Collecting and Analysing Outline Data

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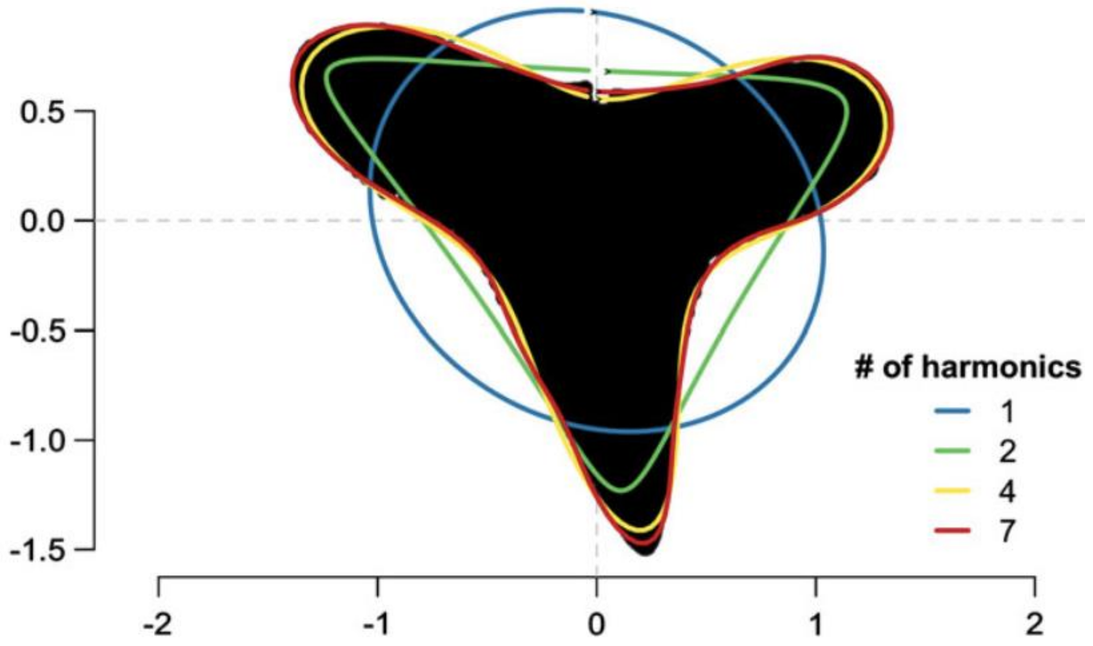
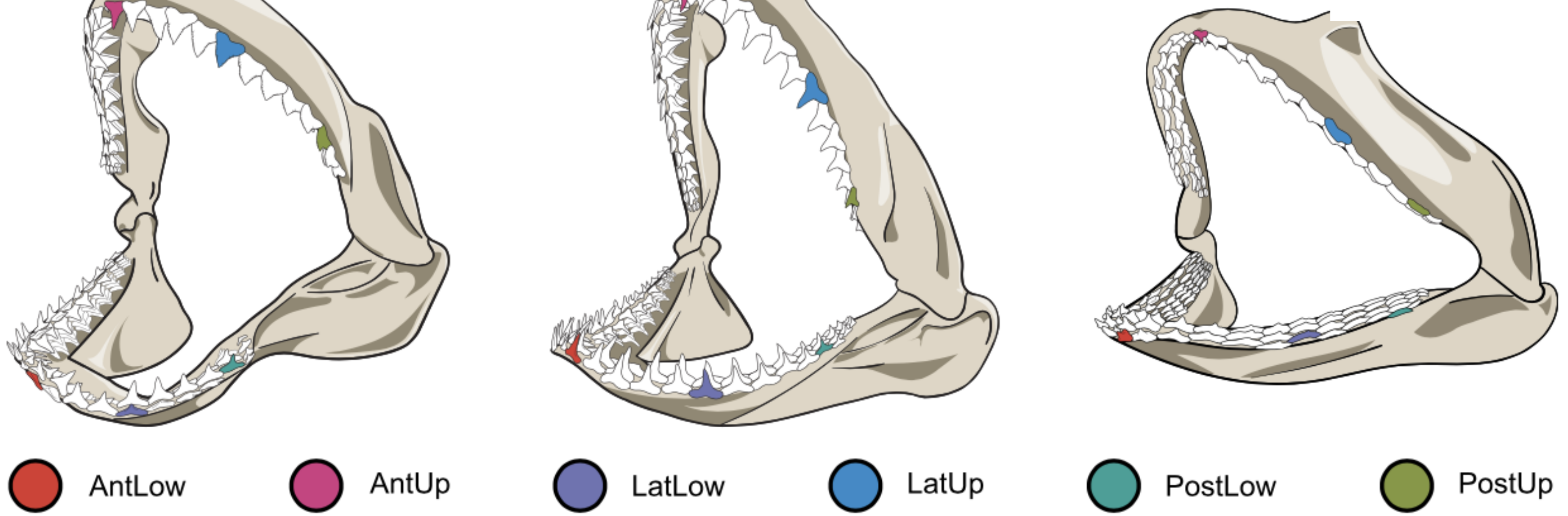
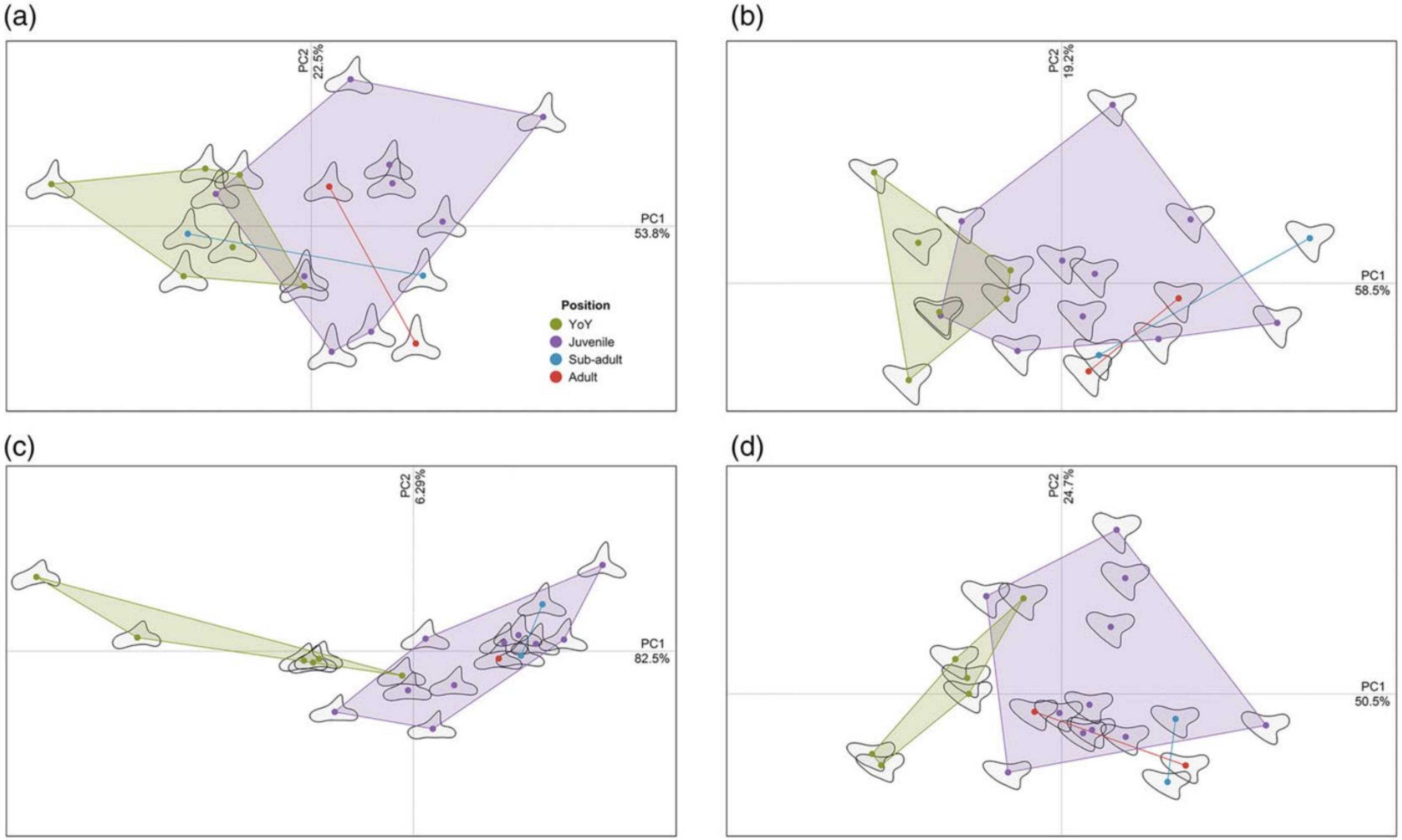
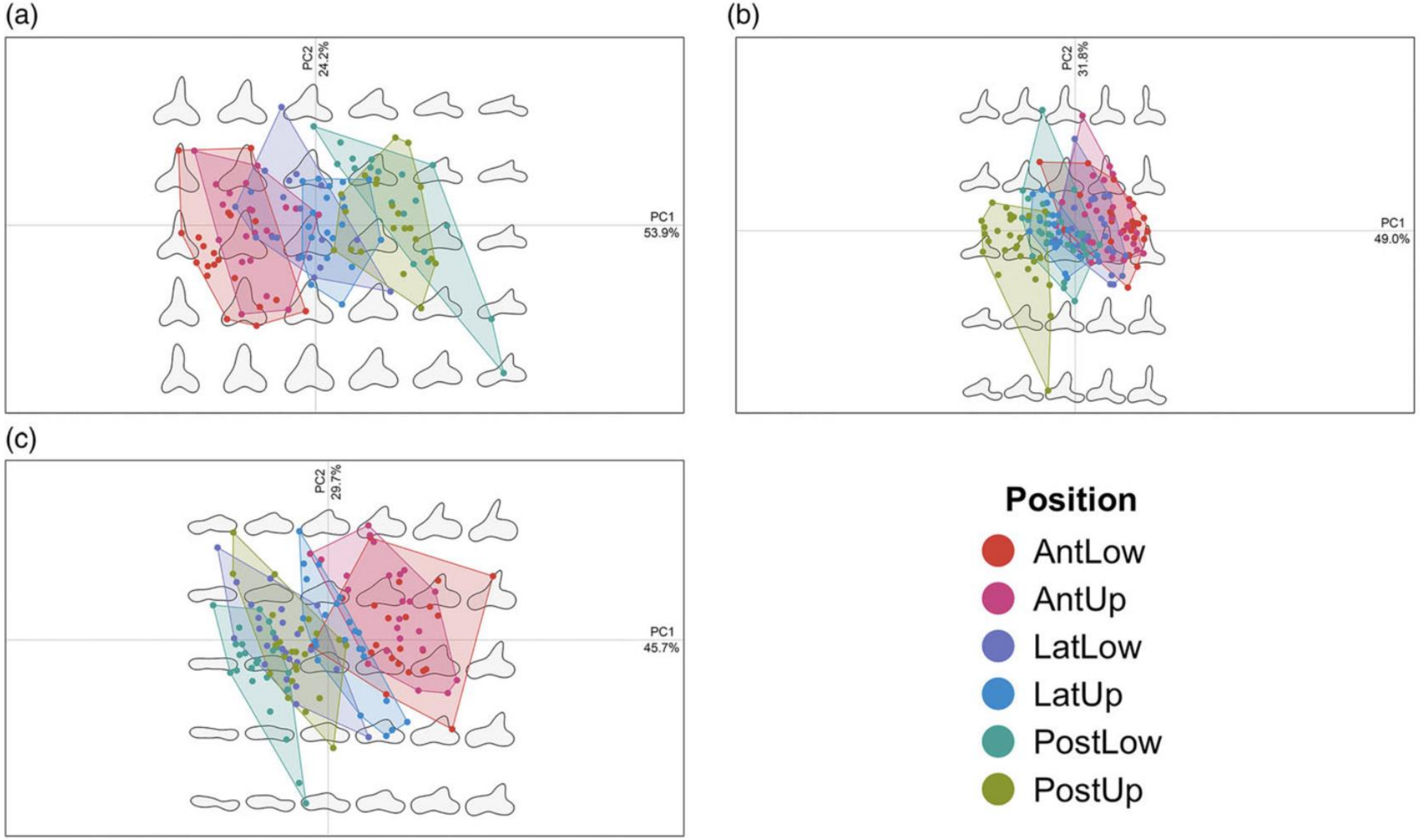


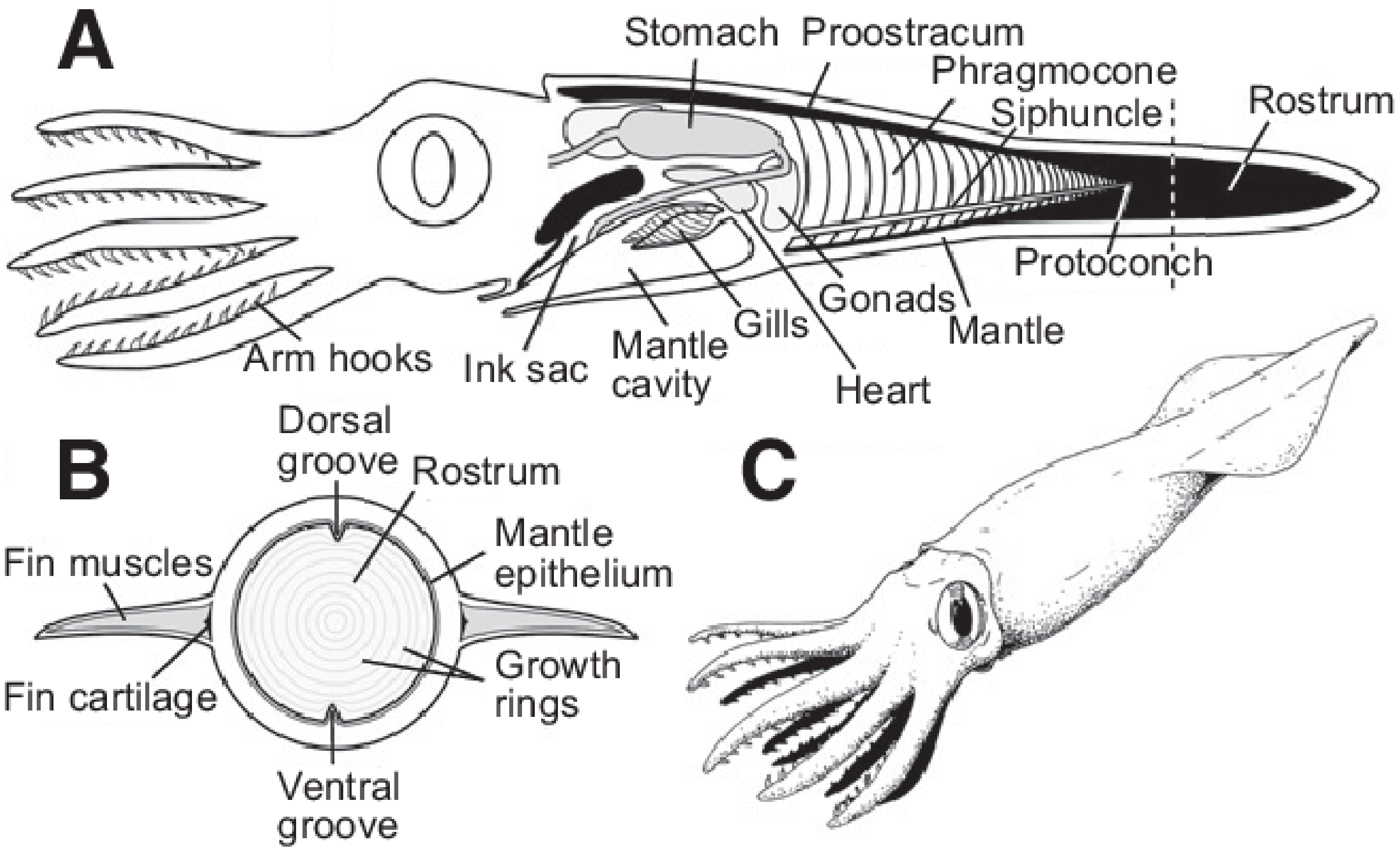


Cullen and Marshall 2019

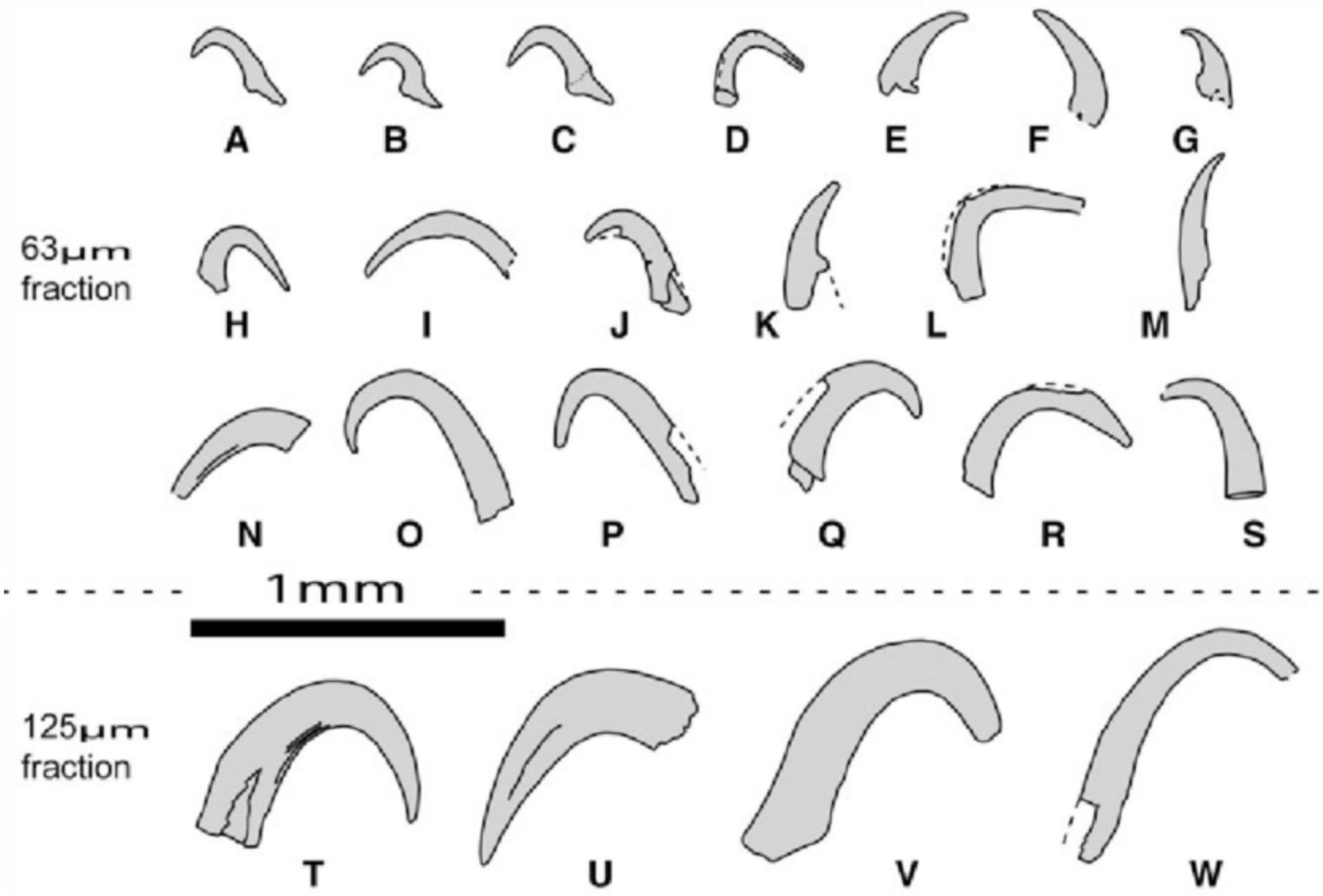

(a)
PC2 22.5%
PC1 53.8%
Position
YoY
Juvenile
Sub-adult
Adult
(b)
PC2 19.2%
PC1 58.5%
(c)
PC2 6.29%
PC1 82.5%
(d)
PC2 24.7%
PC1 50.5%


(a)
PC2
24.2%
PC1
53.9%
(b)
PC2
31.8%
PC1
49.0%
(c)
PC2
29.7%
PC1
45.7%
Position
AntLow
AntUp
LatLow
LatUp
PostLow
PostUp

Belemnites

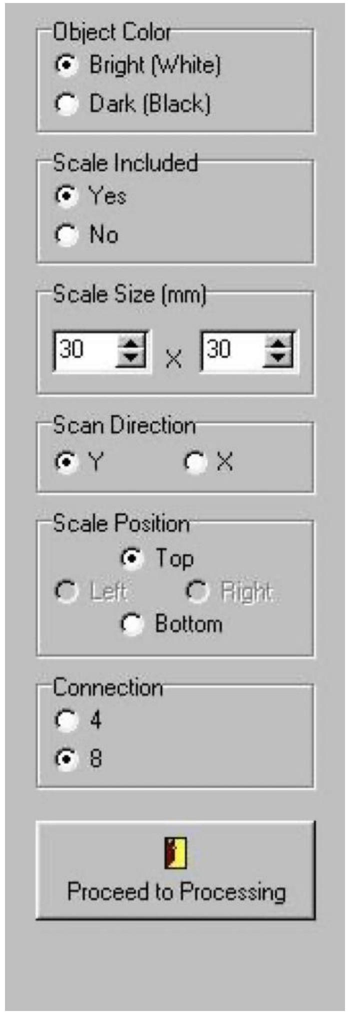


Iba et al 2012


A
B
C
D
E
F
G
63µm fraction
H
I
J
K
L
M
N
O
P
Q
R
S
1mm
125µm fraction
T
U
V
W

So how are we collecting the data?

SHAPE



Object Color
● Bright (White)
○ Dark (Black)

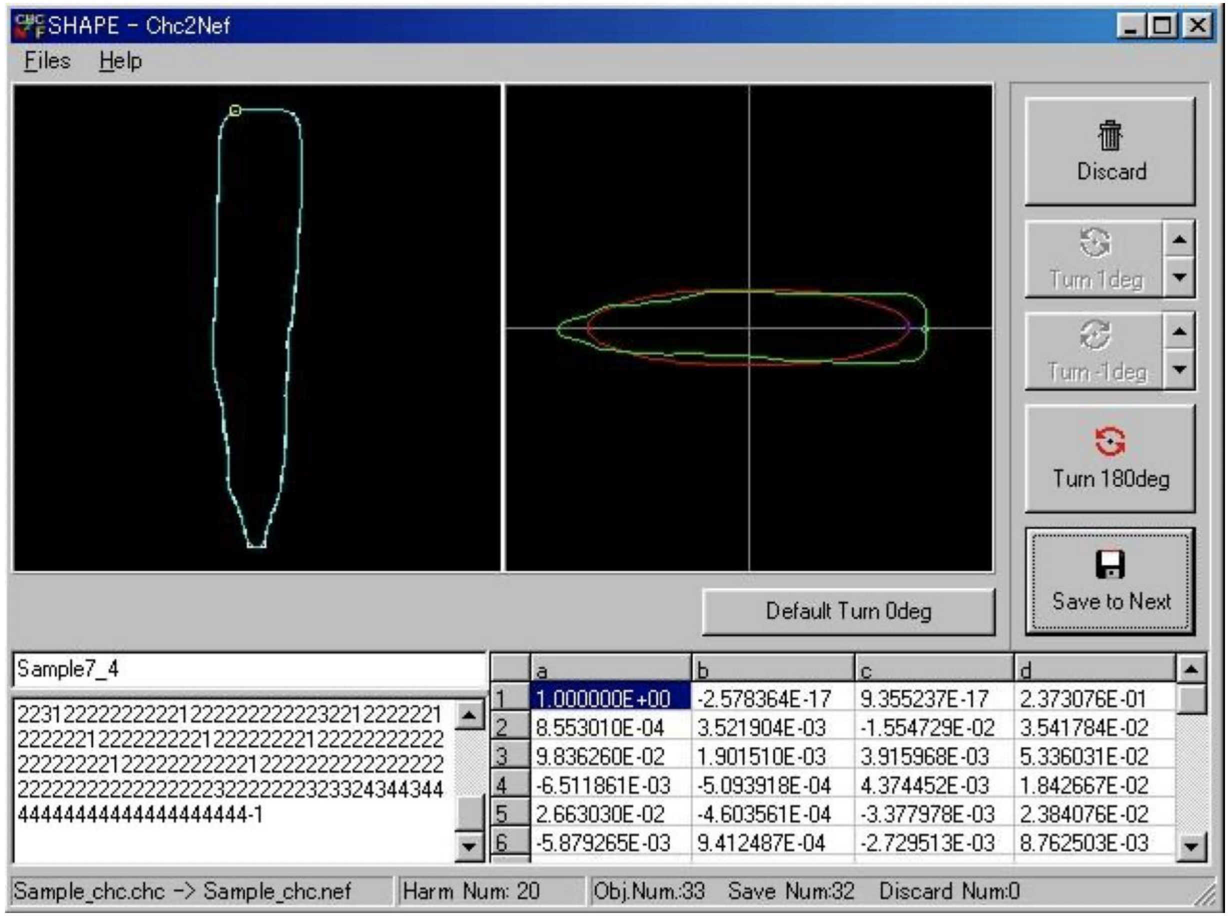
Scale Included
● Yes
○ No

Scale Size (mm)
30 x 30

Scan Direction
● Y ○ X

Scale Position
● Top
○ Left ○ Right
○ Bottom

Connection
○ 4
● 8



Sample7_4

```
2231222222222212222222222232212222221
2222221222222222122222222122222222222
2222222212222222222212222222222222222
22222222222222222322222232332434434 4
44444444444444444444-1
```

	a	b	c	d
1	1.000000E+00	-2.578364E-17	9.355237E-17	2.373076E-01
2	8.553010E-04	3.521904E-03	-1.554729E-02	3.541784E-02
3	9.836260E-02	1.901510E-03	3.915968E-03	5.336031E-02
4	-6.511861E-03	-5.093918E-04	4.374452E-03	1.842667E-02
5	2.663030E-02	-4.603561E-04	-3.377978E-03	2.384076E-02
6	-5.879265E-03	9.412487E-04	-2.729513E-03	8.762503E-03

Sample_chc.chc -> Sample_chc.nef Harm Num: 20 Obj.Num.:33 Save Num:32 Discard Num:0

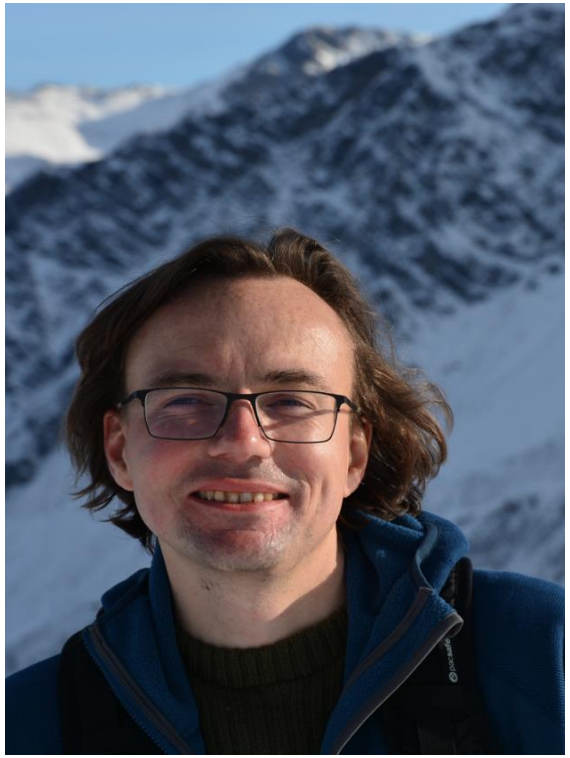
SHAPE

Iwata, H., and Y. Ukai (2002) SHAPE: A computer program package for quantitative evaluation of biological shapes based on elliptic Fourier descriptors. Journal of Heredity 93: 384-385.

http://lbm.ab.a.u-tokyo.ac.jp/~iwata/shape/

Alternative:

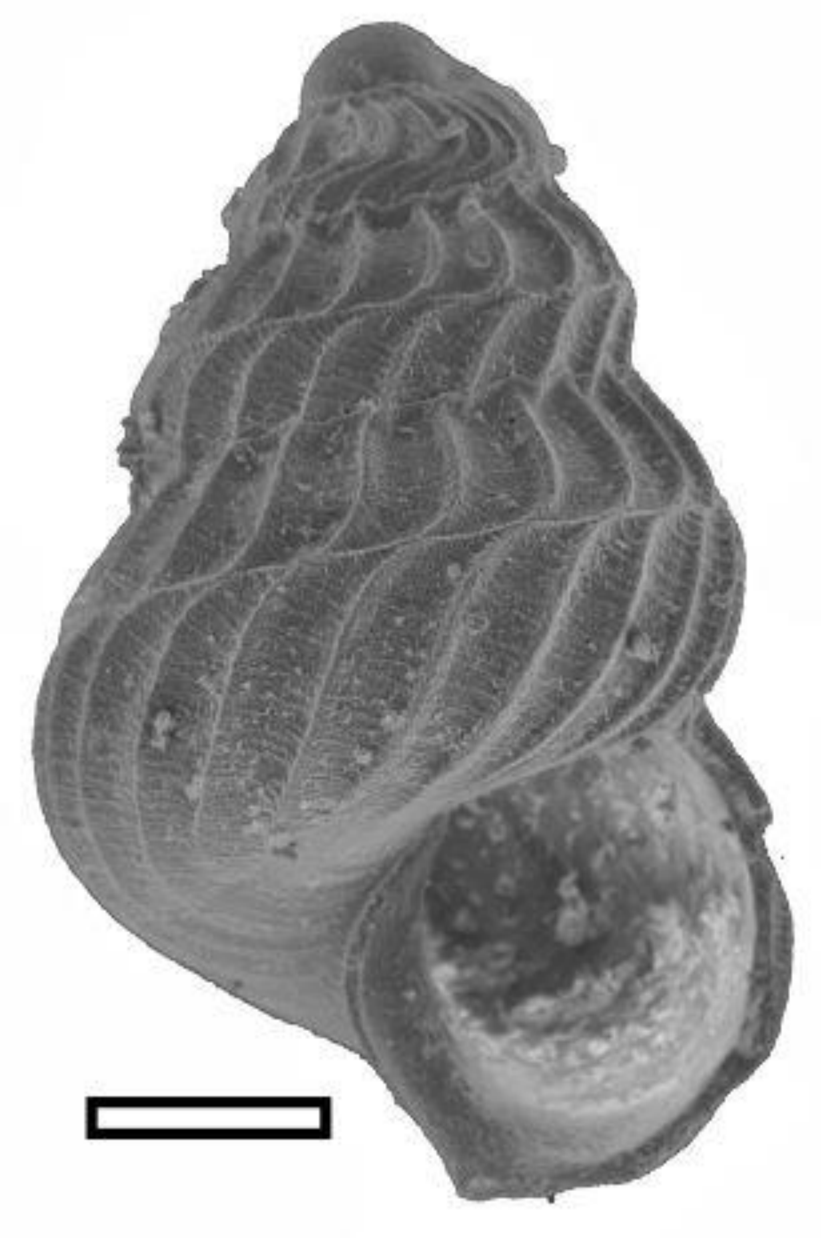
- `Momocs` R package
- Custom code from Manuel F. G. Weinkauf



The workflow

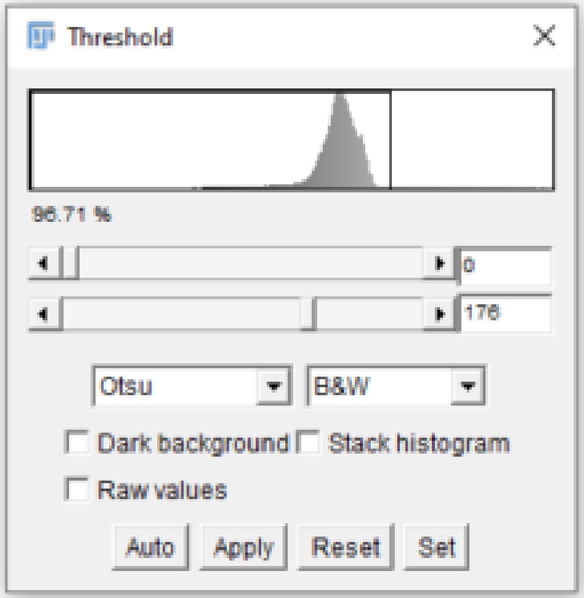
1. Photograph Specimens
2. Binarize Photos
3. Digitize outlines
4. Create Fourier Decomposition
5. Analyze!

Photograph specimens



Binarize Images

FJIJI: **F**iji **I**s **J**ust **I**mageJ



Threshold

96.71 %

0

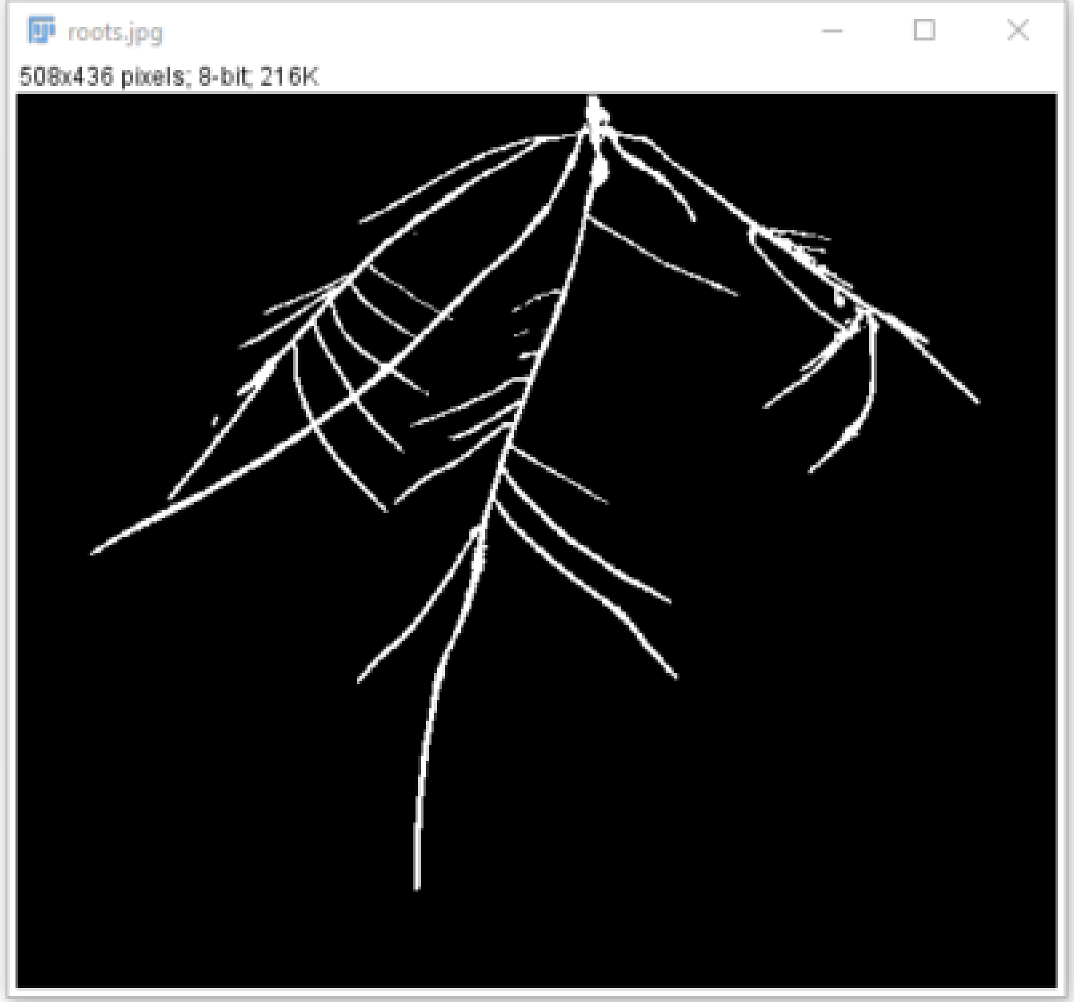
176

Otsu

B&W

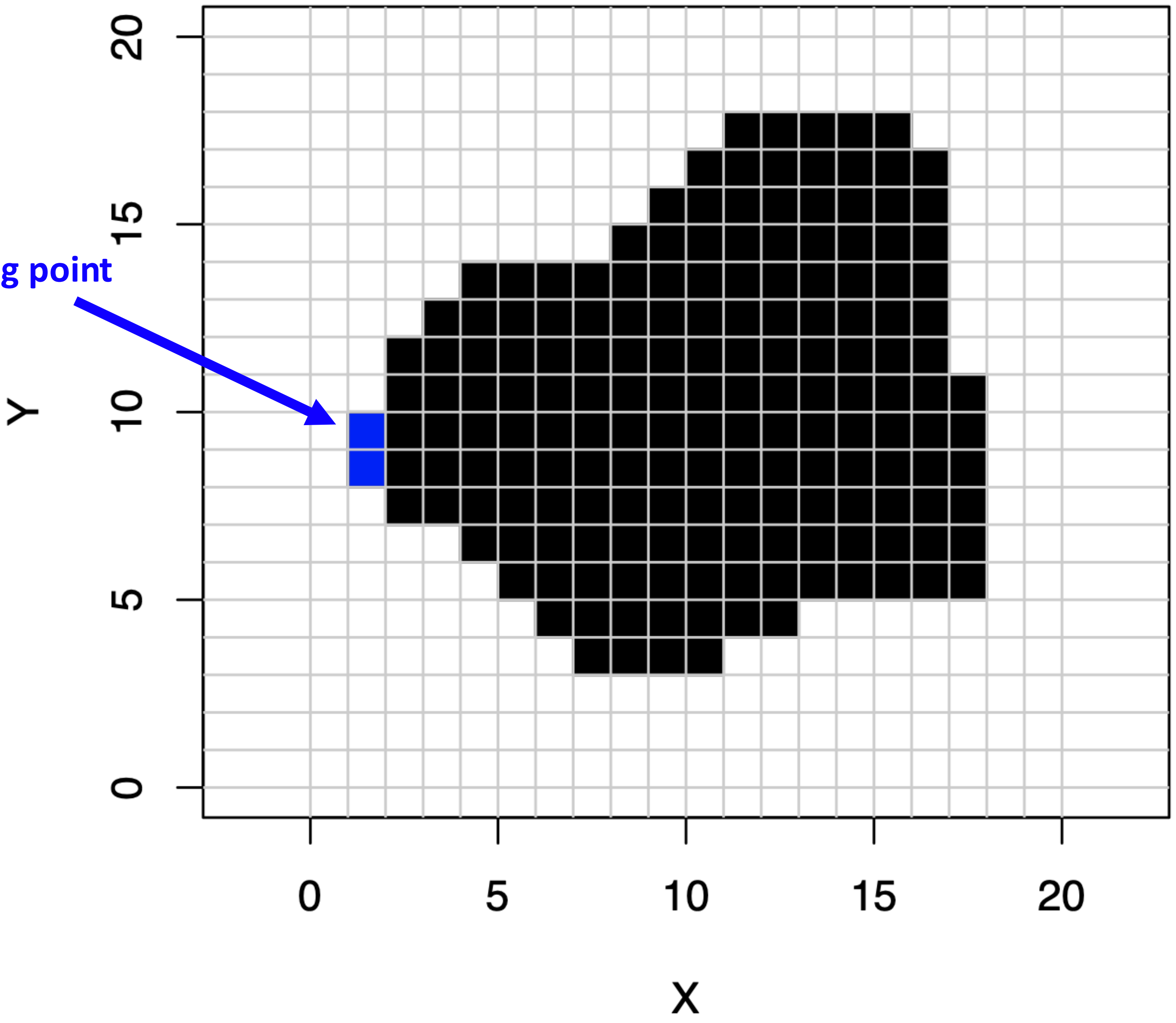
☐ Dark background ☐ Stack histogram

☐ Raw values

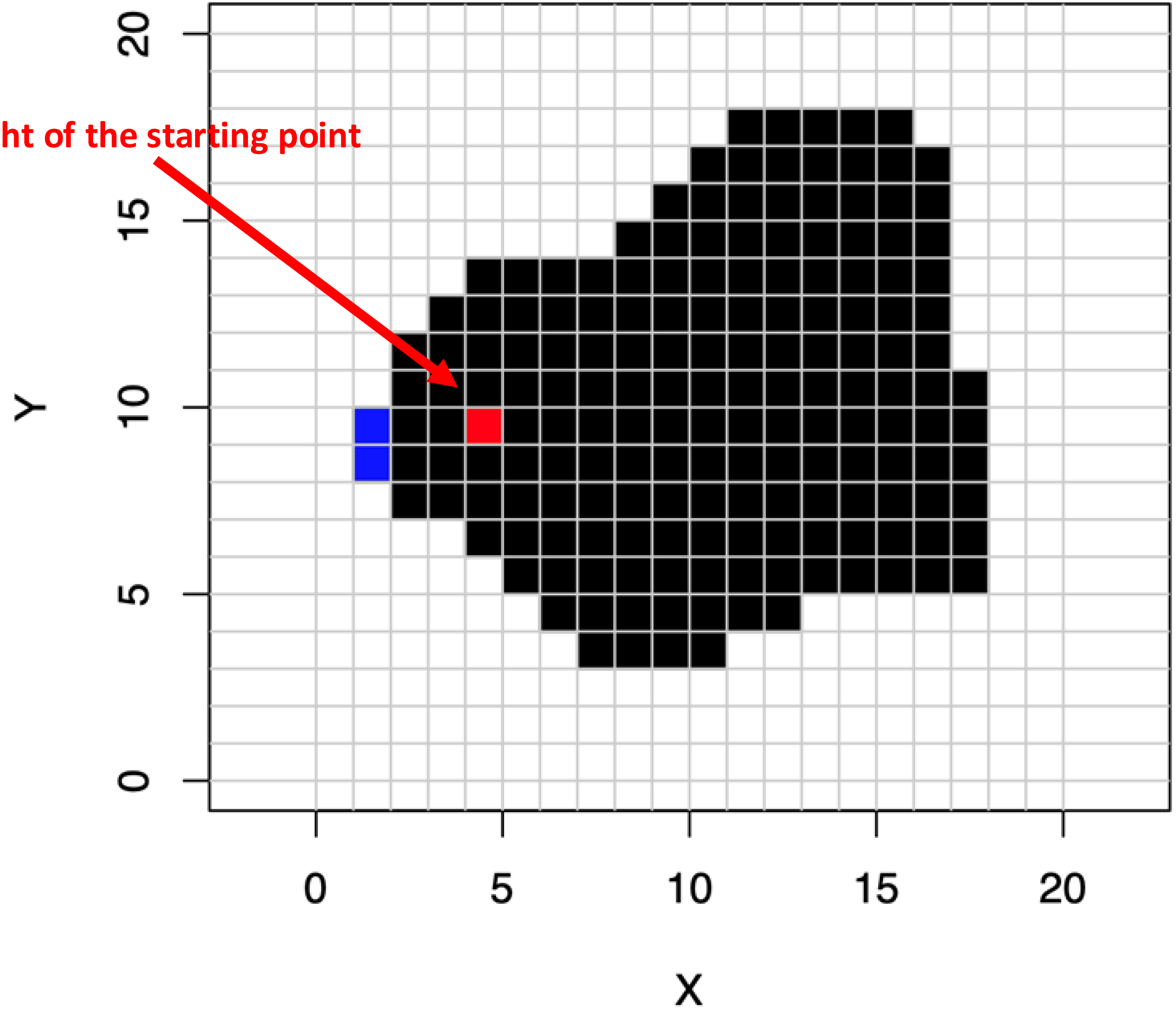


roots.jpg

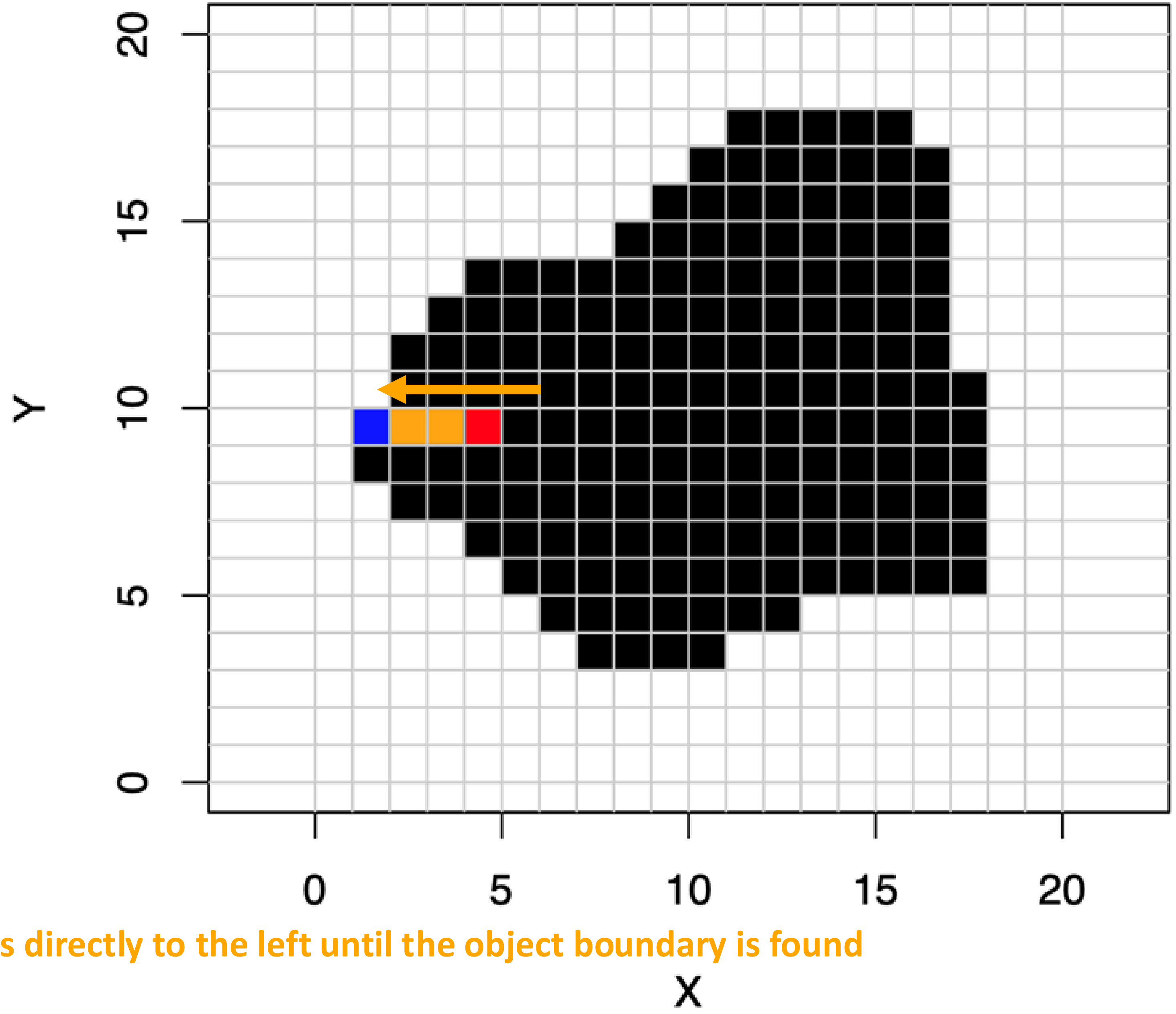
508x436 pixels; 8-bit; 216K



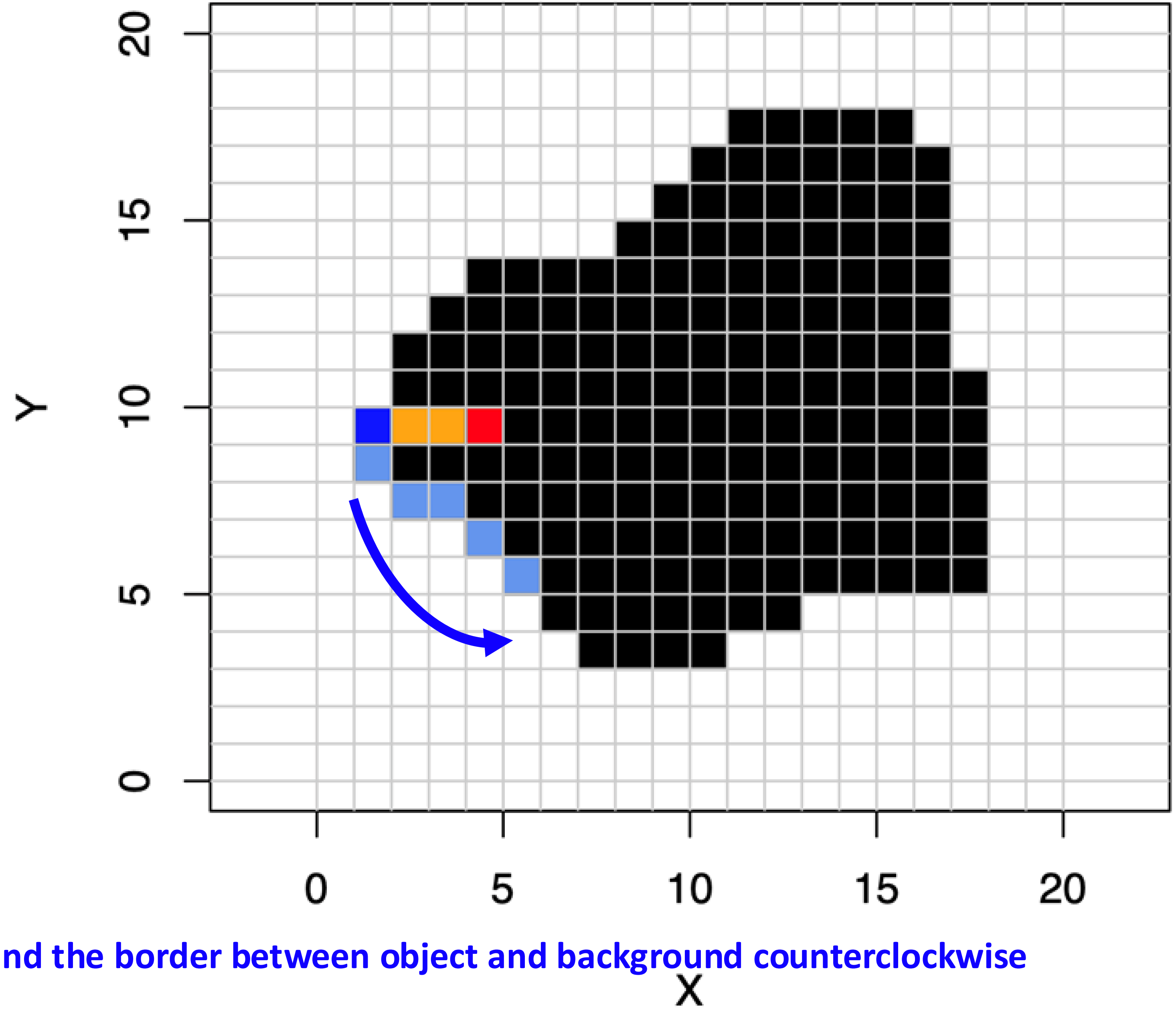
Homologous starting point



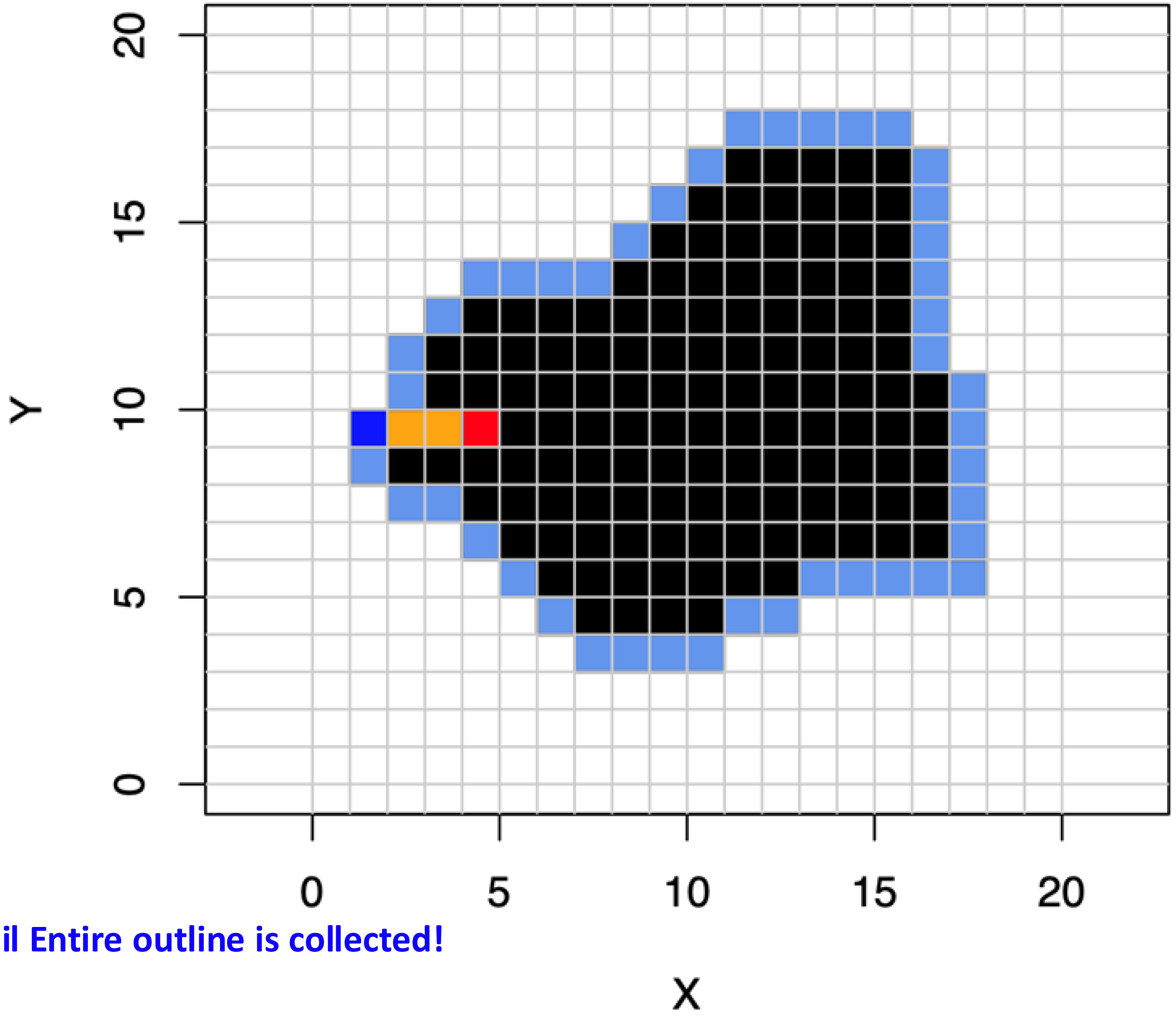
You click to the right of the starting point



Algorithm walks directly to the left until the object boundary is found



Algorithm walks around the border between object and background counterclockwise



Until Entire outline is collected!

Image requirements

- All specimens must be rotated to be roughly the same orientation
- Homologous point has to be to the left