

phenoVein - A software tool for leaf vein segmentation and analysis

Jonas Bühler¹, Louai Rishmawi^{2,3}, Daniel Pflugfelder¹, Gregor Huber¹, Hanno Scharr¹, Martin Hülskamp², Maarten Koornneef³, Ulrich Schurr¹, Siegfried Jahnke¹

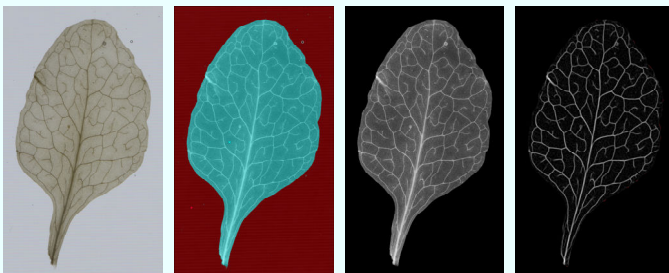
¹ Institute of Bio- and Geosciences: Plant Sciences (IBG-2), Forschungszentrum Jülich GmbH, 52425 Jülich, Germany

² Botanical Institute and Cluster of Excellence on Plant Sciences (CEPLAS), University of Cologne, Cologne Biocenter, 50674 Cologne, Germany

³ Max-Planck Institute for Plant Breeding Research and Cluster of Excellence on Plant Sciences (CEPLAS), 50829 Cologne, Germany

phenoVein is a software tool dedicated to automated segmenting and analyzing images of leaf veins. It includes comfortable manual correction features. Advanced image filtering automatically emphasizes veins from background and compensates for local brightness inhomogeneities. Phenotypical leaf vein traits being calculated are total vein density, vein lengths and widths and skeleton graph statistics. For determination of vein widths, a model based vein edge estimation approach has been implemented. We demonstrate the capabilities of phenoVein on a set of vein structure mutants of *Arabidopsis thaliana*.

Automated vein segmentation

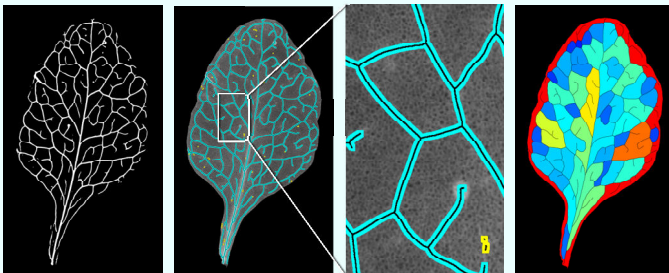


Original image of a cleared leaf of *Arabidopsis thaliana* (hve2, leaf 6, 30 DAS)

Leaf / background segmentation, determination of leaf area

Conversion from color to gray value image, e.g. green channel from RGB

Vesselness filtering of vein structures and compensation of irregular lighting



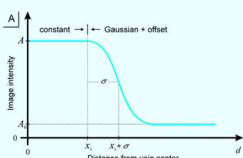
Threshold based vein mask

Skeletonization of the vein mask

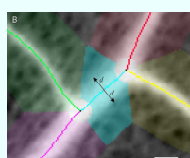
Magnification of skeleton subsection

Color encoded areole sizes

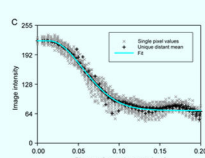
Vein width estimation



Sketch and parameters of vein edge model. The vein is assumed to have a constant brightness. The edge and the areole are modeled by a smooth half-Gaussian



Inverted subsection of leaf image. Vein piece of interest and surrounding area (next closes pixels) are highlighted in cyan.



Pixel intensities vs shortest distance to skeleton (gray). The vein edge model (cyan) is least squares fitted to the pixel intensities.

$$\text{Vein edge function: } v_e(x) = \begin{cases} A & x < x_c \\ A_0 + (A - A_0) \exp(-(x - x_c)^2 / (2\sigma^2)) & x \geq x_c \end{cases}$$

$$\text{Mean vein width: } w_v = 2(x_c + \sqrt{2 \ln(2)} \sigma)$$

Leaf vein traits

Important vein traits

Total vein length

Projected leaf area

Leaf vein density

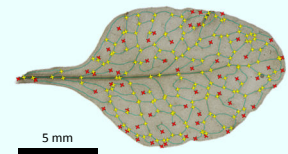
Mean vein width

Vein graph statistics

- Branching points

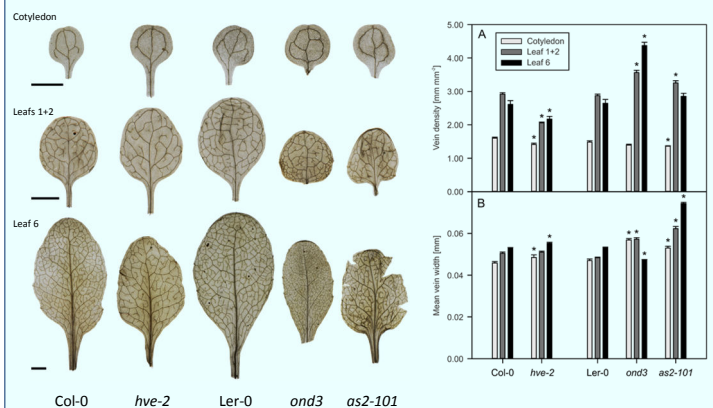
- Free ending points

- Areoles



Total skeleton length	242.7	mm
Leaf area	136.4	mm ²
Vein density	1.78	mm mm ⁻²
Mean vein width	50.3	μm
Single skeleton pieces	273	
Free ending points	63	
Branching points	161	
Areoles	52	

Analysis of venation mutants



Photographs of cleared leaves of *Arabidopsis thaliana* mutants. Cotyledons (14 DAS), pooled leaves 1+2 (14 DAS) and leaf 6 (30 DAS). Scale bar = 2.5mm

Main results of vein analysis. Vein density and mean vein width of different genotypes. * indicate statistically significant differences ($p < 0.05$).

Software

phenoVein is a plug-in for MeVisLab, the source code is freely available as open source software.

phenoVein can be downloaded from:
www.phenovein.de

Publication of phenoVein:
Bühler J, Rishmawi L, Pflugfelder D, Huber G, Scharr H, Hülskamp M, Koornneef M, Schurr U, Jahnke S (2015). phenoVein - A Tool for Leaf Vein Segmentation and Analysis. *Plant Physiology* 10.1104/pp.15.00974

