# Network Analysis of CNN predictions

A set of Matlab programs are provided that were used for the analyses in Xu *et al.*, (2020) and Blonder *et al.,* (2020). These require Matlab 2020a or later. They may work on earlier versions of MatLab, but this has not been tested and cannot be guaranteed.

The output of figures at full resolution uses export\_fig.m originally written by Oliver Woodford (2008-2014) and now maintained by Yair Altman (2015-). This is included in the zip. However, when exporting to vector format (PDF or EPS) this function requires that Ghostscript is installed on your system. Ghostscript can be downloaded from:

<http://www.ghostscript.com>

When exporting images to eps and pdf formats, export\_fig additionally requires pdftops, from the Xpdf suite of functions. This is included in the xpdf tools package and can be downloaded from:

<https://www.xpdfreader.com/download.html>

# Instructions

1. Download the **X\_images\_downsampled.zip** folders from <https://doi.org/10.5281/zenodo.4008614> and unzip to a single data directory. Each folder in the unzipped file contains a sample represented by a CODE with format X-TY-BZ. X represents the name of a plot in the Global Ecosystems Monitoring network database (e.g. 'BEL'). Tree (T) Y indicates the number of a tree within a plot (e.g. '101') and Z represents the light stratum of the canopy where the leaf was collected (either 'S' for 'sunlit' or 'SH' for 'shaded').
2. The following images are present for each sample, downsampled (ds) by a factor of 2 from the original data:
   1. CODE\_ds\_img.png: the raw grayscale image.
   2. CODE\_ds\_mask.png: a hand-traced binary mask indicating the useable region of leaf tissue within the image (of high image quality, i.e. excluding tears, bubbles, dust)
   3. CODE\_ds\_cnn.png: the mean of the predicted vein networks using the CNN method.
   4. CODE\_ds\_roi.png: a binary mask indicating the hand-traced region of interest
   5. CODE\_ds\_seg.png: a binary mask indicating the hand-traced presence/absence of veins within the region of interest
   6. CODE\_ds\_big\_mask.png: a binary mask indicating the hand-traced presence/absence of larger veins within the region of interest. This image is only present when it was determined that larger veins were present in the leaf segment that were not included in the GT used for training.
3. Download the **matlab\_programs.zip** from <https://doi.org/10.5281/zenodo.4008614> and unzip to a working directory on the MatLab path.
4. Start MatLab (2020a or later) and navigate to the data directory.
5. Run *LeafVeinAnalysisBatch\_PR\_NP.m* to compare different enhancement methods using Precision-Recall analysis against the manual ground truth regions.
6. Run *LeafVeinAnalysisBatch\_NP.m* to extract the full network statistics using the optimal threshold from the Precision-Recall analysis.
7. Results are saved in the Summary folder and subfolders.
8. Compiled versions as single pdfs of the figures are also available at: <https://doi.org/10.5281/zenodo.4008361>

# References

## Software GUI:

Xu, H., Blonder, B., Jodra, M., Malhi, Y. and Fricker, M.D. (2020) Automated and accurate segmentation of leaf venation networks via deep learning. **New Phytol**. (In press).

## Analysis of trait data:

Blonder, B., S. Both, M. Jodra, H. Xu, M. Fricker, I. S. Matos, N. Majalap, D. F. R. P. Burslem, Y. Teh and Y. Malhi (2020) Linking functional traits to multiscale statistics of leaf venation networks. **New Phytol**. (In press).

## Original image data set and ground truths

Blonder, B., Both, S., Jodra, M., Majalap, N., Burslem, D., Teh, Y. A., and Malhi, Y. (2019) Leaf venation networks of Bornean trees: images and hand‐traced segmentations. **Ecology** 100: e02844.[10.1002/ecy.2844](https://doi.org/10.1002/ecy.2844).

Available from: <https://ora.ox.ac.uk/objects/uuid:de65fc07-4b8f-4277-a6c4-82836afbdeb3>