points on the map and add a colour gradient according to its value

Result



Heterozygozity per population of P.Oceanica
Latitude
50
40
30
20
-10
0
10
20
30
40
Longitude
Ho
0.6
0.5
0.4
0.3
0.2
Google

Hiccups along the way…

- Finding the right code to use (R)
- Discovering that certain functions were not compatible with each other
- Inexperience

Part II: Human impacts data

	Fishing_deme	Nutrient_Input	Commercial_Shipping	Organic_Pollution	UV_Radiation	Urban_Runof	Ocean_Acidificatio	Sea_Surface	Oil_Spills	Risk_of_Hypoxia	cumulative_thre
r	0.226	0.005	0.468	0	0.833	0.039	0.846	0.226	0	0	9.89
n	0.228	0.198	0.283	0.014	0.833	0.255	0.869	0.139	0	0.439	11.49
C	0.204	0.284	0.262	0.031	0.833	0.231	0.869	0.242	0	0.044	2.76
F	0.147	0.213	0.225	0.016	0.737	0.303	0.88	0.143	0	0	3.22
u	0.149	0.416	0.115	0.092	0.737	0.337	0.857	0.075	0	0.476	3.17
	0.149	0.244	0.295	0.022	0.737	0.182	0.857	0.045	0	0	6.88
a	0.259	0.056	0.212	0.002	0.909	0.107	0.869	0.006	0.005	0.44	4.65
	0.26	0.018	0.181	0	0.909	0.062	0.869	0.009	0.001	0.34	4.37
l	0.316	0.135	0.252	0.007	0.873	0.035	0.869	0.162	0	0.142	4.29
a_	0.316	0.08	0.192	0.003	0.873	0.018	0.869	0.149	0	0.071	3.36
a_	0.316	0.08	0.192	0.003	0.873	0.018	0.869	0.149	0	0.071	3.36
	0.111	0.063	0.246	0.003	0.833	0.079	0.869	0.027	0.001	0	2.79
te	0.087	0.156	0.146	0.041	0.737	0.207	0.869	0.004	0	0	6.12
	0.09	0.07	0.023	0.013	0.816	0.196	0.857	0.086	0.002	0	1.34
	0.098	0.006	0.271	0.001	0.679	0.062	0.869	0.283	0	0.327	3.26
	0.102	0.334	0.12	0.174	0.909	0.261	0.857	0.009	0	0	4.07
hi	0.118	0.129	0.023	0.03	0.909	0.19	0.88	0.075	0	0	4.32
	0.124	0	0.093	0	0.788	0	0.88	0.258	0	0	2.46
	0.138	0.199	0.107	0.063	0.833	0.194	0.869	0.009	0	0	5.76
e	0.094	0.037	0.012	0.006	0.788	0.2	0.88	0.182	0	0	6.1

Micheli et al., (2013)

Reformat Data

Step 1: Replace commas for tabs:

Find: ,

Replace: \t

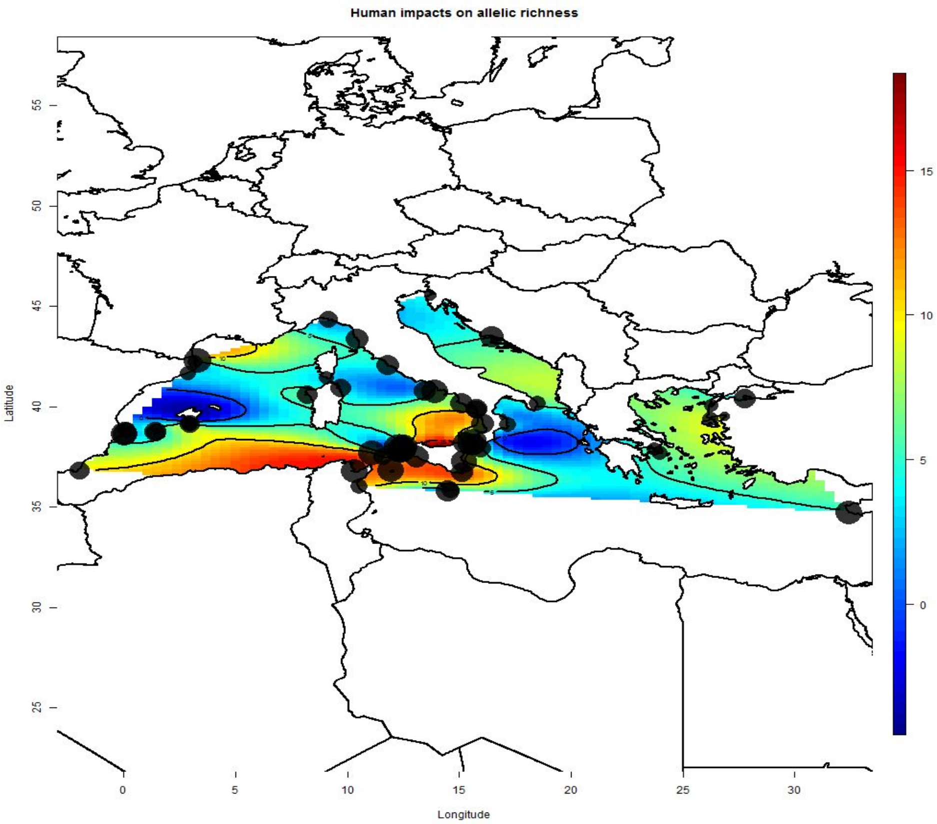
```
fish	nut	ship	pol	uv	uvb	oa	sst	inv	pop	oil	hypox	cthreat	Long	Lat
0.122	0.005	0.468	0	0.833	0.039	0.846	0.226	0	0	0	0	9.89	-1.99	36.82
0.145	0.198	0.283	0.014	0.833	0.255	0.869	0.139	0	0	0	0.439	11.49	0.01	38.62
0.132	0.284	0.262	0.031	0.833	0.231	0.869	0.242	0.049	0.249	0	0.044	2.76	0.05	38.63
0.111	0.213	0.225	0.016	0.737	0.303	0.88	0.143	0.393	0.25	0	0	3.22	2.84	41.69
0.132	0.416	0.115	0.092	0.737	0.337	0.857	0.075	0	0	0	0.476	3.17	3.19	42.21
0.132	0.244	0.295	0.022	0.737	0.182	0.857	0.045	0.147	0.612	0	0	6.88	3.3	42.3
0.17	0.056	0.212	0.002	0.909	0.107	0.869	0.006	0.721	0.31	0.005	0.44	4.65	1.41	38.75
0.17	0.018	0.181	0	0.909	0.062	0.869	0.009	0.721	0.307	0.001	0.34	4.37	1.46	38.74
0.221	0.135	0.252	0.007	0.873	0.035	0.869	0.162	0.783	0	0	0.142	4.29	2.93	39.15
0.221	0.08	0.192	0.003	0.873	0.018	0.869	0.149	0.348	0.228	0	0.071	3.36
```

R

Goal: make a map of the data generated from the python file

- Import the data
- Make a map of mediterranean
- Put the data points on the map and add a colour gradient based on whichever variable is called upon (e.g. ocean acidificaton or nutrient input)

Result



Human impacts on allelic richness
Latitude
Longitude
55
50
45
40
35
30
25
0
5
10
15
20
25
30
15
10
5
0