

Cranium

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Abstract

Collaborated with the Barresi Lab, we continued Δ SCOPE by extending functionalities in R package—Cranium. We modified existed functions in Cranium, built new functions and optimized parameters so that evaluating sample alignments is no longer vulnerable to subjective biases. Additionally, alignments will be able to run automatically without labor-intensive manual correction that would introduce more researcher biases.

Author summary

This is our first draft.

Abstract

Introduction

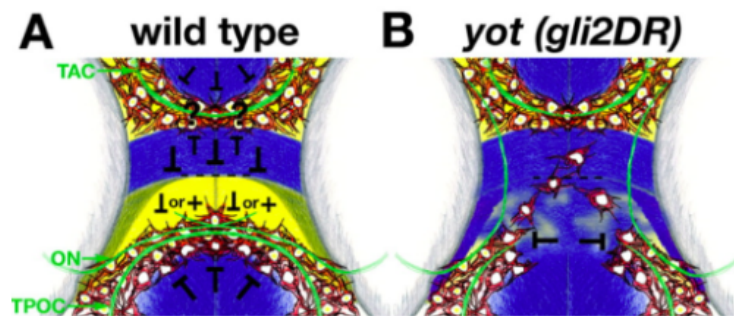


Fig 1. Wild Type and Mutant Commissure

Data

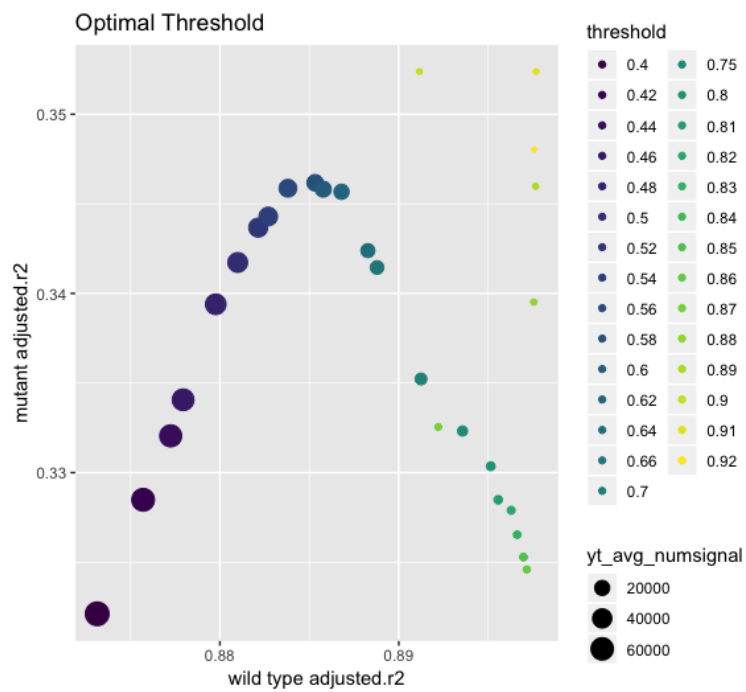
3

Programming Languages

4

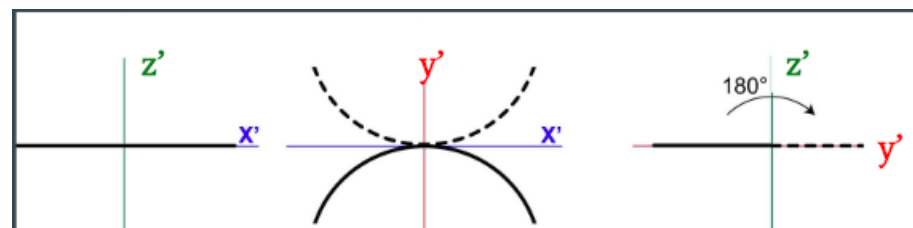
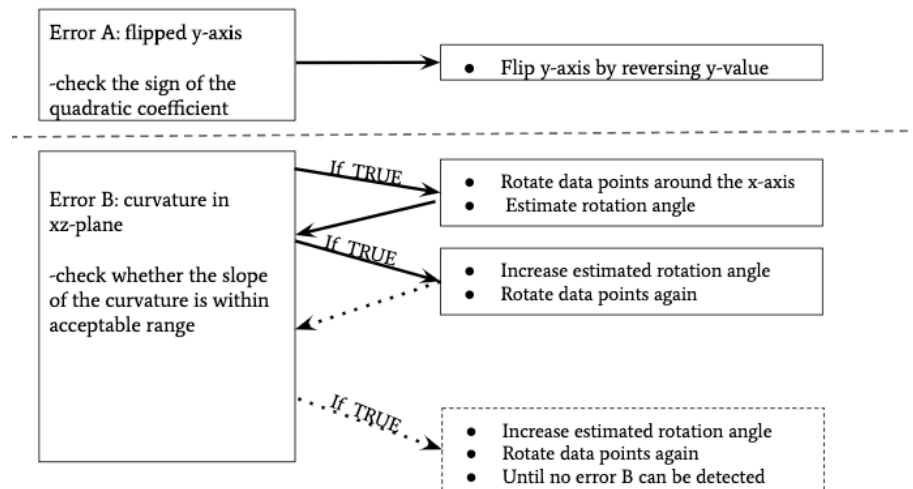
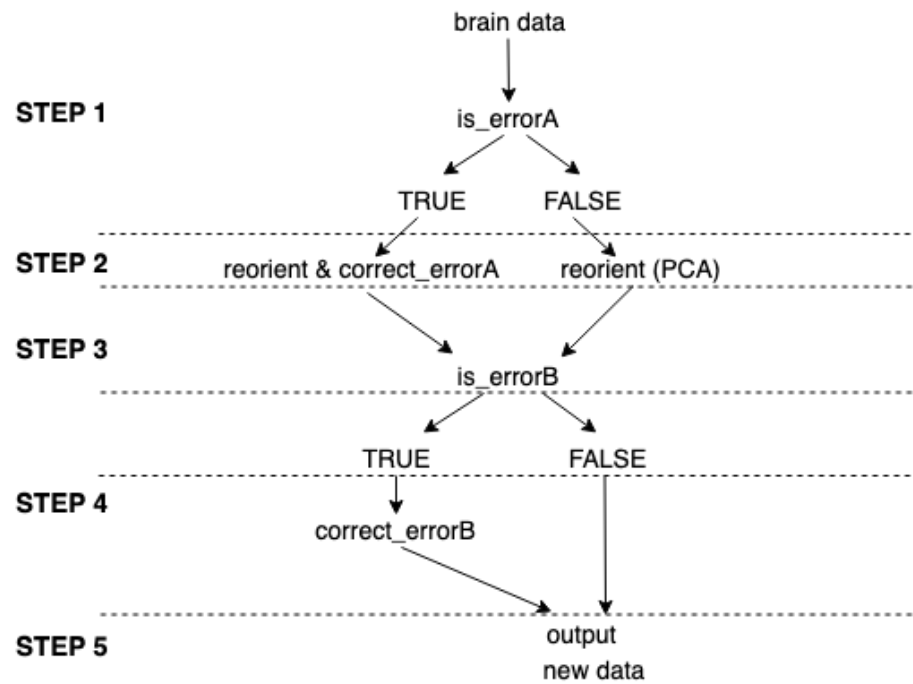
Pre-Correction

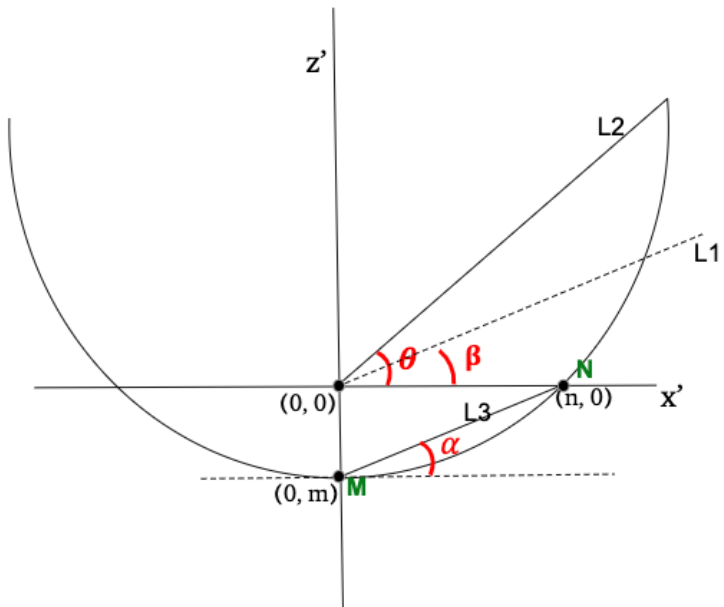
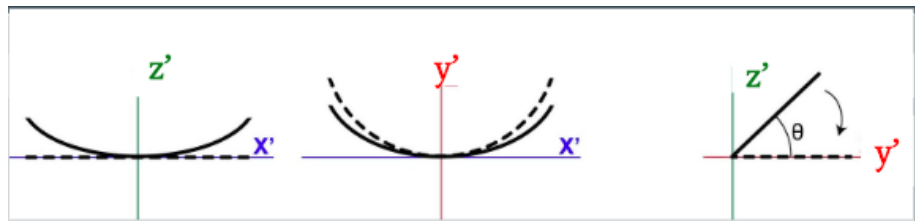
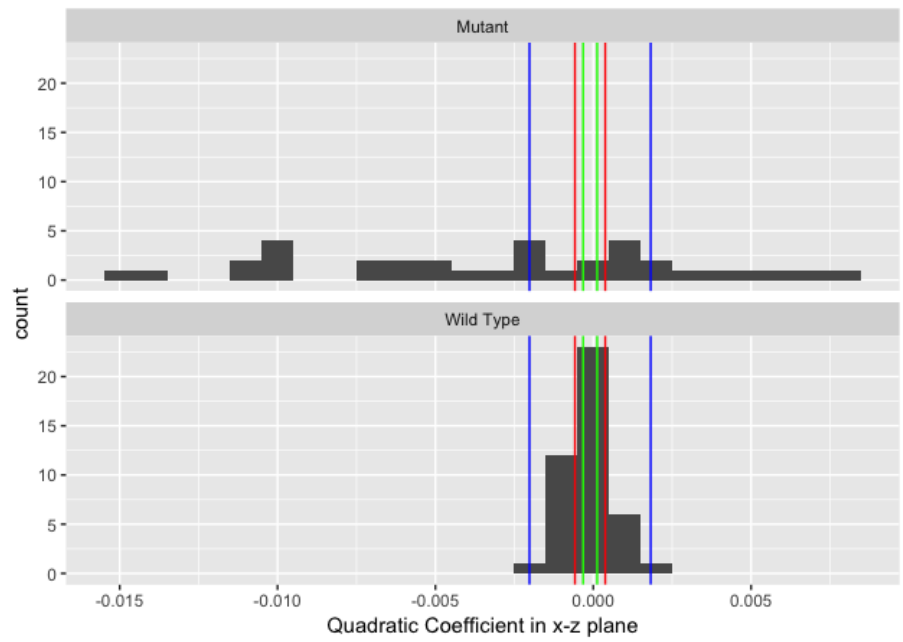
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Correction

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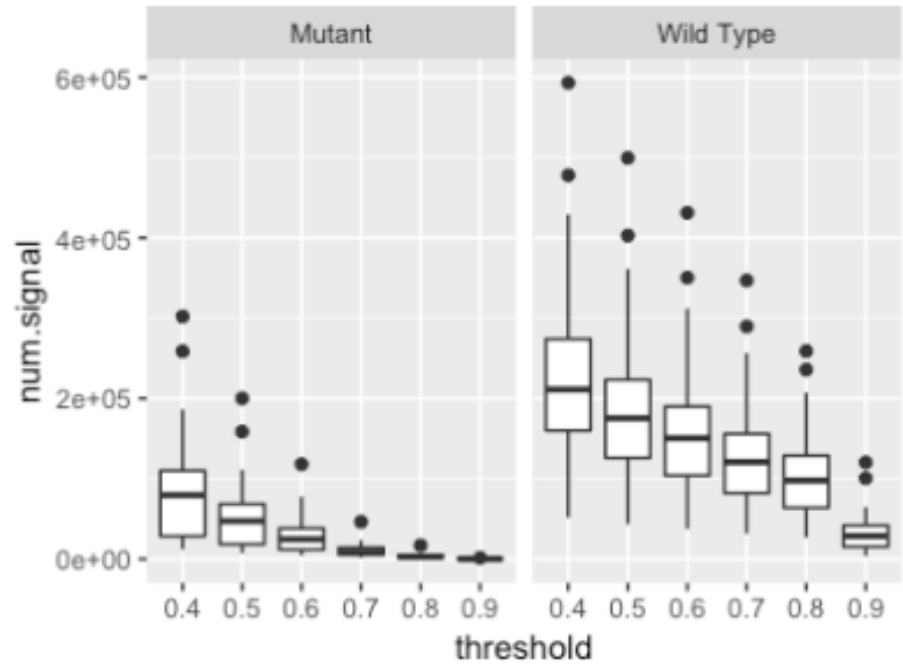


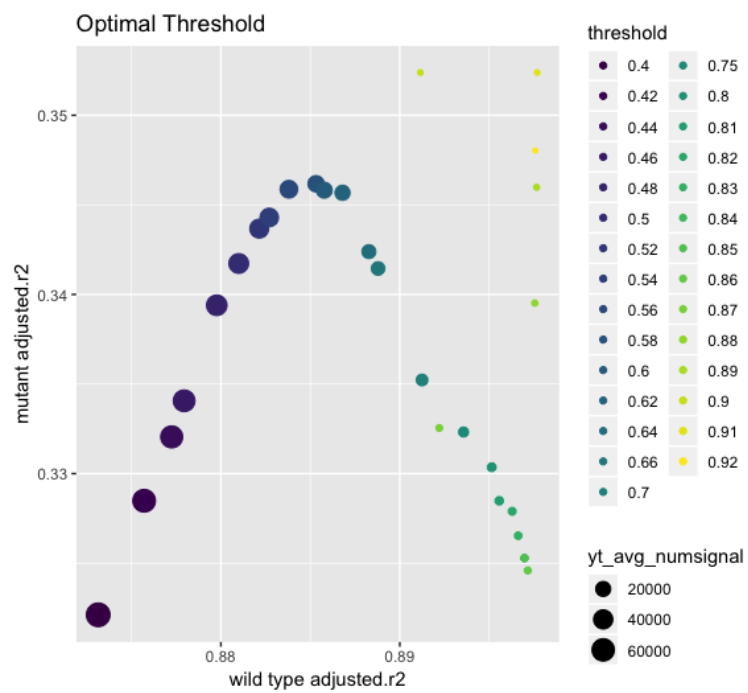
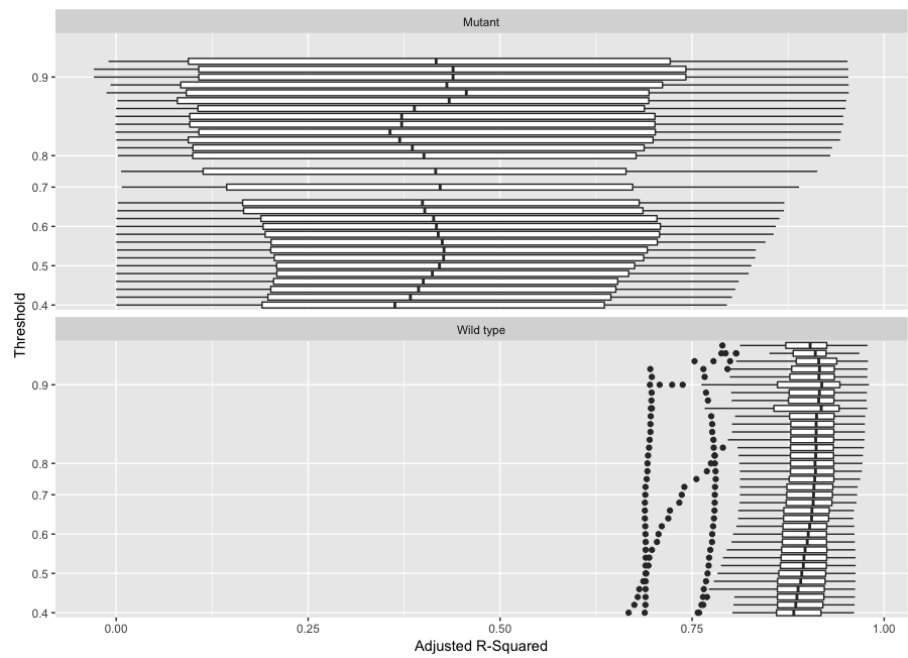


$$R_x(\theta) = \begin{bmatrix} 1 & 0 & 0 \\ 0 & \cos \theta & -\sin \theta \\ 0 & \sin \theta & \cos \theta \end{bmatrix}$$

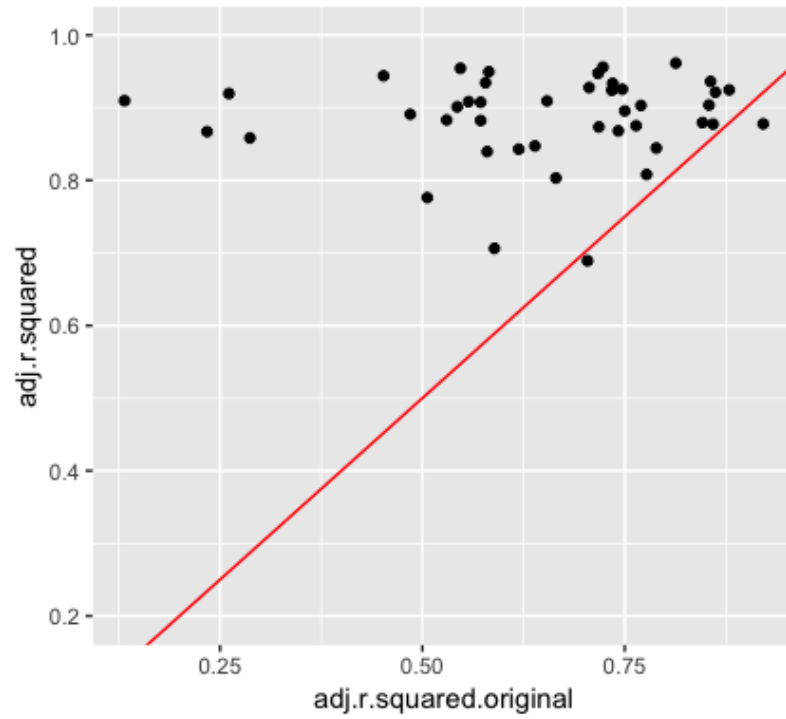
Results

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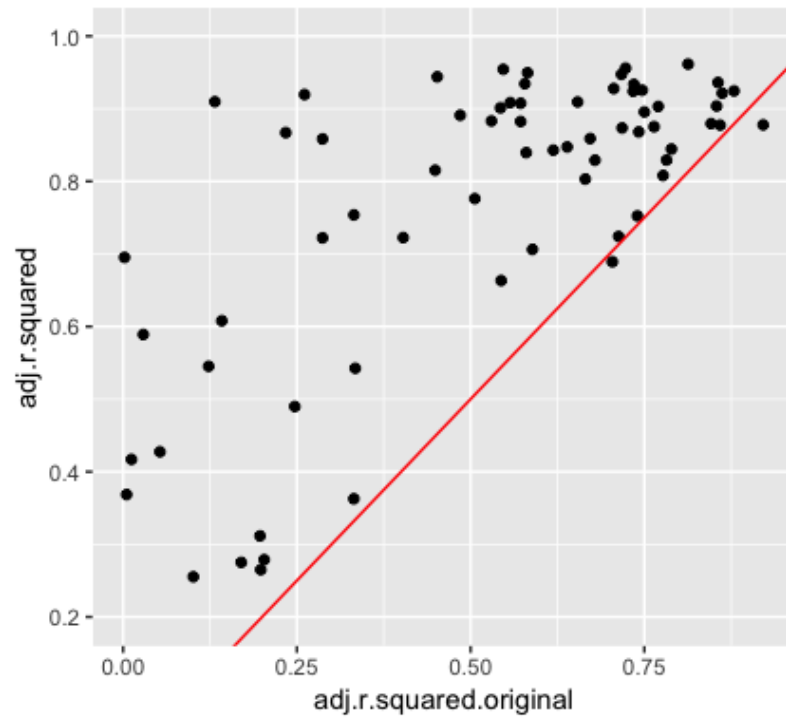




Adjusted R square before and after reorientation



Adjusted R square before and after reorientation



Conclusion

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Future Research

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