Integrating digital datasets to quantify morphological variability and understand species delimitation: an innovative approach using terebratulide brachiopods

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UC DAVIS

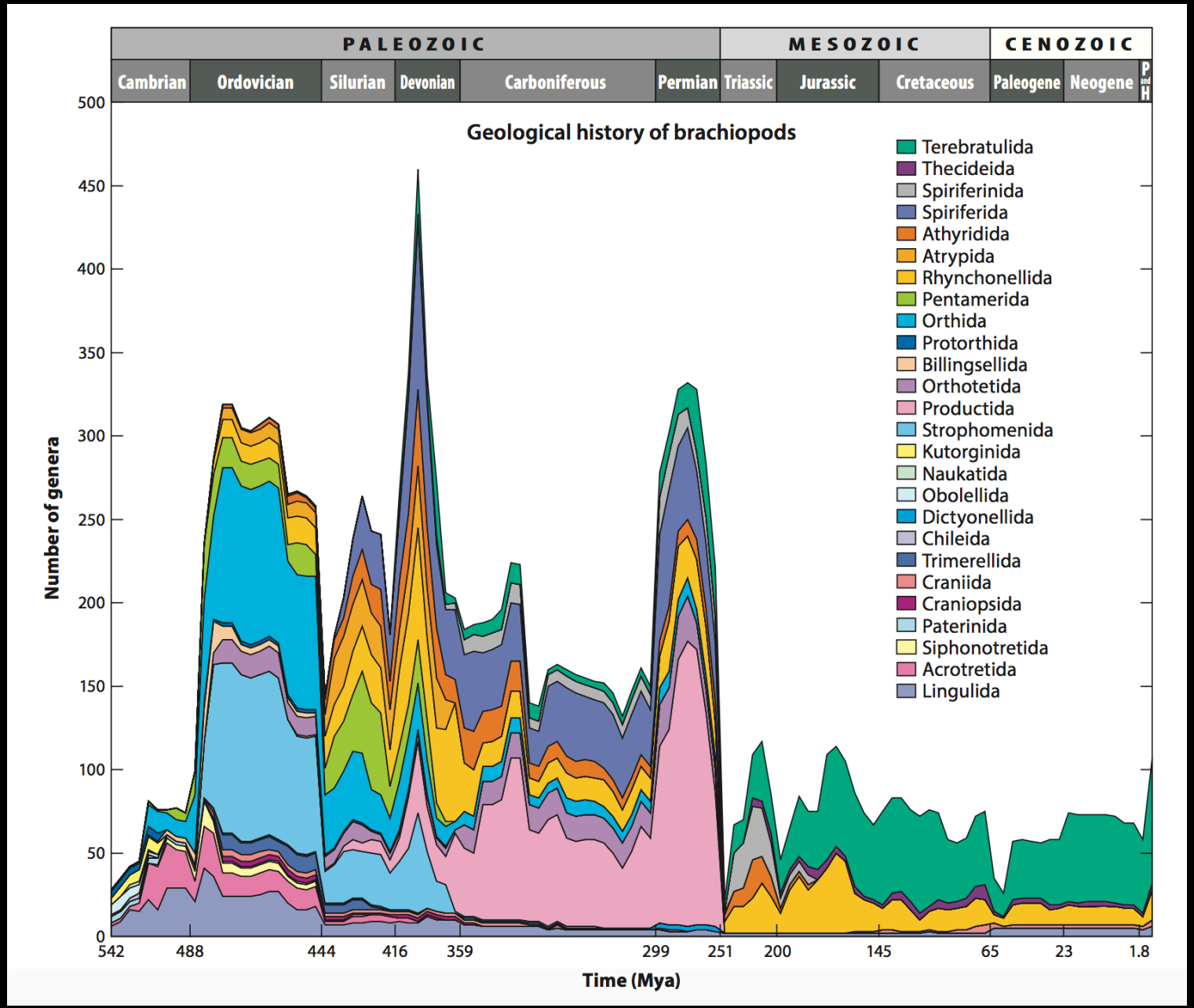
DEPARTMENT OF EARTH AND PLANETARY SCIENCES

What are brachiopods?

- Marine invertebrates
- Lophotrochozoans—related to phoronids, bryozoans, annelids, and nemertreans
- Shells with two valves
- Lophophore—feeding and respiratory organ

Brachiopod diversity through time

- Highly diverse and abundant during Paleozoic
- Dramatic decline after Permian-Triassic extinction
- Current populations seem to be decreasing



Taken from Carlson (2016) adapted from Curry and Brunton (2007)

What drives our research?

- Commonly thought that external morphology offers little resolution for classification in terebratulide brachiopods
- Internal morphology is necessary but rarely analyzed quantitatively
- Testing validity of named species
- Biodiversity estimation

Dallinella occidentalis

Terebratalia transversa

Terebratalia coreanica

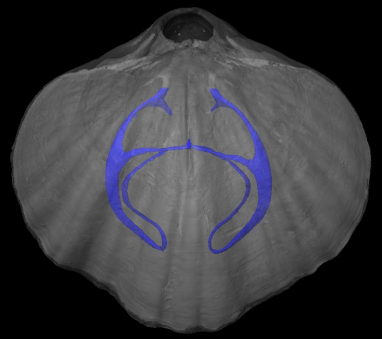
Laqueus erythraeus

Laqueus vancouveriensis

Laqueus rubellus

Research questions

- Is it possible to discriminate named species based on loop morphology?
- Can we discriminate named species based on shell outlines?
- Is there a correspondence between loop shape and shell outline?



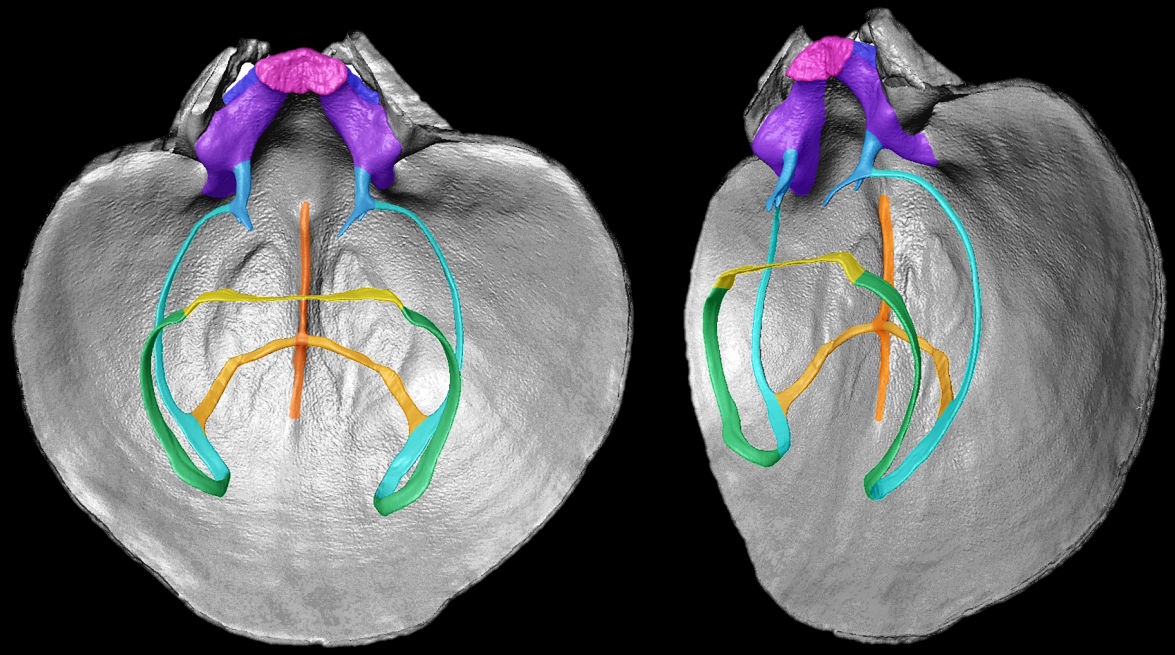
Dallinella occidentalis

Dallinella occidentalis

Terebratalia occidentalis?

Long loops in brachiopods

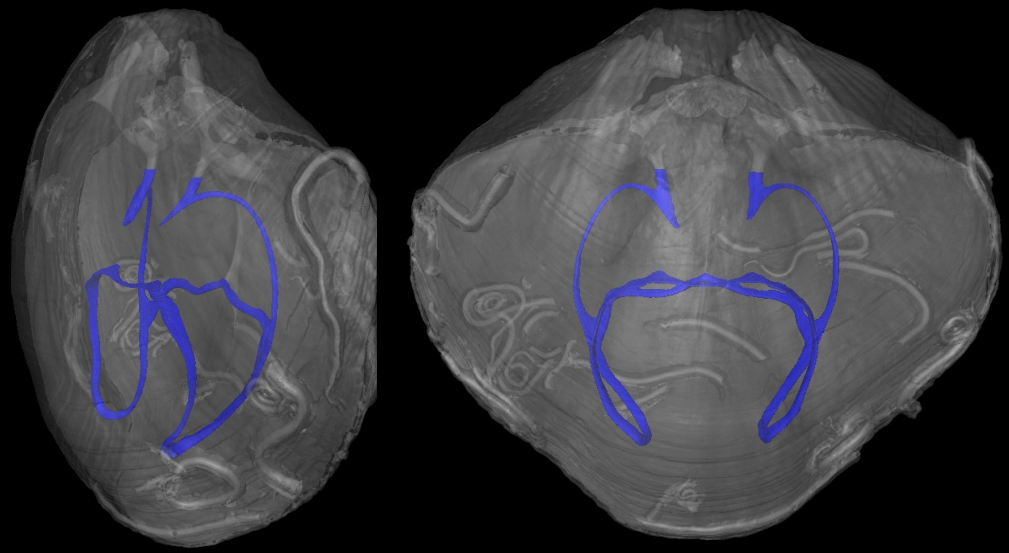
- Calcareous structure that supports the lophophore
- Most conspicuous morphological character in terebratulids
- Phylogenetically and taxonomically important



Terebratalia transversa

How do we study long loops?

- To capture the shape and its variability in a quantitative manner, it is necessary to work with 3D reconstructions and 3D geometric morphometrics.

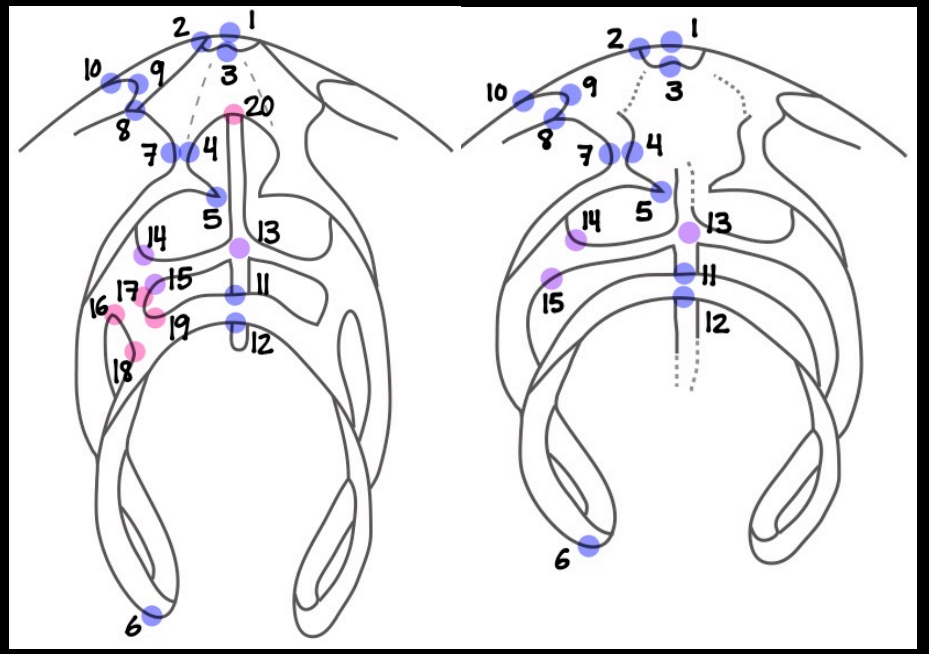


Terebratalia transversa

Methods

3D isosurface models	• From CT scans • Amira
Landmark and semilandmark registration	• Based on proposed landmark schemes • Stratovan Checkpoint
Landmark superimposition	• Generalized Procrustes Analysis • Semilandmark sliding using bending energy
Ordination Methods	• Principal Component Analyses (PCA) • Canonical Variate Analyses (CVA)
Statistical methods	• Procrustes ANOVA

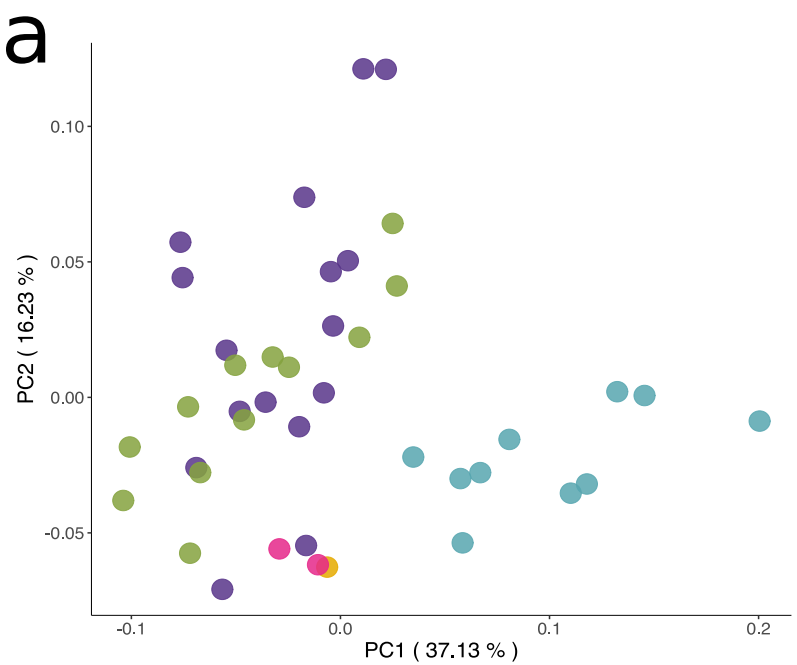
R packages geomorph and Morpho

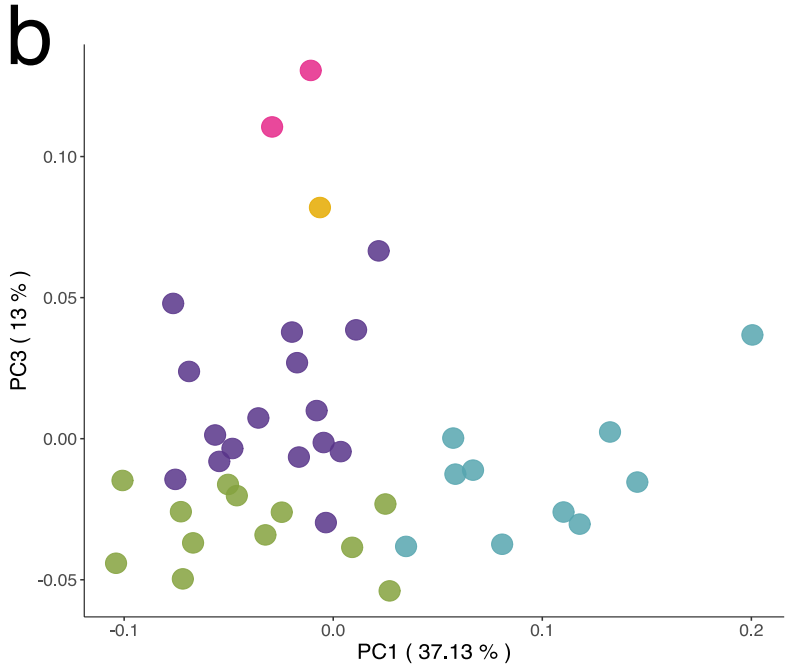


Results—are loops informative?

Overall classification accuracy: 100%

Named species statistically different in shape (p=0.001)





L. blanfordi
L. erythraeus
L. quadratus
L. rubellus
L. vancouveriensis

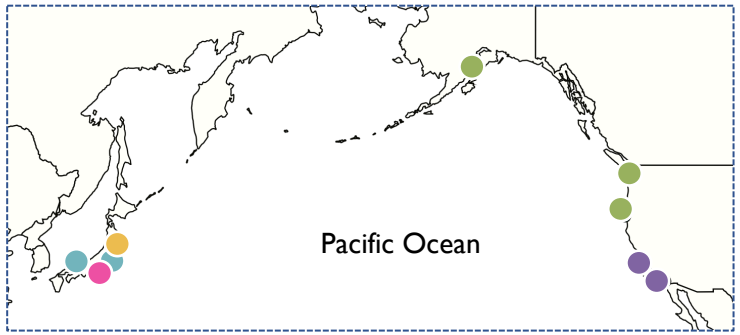
L. blanfordi

L. erythraeus

L. quadratus

L. vancouveriensis

L. rubellus

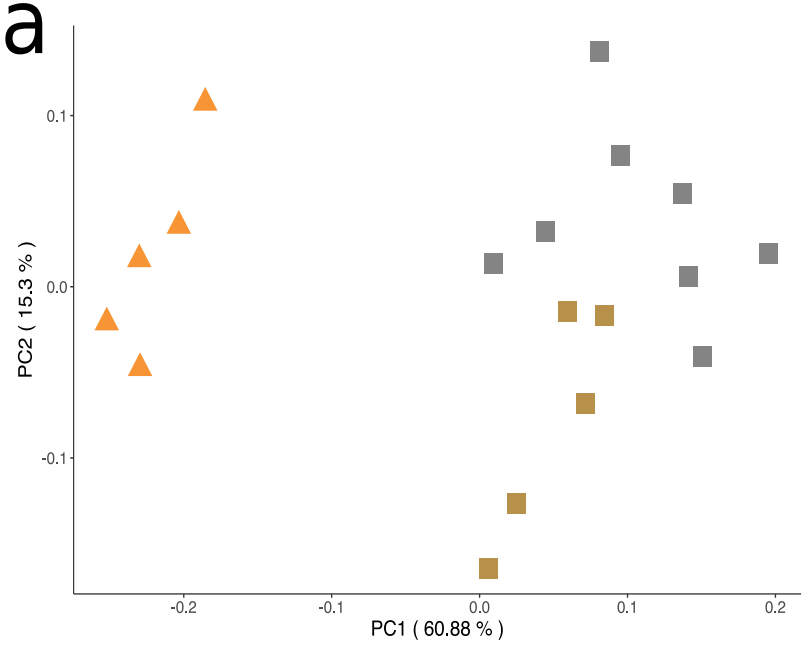


Results—are loops informative?

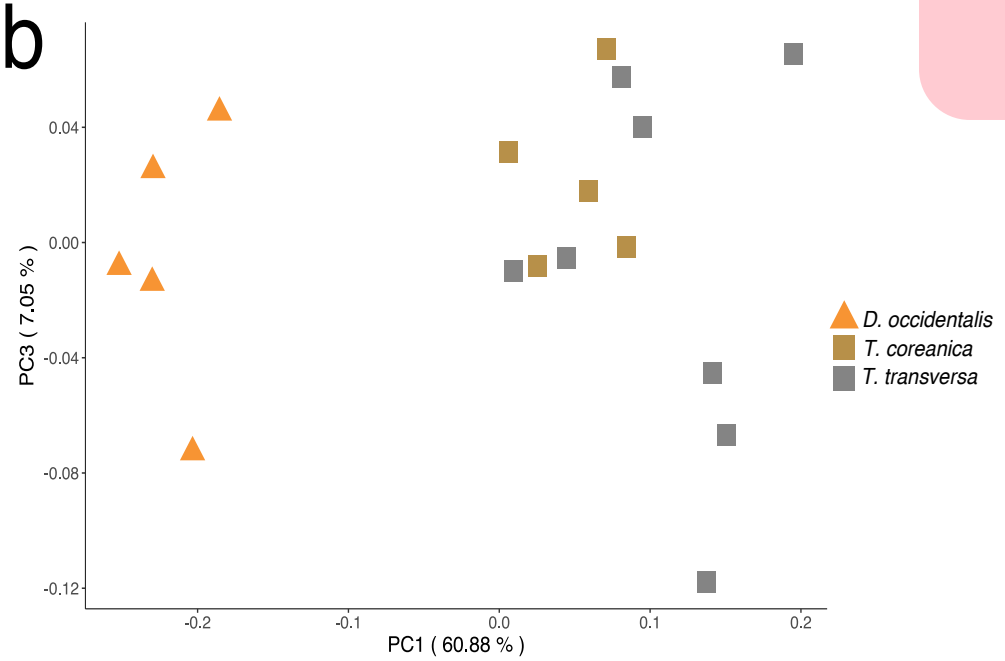
Overall classification accuracy: 72.22%

Named species statistically different in shape (p=0.001)

a



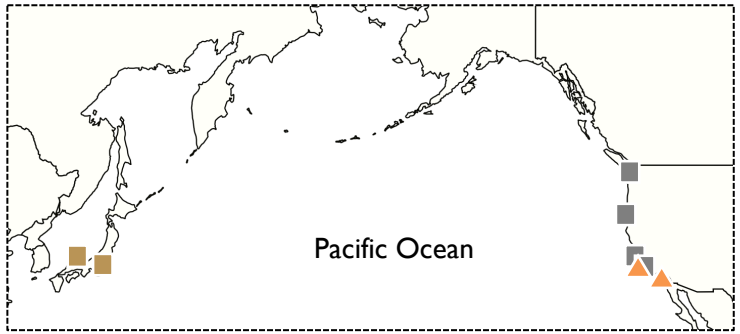
b



Dallinella occidentalis

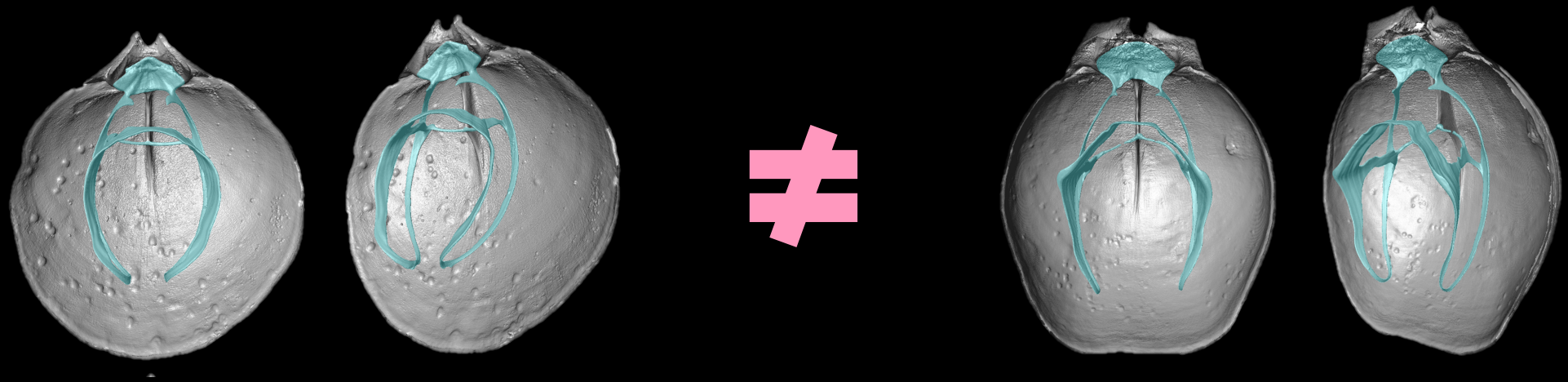
Terebratalia transversa

Terebratalia coreanica



Results—are loops informative?

- Yes!
- Loops offer sufficient resolution to discriminate between named species.



Laqueus vancouveriensis ≠ *Laqueus erythraeus*

What happens when loops are not present?

- Loops are rarely preserved in fossils
- Are outlines a good proxy for loops?

Exceptional

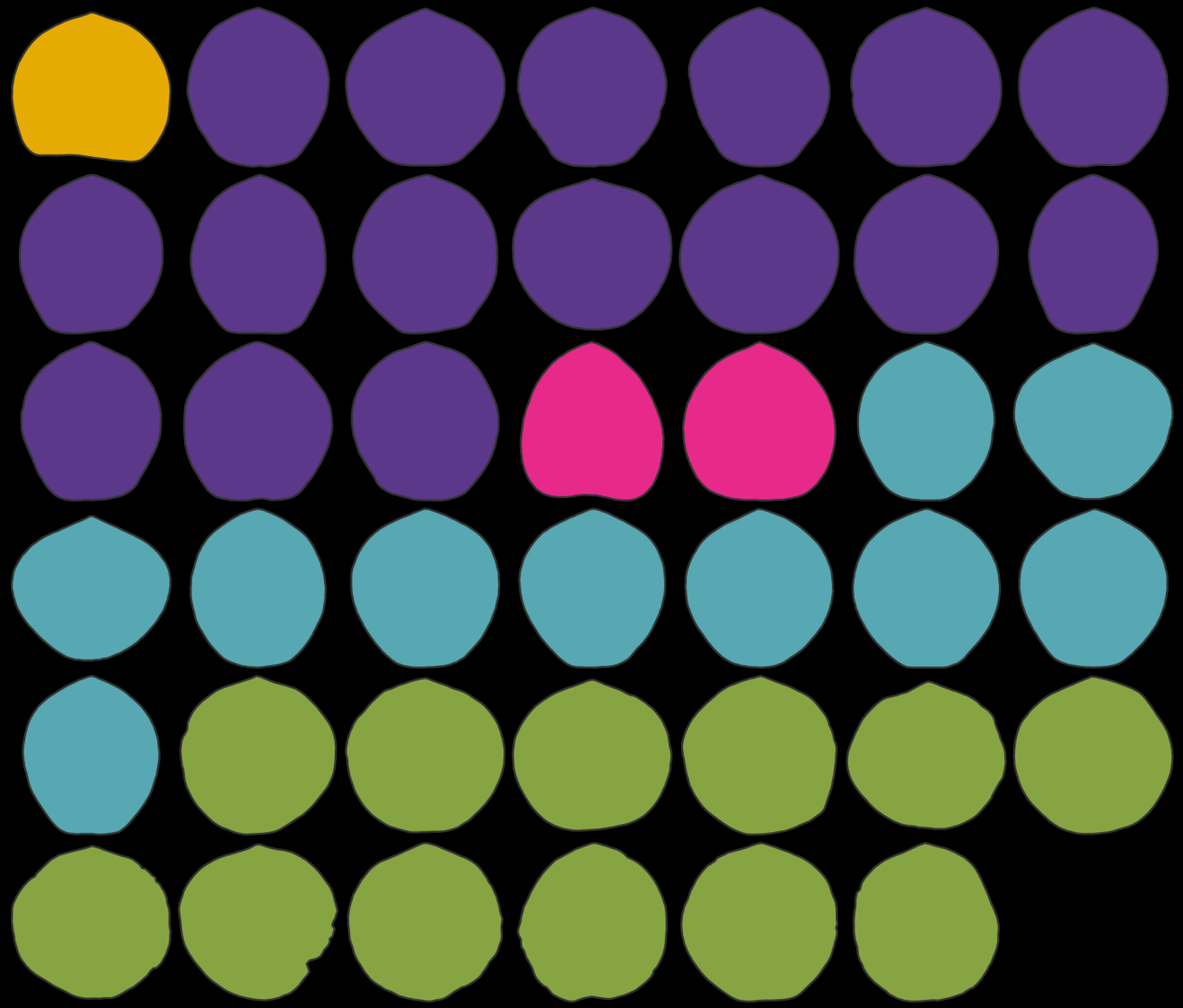
Terebratalia smithi? Late Pliocene

Common

Laqueus vancouveriensis, Pliocene

Outlines

- *Laqueus*
- Same specimens as 3D GM analysis
- Outlines of dorsal valve

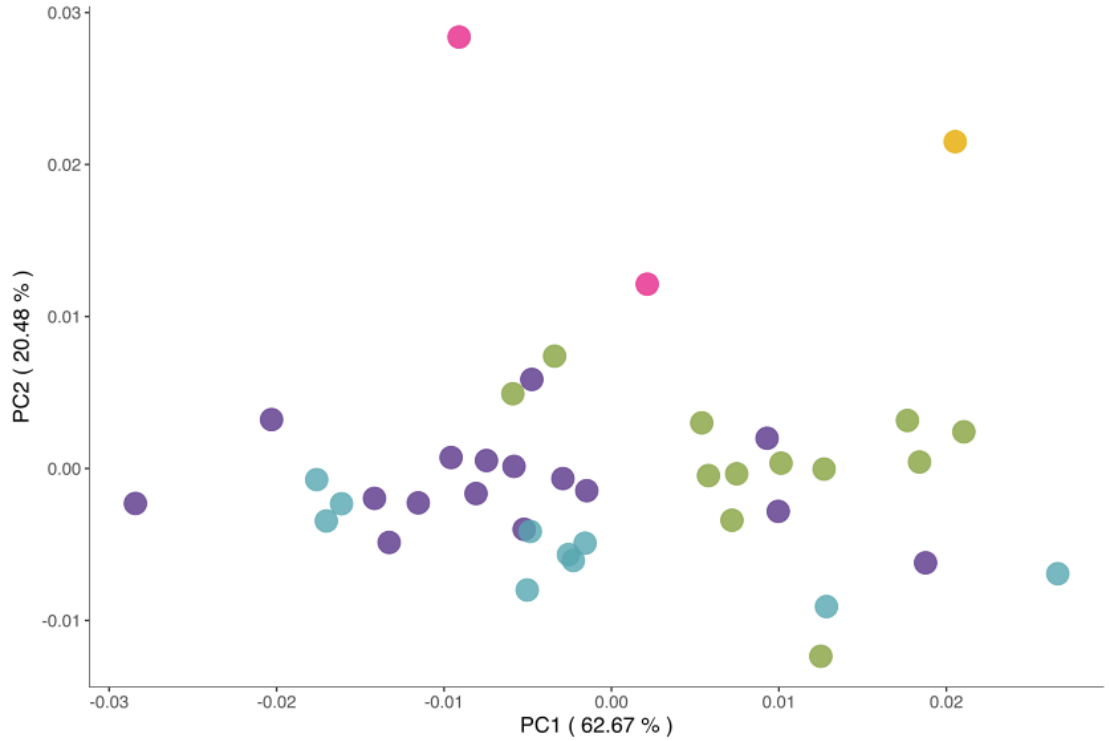


Methods

Outline digitization	• From CT scans • Illustrator
Elliptical Fourier Analysis	• Procrustes Analysis to align outlines • EFA
Ordination Methods	• Principal Component Analyses (PCA)
Morphological integration	• Partial least squares analysis • Long loop CT dataset and outlines

R packages Momocs and geomorph

Outline results



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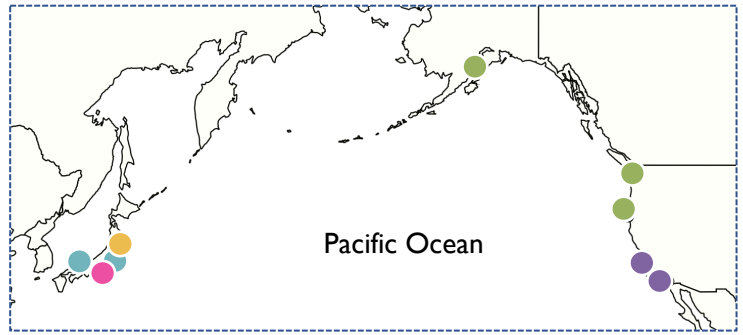
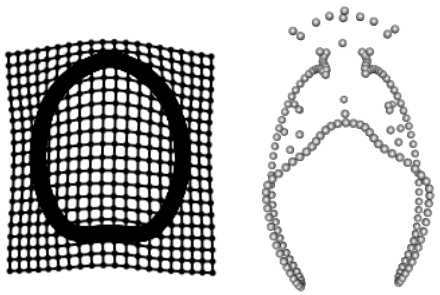
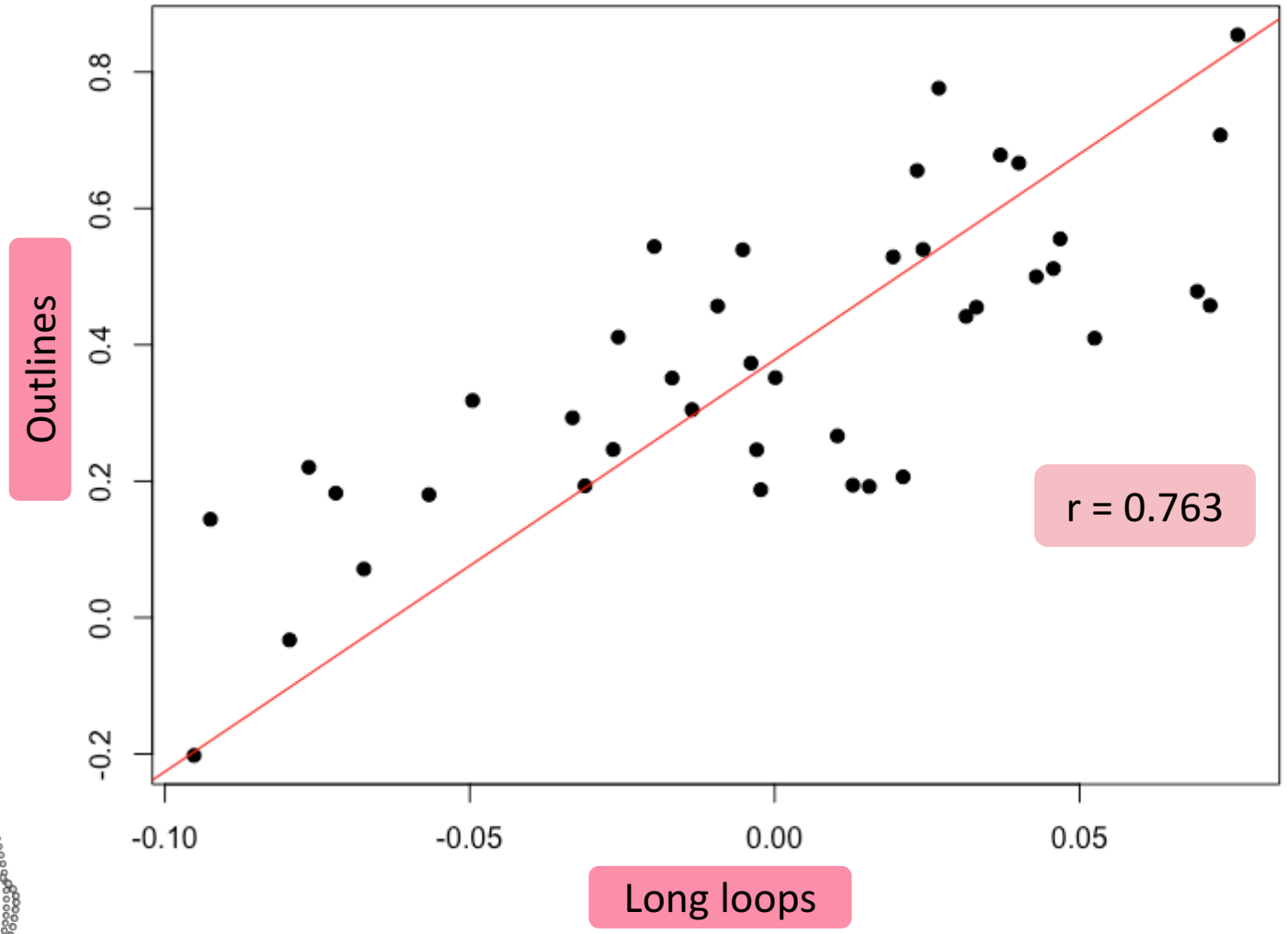
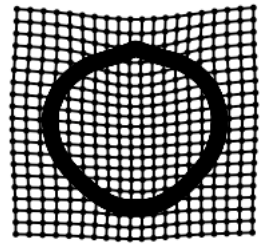


Is there a correspondence between loop shape and shell outline?

PLS







Going further

- How can we take these morphological analyses a step further?
- Can we test our morphological predictions using a genetic data?
- Species delimitation analyses using genetic data.

Genetic analysis

Collection of specimens

- East and West Pacific localities
- Approx. 10-15 indiv/ loc

DNA extraction and sequencing

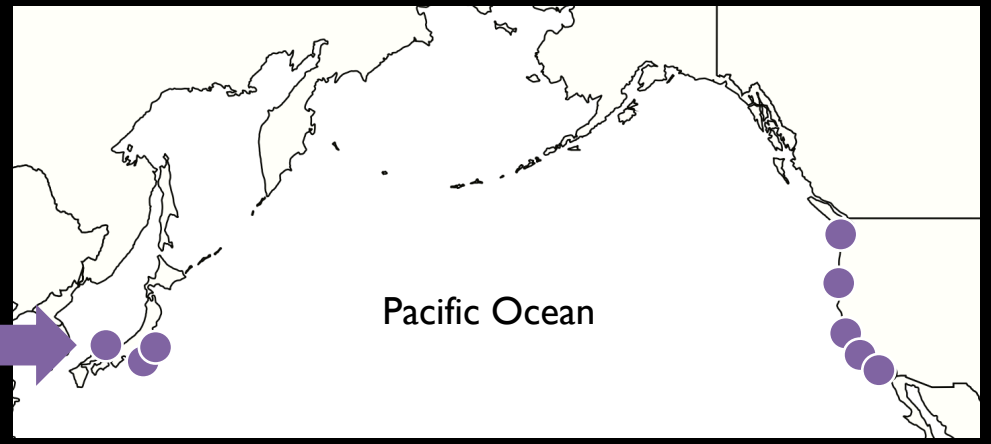
- RADSeq—uses restriction enzyme to cut DNA in fragments
- Illumina sequencing

Phylogenetic analysis

- Single nucleotide polymorphisms (SNPs), heterozygosity, population differentiation
- Maximum Likelihood and Bayesian phylogenetic inference

Species delimitation

- Bayesian analysis of sequence data using the multispecies coalescent model



L. rubellus
T. coreanica

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Conclusions

- We can discriminate named species based on loop morphology. Species are statistically significantly different.
- Shell outlines offer less resolution when trying to discriminate between named species. However, outline data is valuable when loops are not present.
- Importance of treating named species as hypotheses to be tested.
- Importance of accurately estimating biodiversity.

Acknowledgments

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