

INTRODUCTION

Image analysis is, by definition, the obtention of **metrics** describing the objects contained in a particular image. In a perfect situation, these descriptors would accurately represent the biological object in the image and we could consider that the difference between the descriptors and the biological truth is negligible. However, in many cases, **artefacts** might be present in images in such a way that the representation of the biological object is not accurate anymore. These are likely to impede the image analysis and create a gap between the descriptors and the data.

LIBRARY OF ROOTS

We used the structural root model **ArchiSimple** to create a large library of random root systems (10 000, with 3 image degradation levels, **fig A**).

For each root system, we created an RSML file that contained to whole root system structure. From that RSML file we could then compute (i) the **ground-truth** metrics for the root system and (ii) and a **2D image** of the root system.

The **root system library** is freely available on Zenodo: <http://bit.ly/root-lib>

VALIDATION

We used a custom-made image analysis pipeline to extract classical **root system descriptors** from each image of the library. Example of descriptors are the width, depth, total length or number of root tips.

We compared these descriptors with the ground-truth data and observed (i) that large **errors** are likely to arise for large root system and (ii) that these errors are **non-linear** and hard to predict (**fig B**).

The errors were dependent on the **image quality**, the root system **size**, the considered **metric** and the root system **type** (tap-rooted or fibrous)

IMPROVEMENT

In order to improve the quality of the metrics obtained from the images, we train a **Random Forest** algorithm to predict parameters of interest (that are to obtain) from image descriptors (that are easy to obtain but with limited biological relevance).

We tested this approach both on our simulated root system library [Lobet, Koevoets, Noll et al. 2017] (**fig. C**) and on experimental images [Atkinson, Lobet et al. 2017]. In both cases, the Random Forest predictors were better than the conventional approach.

CONCLUSION

We have used a combinaison of structural root models and machine learning to improve root image analysis pipeline.

Our pipeline was bundled into a R Shiny app and is available at <http://bit.ly/primal-app>

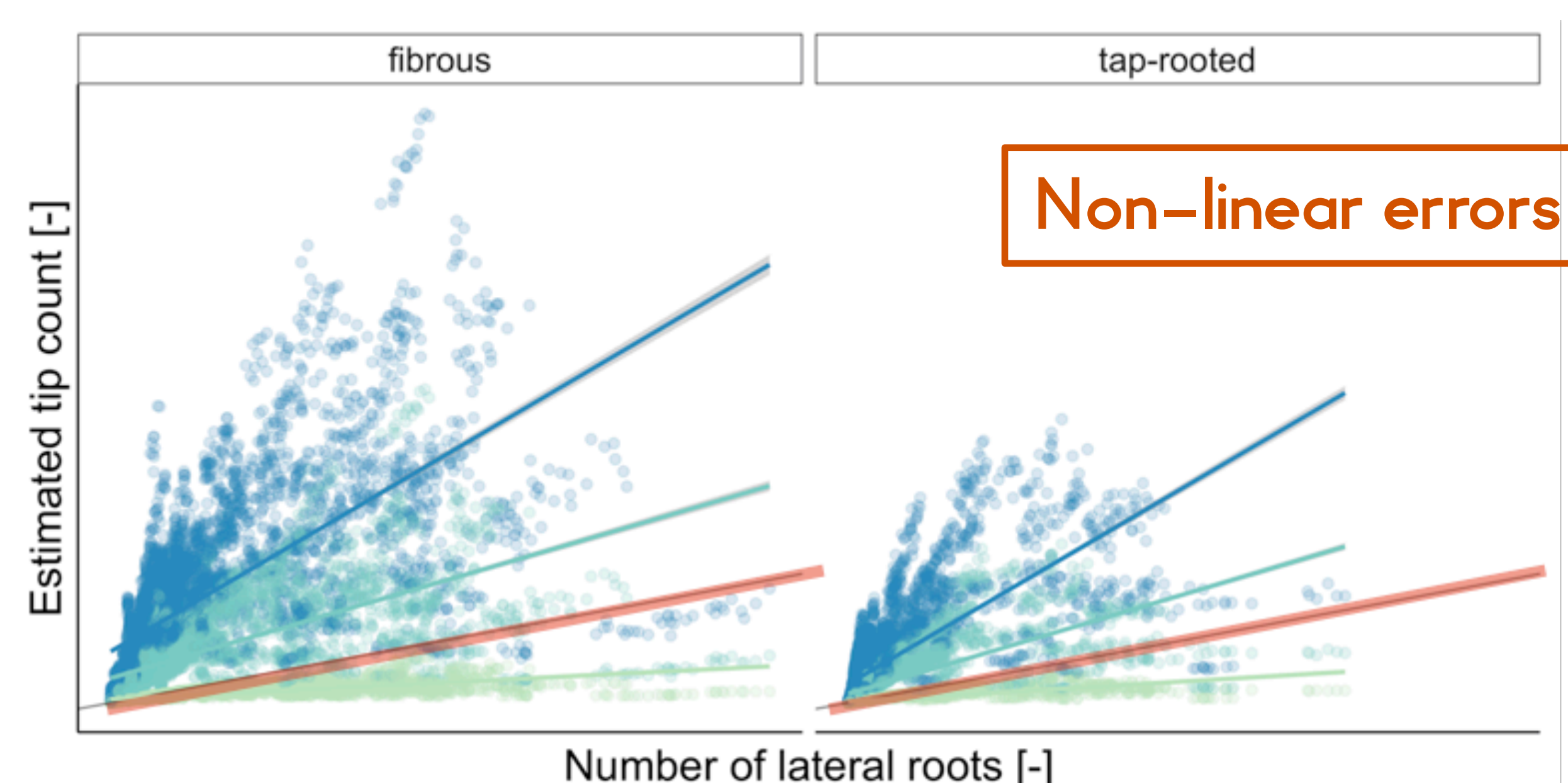
A

LIBRARY OF 10 000 ROOT SYSTEMS



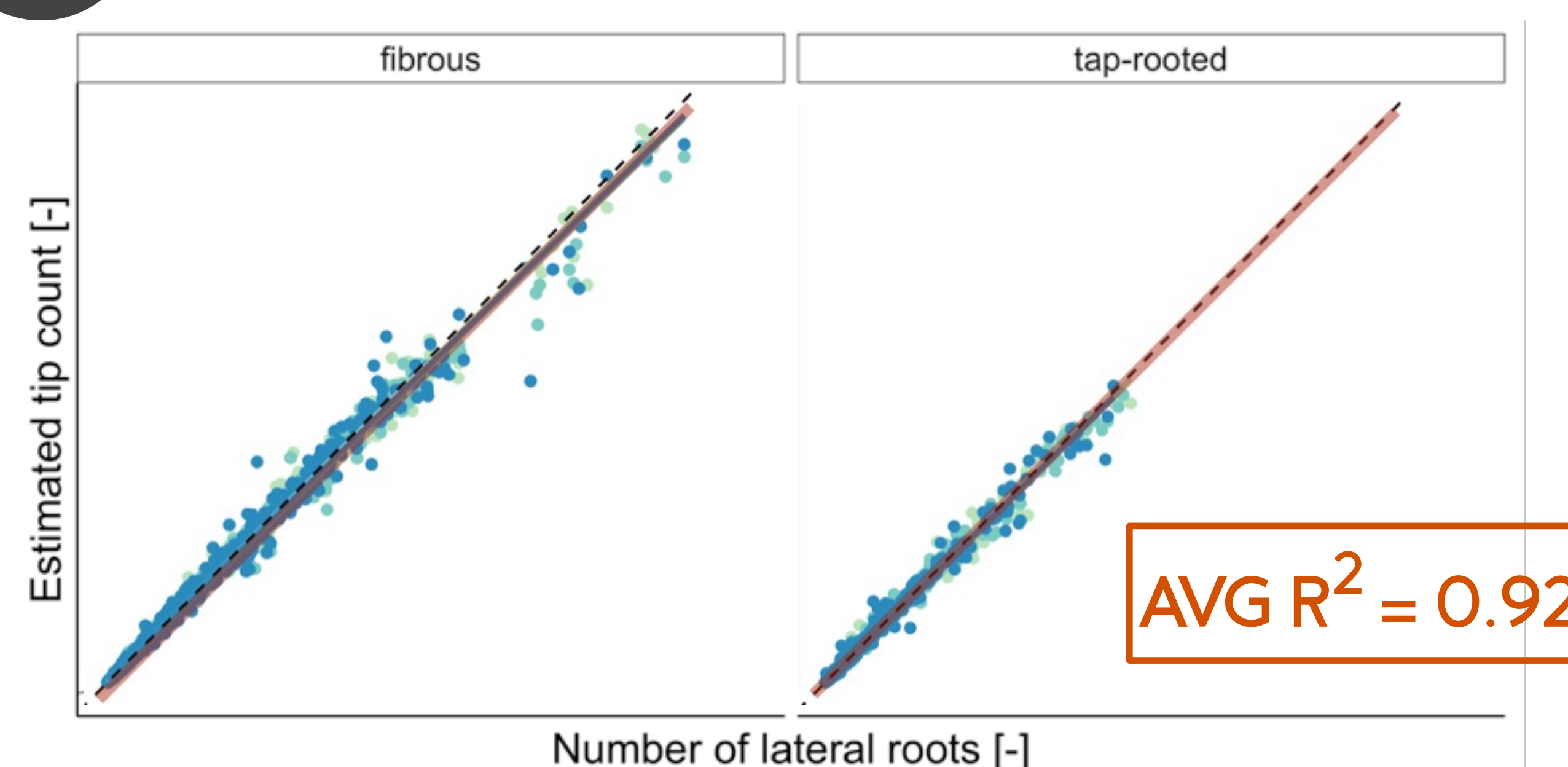
B

IMAGE ANALYSIS PIPELINE FAILS FOR LARGE ROOT SYSTEMS



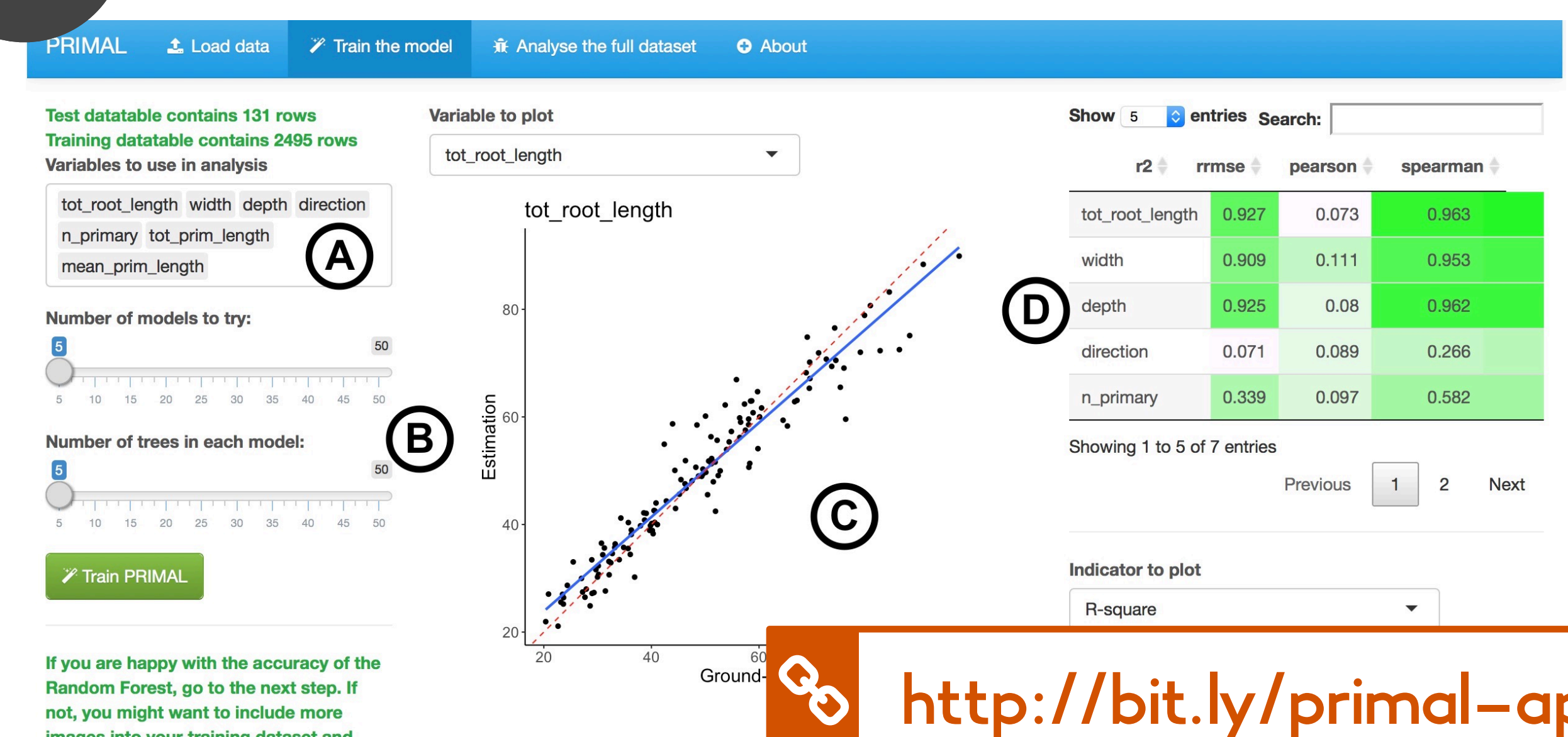
C

RANDOM FOREST AT THE RESCUE



D

TRY IT YOURSELF USING OUR APP!



MORE ABOUT THIS WORK

Lobet et al. 2017 (doi: 10.3389/fpls.2017.00447)
Atkinson, Lobet et al. 2017 (doi: 10.1101/152702)

ABOUT US

@guillaumelobet
<http://www.plantmodelling.xyz>

OUR FUNDERS

