Deep Neural Networks for Root System Analysis

Hanno Scharr¹, Patrick M. Schwehn^{1,2}, Max Riedel¹, Katrin Heinz¹, Kerstin Nagel¹ ¹ Institute of Bio- and Geosciences: Plant Sciences (IBG-2) Forschungszentrum Jülich, Germany ² Faculty of Electrical Engineering and Information Technology, RWTH Aachen University, Germany



Figure 1: Typical rhizotron data and results. Left: input image. Middle: automatic labelling result. Right: manually labelled image. Main roots are green, side root red.

In this contribution we describe a deep neural network (DNN) solution for labelling of roots according to their root order, *i.e.* main or side-root.

A wide range of image-based plant phenotyping methods for above-ground organs exist, where automated camerabased methods are abundant [3, 5, 14, 15]. For belowground organs like root systems noninvasive measurements require either growing plants in special ways, like in transparent agar [8], on paper [2] or in hydro- or aeroponics. Or special 3D imaging equipment is required when grown in soil, e.g. magnetic resonance imaging (MRI) [12], positron emission tomography (PET) [4], or computed tomography (CT) [7]. Simple camera-based imaging of root systems in soil can be achieved, when using special flat pots, so-called rhizotrons [9], where one side is made from transparent material. During plant growth they are inclined such that roots grow along the transparent window. In contrast to other above mentioned root system imaging setups where the full root system is visible, rhizotron imagery shows only fragments of the root system, as roots growing along the window vanish into the opaque soil from time to time. Well established root image analysis solutions (like e.g. [6, 13]) are designed to reconstruct complete root graphs, thus not being suitable in this application scenario. Due to this lack of fully automated, high quality solutions state-of-the-art analysis still involves some human post-processing or labelling.

Human generated labels are 1 pixel wide lines indicating where roots are, *i.e.* labelled root skeletons, rather than segmentations. Drawing precision is in the range of few pix-

els, therefore skeletons are not always reliably centered on roots, introducing some position noise in the labels. Having such hand-labelled data available, enables us to investigate different DNN architectures for root labelling. Biologically relevant root system parameters like branching angles or frequencies, root densities etc. are then derived in a subsequent step.

We investigate two different DNN architectures. The first one is a modification of the four-fold hourglass introduced by [10] and established for plant phenotyping applications like grain, ear or ear tip detection [11]. This network is designed for heat-map generation, indicating where sough for objects are in an image. There, training is performed using mean square error as loss. Here, we appended softmax layers at each layer used for loss calculation, such that pixelwise classification can be learned using categorical cross entropy. The network was trained end-to-end, from scratch, using RMSProp with batch size 50, 100 epochs and learning rate $2.5 \cdot 10^{-4}$ as in [11]. As image data is typically 15Mpix, we employed tiling such that outputs are 64×64 as in [11] in order to make the network trainable on a single Nvidia 1080Ti GPU with 11GB memory. The resulting network has 25M parameters.

Results using the four-fold hourglass architecture are shown in Figure 1. The general root system properties are already very well captured. However, there is still room for improvement, compare e.g. the topmost main roots not being completely captured by the DNN.

In order to enlarge spatial reach, in an ongoing project,

we currently investigate a DNN architecture introduced for Acknowledgements We thank Anna Galinski, Carmen fast image processing [1] using dilated convolutions [16]. Müller, Jonas Lentz, Ann-Katrin Kleinert, and Bernd Kas-Using the same GPU for training, the smaller size of the network allows for larger tiles, 320×320 in our case. Prelim-supported by a third-party project of the German Fedinary results are comparable to the ones shown in Figure 1, eral Ministry of Education and Research: German-Plantwhile the network has only in the order of 100k parameters. Phenotyping Network (DPPN), BMBF Fz. 031A053.

References

- [1] Q. Chen, J. Xu, and V. Koltun. Fast image processing with fully-convolutional networks. In International Conference on Computer Vision (ICCV), 2017.
- [2] T. Gioia, A. Galinski, H. Lenz, C. Müller, J. Lentz, K. Heinz, C. Briese, A. Putz, F. Fiorani, M. Watt, U. Schurr, and K.A. Nagel. Growscreen-page, a noninvasive, high-throughput phenotyping system based on germination paper to quantify crop phenotypic diversity and plasticity of root traits under varying nutrient supply. Functional Plant Biology, 44:6-93, 2016.
- [3] C. Granier, L. Aguirrezabal, K. Chenu, S. J. Cookson, M. Dauzat, P. Hamard, J.-J. Thioux, G. Rolland, S. Bouchier-Combaud, A. Lebaudy, B. Muller, T. Simonneau, and F. Tardieu. PHENOPSIS, an automated platform for reproducible phenotyping of plant responses to soil water deficit in Arabidopsis thaliana permitted the identification of an accession with low sensitivity to soil water deficit. New Phytologist, 169 (3):623-635, January 2006.
- [4] S. Jahnke, M.I. Menzel, D. van Dusschoten, G.W. Roeb, J. Bühler, S. Minwuyelet, P. Blümler, V.M. Temperton, T. Hombach, M. Streun, S. Beer, M. Khodaverdi, K. Ziemons, H.H. Coenen, and U. Schurr. Combined mri-pet dissects dynamic changes in plant structures and functions. The Plant Journal, 59(4):634-644, 2009. doi: 10.1111/j.1365-313X.2009.03888.x.
- [5] M. Jansen, F. Gilmer, B. Biskup, K.A. Nagel, U. Rascher, A. Fischbach, S. Briem, G. Dreissen, S. Tittmann, S. Braun, I. De Jaeger, M. Metzlaff, U. Schurr, H. Scharr, and A. Walter. Simultaneous phenotyping of leaf growth and chlorophyll fluorescence via GROWSCREEN FLUORO allows detection of stress tolerance in Arabidopsis thaliana and other rosette plants. Functional Pant Biology, 36(10/11): 902–914, 2009.
- [6] S. Mairhofer, S. Zappala, S. Tracy, C. Sturrock, M. Bennett, S. Mooney, and T. Pridmore. Rootrak: Automated recovery of 3d plant root architecture in soil from x-ray micro computed tomography using visual tracking. Plant Physiology, 2011. doi: 10.1104/pp. 111.186221.
- [7] S. J. Mooney, T. P. Pridmore, J. Helliwell, and M. J. Bennett. Developing x-ray computed tomography to non-invasively image 3-d root systems architecture in soil. Plant and Soil, 352(1):1-22, Mar 2012. ISSN 1573-5036. doi: 10.1007/ s11104-011-1039-9. URL https://doi.org/ 10.1007/s11104-011-1039-9.
- [8] K.A. Nagel, B. Kastenholz, S. Jahnke, D. van Dusschoten, T. Aach, M. Mühlich, D. Truhn, H. Scharr, S. Terjung, A. Walter, and U. Schurr. Temperature responses of roots: impact on growth, root system architecture and implications for phenotyping. Func-

tenholz for providing labelled data. This work has been

tional Pant Biology, Special Issue: Plant Phenomics, 36(10/11):947-959, 2009.

- [9] K.A. Nagel, A. Putz, F. Gilmer, K. Heinz, A. Fischbach, J. Pfeifer, M. Faget, S. Blossfeld, M. Ernst, C. Dimaki, B. Kastenholz, A.-K. Kleinert, A. Galinski, H. Scharr, F. Fiorani, and U. Schurr. GROWSCREEN-Rhizo is a novel phenotyping robot enabling simultaneous measurements of root and shoot growth for plants grown in soil-filled rhizotrons. Functional Plant Biology, 39:891-904, 2012.
- [10] A. Newell, K. Yang, and J. Deng. Stacked hourglass networks for human pose estimation. In European Conference on Computer Vision, pages 483--499. Springer, 2016.
- [11] M.P. Pound, J.A. Atkinson, D.M. Wells, T.P. Pridmore, and A.P. French. Deep learning for multi-task plant phenotyping. In Computer Vision Workshop (ICCVW), 2017 IEEE International Conference on Computer Vision: Computer Vision Problems in Plant Phenotyping, Venice, Italy, 2017.
- [12] U. Rascher, S. Blossfeld, F. Fiorani, S. Jahnke, M. Jansen, A.J. Kuhn, S. Matsubara, L.L.A. Märtin, A. Merchant, R. Metzner, M. Müller-Linow, K.A. Nagel, R. Pieruschka, F. Pinto, C.M. Schreiber, V.M. Temperton, M.R. Thorpe, D. van Dusschoten, E. van Volkenburgh, C.W. Windt, and U. Schurr. Noninvasive approaches for phenotyping of enhanced performance traits in bean. Functional Plant Biology, 38 (12):968-983, 2011.
- [13] H. Schulz, J.A. Postma, D. van Dusschoten, H. Scharr, and S. Behnke. Plant root system analysis from mri images. In Computer Vision, Imaging and Computer Graphics. Theory and Application, CCIS 359, pages 411–425. Springer Berlin Heidelberg, 2013.
- [14] Sotirios Tsaftaris and Christos Noutsos. Plant phenotyping with low cost digital cameras and image analytics. In IoannisN. Athanasiadis, AndreaE. Rizzoli, PericlesA. Mitkas, and JorgeMarx Gómez, editors, Information Technologies in Environmental Engineering, Environmental Science and Engineering, pages 238-251. Springer Berlin Heidelberg, 2009. ISBN 978-3-540-88350-0.
- [15] A. Walter, H. Scharr, F. Gilmer, R. Zierer, K.A. Nagel, M. Ernst, A. Wiese, O. Virnich, M.M. Christ, B. Uhlig, S. Jünger, and U. Schurr. Dynamics of seedling growth acclimation towards altered light conditions can be quantified via GROWSCREEN: a setup and procedure designed for rapid optical phenotyping of different plant species. New Phytologist, 174(2):447-455, 2007.
- [16] F. Yu and V. Koltun. Multi-scale context aggregation by dilated convolutions. In International Conference on Learning Representations (ICLR), 2016.