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Using the classic Raup shell growth model as a morphometric tool to investigate genetic variation

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Two ecotypes of the marine snail species *Littorina saxatilis* have, as a result of strong natural selection, maintained different shell shapes in distinct, adjacent environments. Being able to quantify and compare the underlying growth structure for the two ecotypes should provide a better insight into the reasons behind the variability of shell shapes, and connect this to the genetics and selective pressures in their respective habitats.

Building on the ideas of Raup, we can construct models of snail shells using logarithmic curves containing a set of biologically descriptive growth parameters. This way of modelling illustrates the construction process of the shells, and the growth parameters are therefore expected to relate closely with the underlying genetics.

Previous biological shape research has mainly analysed the shells using variation of a set of landmarks after Procrustes alignment. This method can quantify the shape differences, but does not give an explicit explanation of how or why they occur. Because of the substantial amount of landmark coordinate data available for *L. saxatilis*, we have developed a geometric method for inferring the growth parameters from these points.

Applying this new analysis to snails collected across contact zones between ecotypes gives the result that growth parameters differ between them and that snails from the hybrid zone show intermediate values, which is consistent with the previous morphometric analysis. However, since the growth parameters are biologically meaningful they should be more informative from a developmental and genetic point of view, and we are going to investigate the performance of both shape characterizations in explaining the genetic variation.

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