

Using Satellite Data to Locate and Phenotype Plants from Space

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Introduction

Grave food insecurity concerns from a growing population and climate change have led to significant interest in improving the yield and resilience of staple crops through crop breeding. [1]

Remote sensing potentially offers a cheap and non-destructive method to collect plant growth data more frequently than previously possible. Recently, satellite images have become precise enough to resolve individual plots in crop breeding trials from space.

The main technical challenge is, then, mapping from pixels to growth traits. Convolutional Neural Networks (CNNs) are used in many other computer vision tasks, and thus were chosen as the main model type for this task.

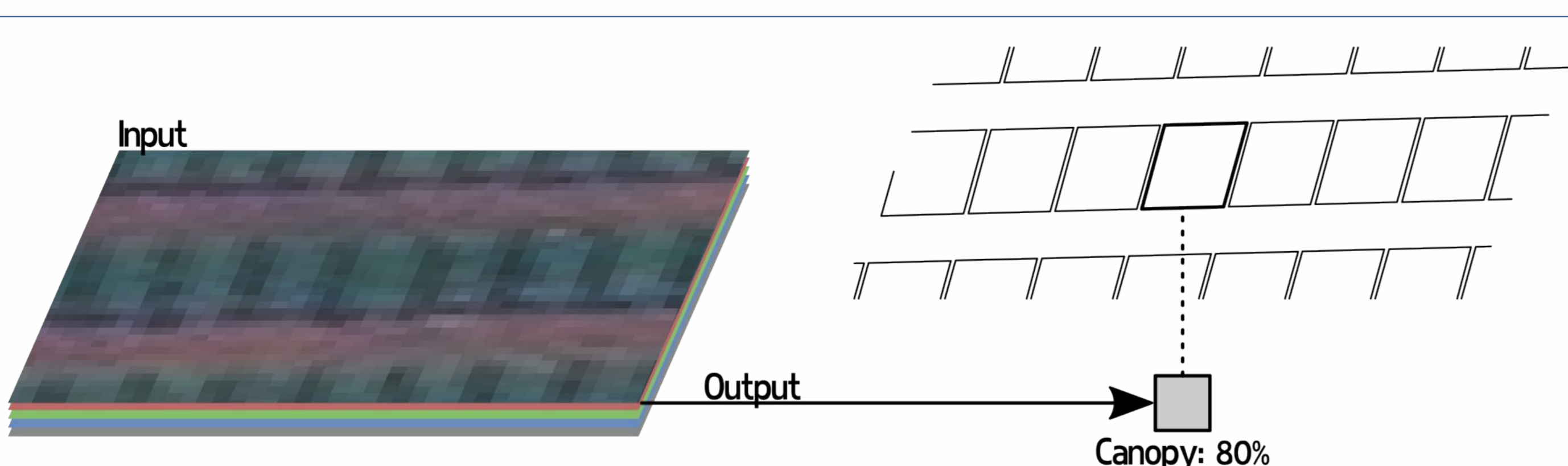
Aims

To train and compare several machine learning and deep learning models that map from pixels to growth traits using a small collection of images of crop breeding trials and corresponding ground measurements. In particular, explore predicting for small areas while using whole-image models (e.g. classification) or per-pixel models (e.g. segmentation).

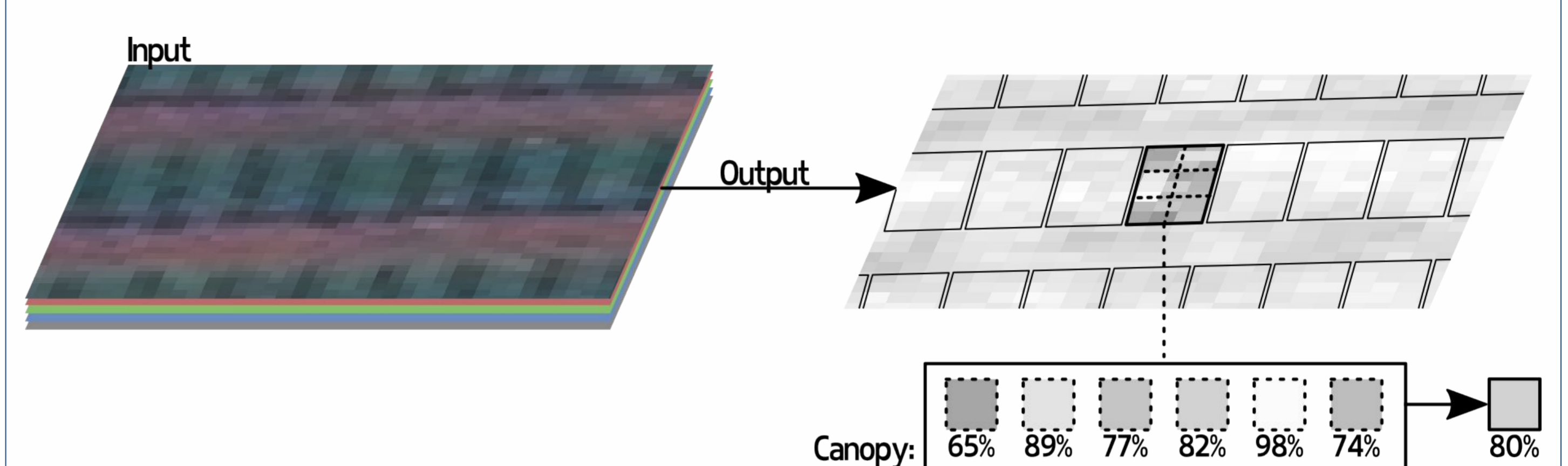
Methods

Existing work uses superpixels, where the pixels within the plot boundary are aggregated into a fixed-length vector. This lacks contextual information.

We propose two methods to use CNNs to provide contextual information, and apply to tiny areas. First is the Centred method, analogous to classification, which makes a single regression prediction for a small image patch. Second is Per-pixel - analogous to segmentation - which predicts per pixel and is aggregated afterward - like the input aggregation of superpixels.



The Centred method - Take a whole image patch as input; predict for just the central plot



The Per-Pixel method - predict per-pixel, then apply a fixed function to aggregate to a per-plot prediction afterwards.

Results

Multiple models per method were trialled, and a simple Centred ResNet18 [2] performed the best, on average, overall. Per-Pixel UNet++ [3] performed almost as well as ResNet18, but was sensitive to aggregation parameters. The Superpixel methods were all outperformed by most CNN models. This implies the CNN models were able to utilise extra contextual information.

Measured absolute R^2 values are large due to correlations in the data, so we include a hypothetical model which perfectly predicts the average trait value per image as a reference point. When evaluated on each image separately, the R^2 were lower, but still much better than random.

Method	Model	Flowering	Canopy Cover	Green	Height
Superpixel	RF	0.825 ±0.008	0.991 ±0.003	0.982 ±0.004	0.963 ±0.005
	MLP	0.858 ±0.006	0.994 ±0.001	0.985 ±0.001	0.969 ±0.001
Centred	VGG-A	0.880 ±0.009	0.989 ±0.002	0.985 ±0.001	0.973 ±0.003
	ResNet18	0.888 ±0.015	0.993 ±0.000	0.986 ±0.001	0.975 ±0.001
	ResNet50	0.886 ±0.010	0.989 ±0.002	0.983 ±0.003	0.969 ±0.003
	DenseNet161	0.863 ±0.017	0.991 ±0.003	0.983 ±0.002	0.970 ±0.004
Per-pixel	UNet++	0.871 ±0.029	0.994 ±0.001	0.986 ±0.002	0.974 ±0.002
	DeepLabv3	0.824 ±0.008	0.994 ±0.001	0.983 ±0.002	0.966 ±0.002
Hypothetical use avg per img		0.782 ±0.010	0.991 ±0.002	0.978 ±0.003	0.952 ±0.003

Results - R^2 - error bars across 5-fold validation - A simple ResNet18 performed best on each predicted trait, and overall.

References

- [1] J. White, et al., Field-based phenomics for plant genetics research, in *Field Crops Research* 133 (2012) 101–112. doi:10.1016/j.fcr.2012.04.003.
- [2] K. He, et al., Identity Mappings in Deep Residual Networks, in *Computer Vision - ECCV 2016*. doi: 10.1007/978-3-319-46493-0_38.
- [3] Z. Zhou, et al., UNet++: A Nested U-Net Architecture for Medical Image Segmentation, in *Deep Learning in Medical Image Analysis and Multimodal Learning for Clinical Decision Support* doi: 10.1007/978-3-030-00889-5.

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