

Counting and classification of bacterial colonies using deep learning

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Introduction

Counting bacterial colonies is a fundamental task in microbiology. Currently, manual counting remains the gold standard. This is a time-consuming and error-prone process, which requires a trained professional. To avoid these issues, the automated method can be applied for the task. The goal of our work was to design a model that counts and classifies bacterial colonies in Petri dishes using RGB images.

Methods

A common way of counting and classifying objects using deep learning is to first detect them and then count found instances of different categories. We tested multiple detectors that achieved state-of-the-art performance on MS COCO dataset:

- 1 Composite Backbone Network (CBNet) [1]
- 2 TridentNet [2]
- 3 Global Context Network (GCNet) [3]
- 4 Fully Convolutional One Stage Object Detector (FCOS) [4]

Additionally, only for counting, we investigated an approach based on density map estimation. It is a simpler method, that was proven effective when applied to cell and crowd counting. We tested three models:

- 1 Context Aware Network (CAN) [5]
- 2 Congested Scene Recognition Network (CSRNet) [6]
- 3 U-Net [7]

An example of true and predicted images for both approaches are presented in Figure 1.

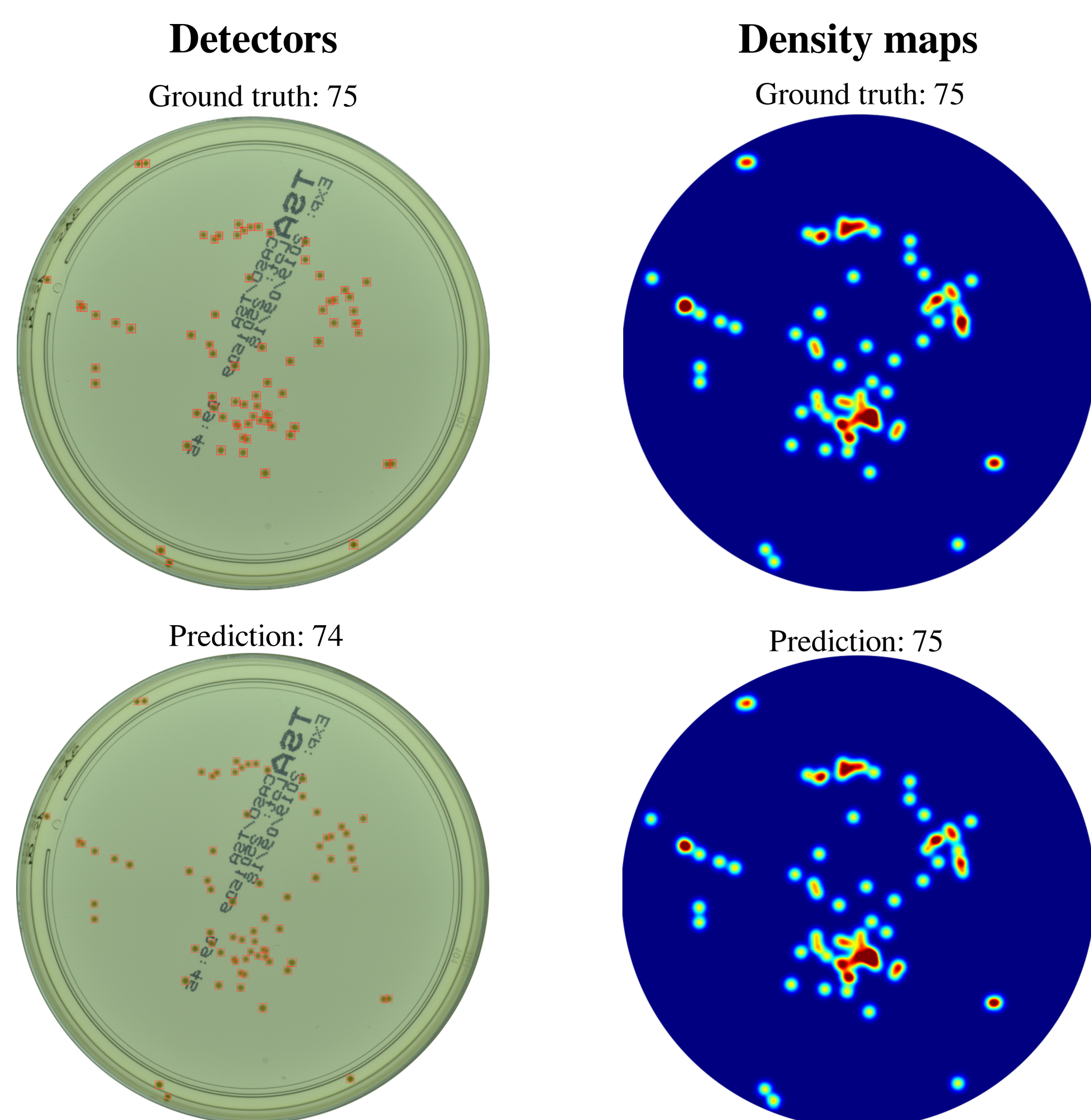


Figure 1: An example of true and predicted bounding boxes and density maps together with the colony count.

Dataset

In cooperation with the University of Wrocław we collected a dataset consisting of 2211 images of microorganisms grown inside Petri dishes. The data were annotated with bounding boxes, together 115619 colonies were found and 5 different types of bacteria were distinguished (Figure 2).

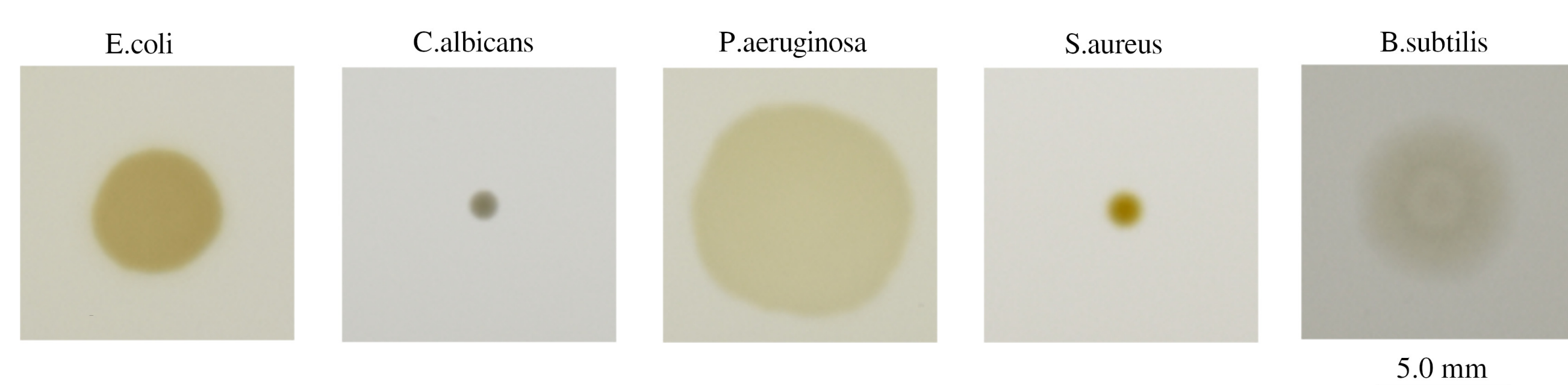


Figure 2: Different types of bacteria grown inside a Petri dish.

Results

Table 1. Mean Absolute Error (MAE) and Mean Absolute Percentage Error (MAPE) obtained using different methods.

Object detection			Density map estimation		
Model	MAE	MAPE	Model	MAE	MAPE
CBNet [1]	1.86	6.13 %	CAN [5]	1.22	4.76 %
TridentNet [2]	1.57	7.92 %	CSRNet [6]	1.69	5.40 %
GCNet [3]	2.04	6.02 %	U-Net [7]	1.64	5.33 %
FCOS [4]	1.47	8.40 %			

Table 2. Mean Absolute Percentage Error (MAPE) obtained using GCNet for different types of bacteria.

	E.coli	C.albicans	P.aeruginosa	S.aureus	B.subtilis
MAPE [%]	5.82	3.71	8.72	3.16	3.09

For counting bacterial colonies the best results in terms of MAPE were obtained using Context Aware Network (Table 1). When we additionally take into account classification, the best performance can be achieved with Global Context Network. MAPE for different bacteria types is presented in Table 2. Performance of bacterial colonies counting and classification is shown in Figures 3 and 4.

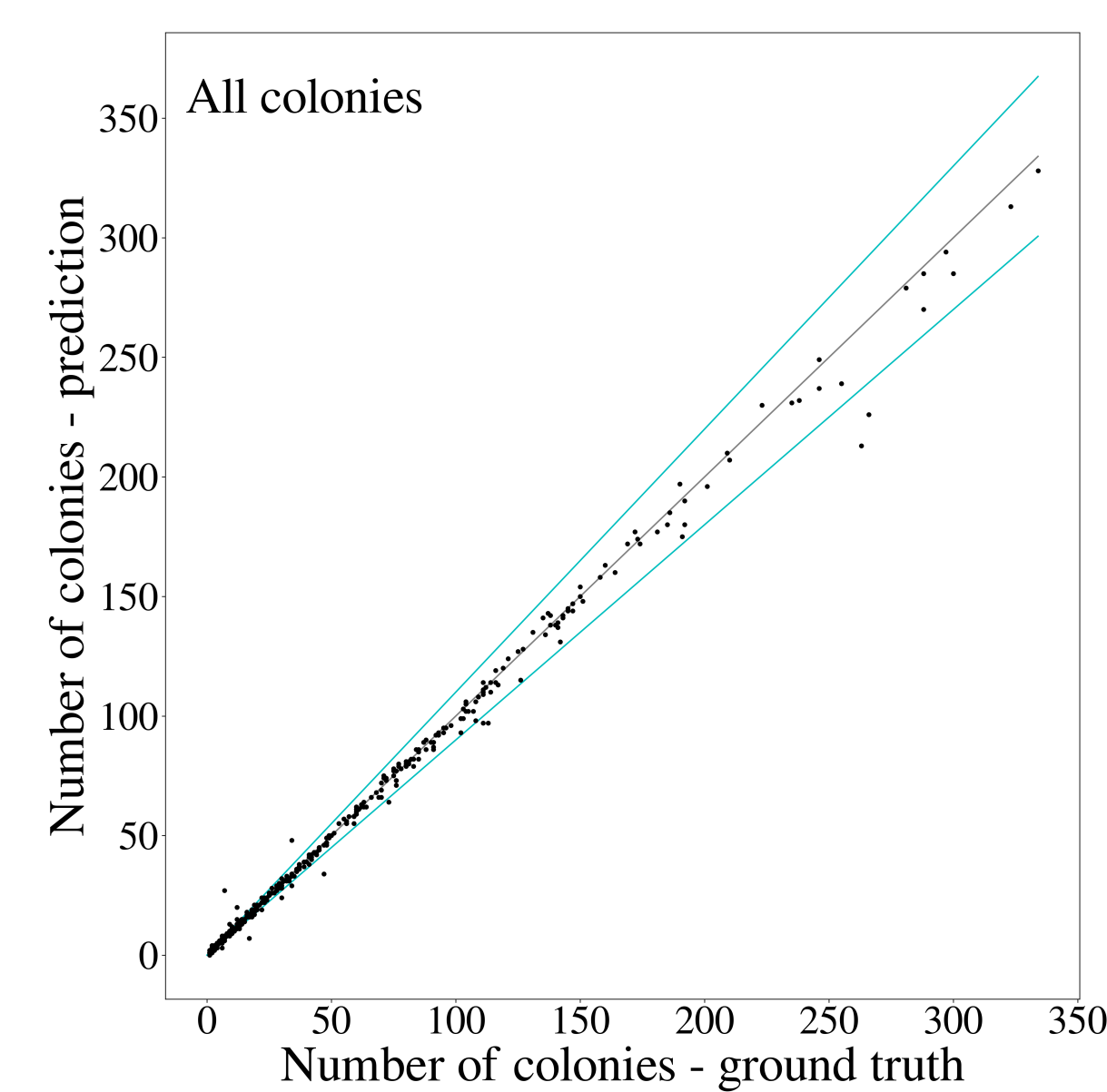


Figure 3: Performance of bacterial colony counting using CAN.

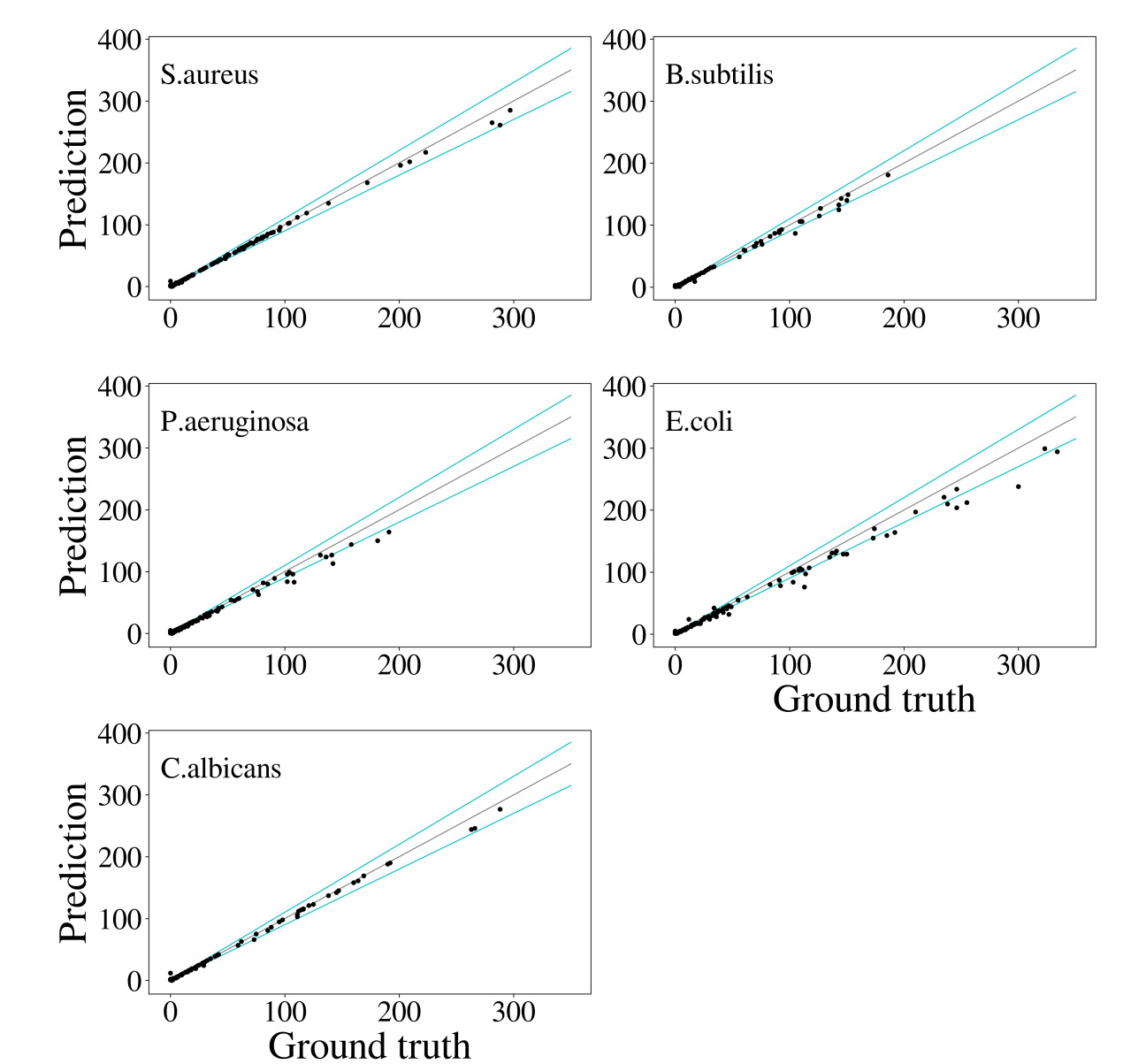


Figure 4: Performance of bacterial colony counting and classification using GCNet.

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