

Background

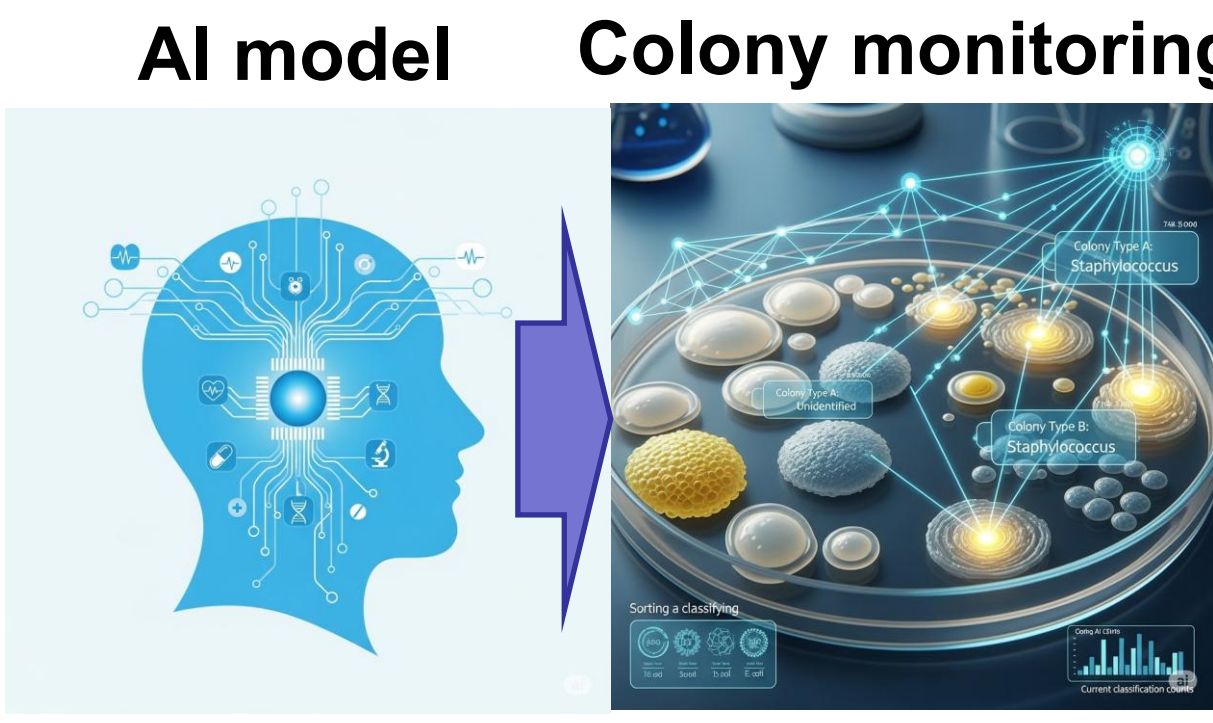
The Need for Faster Bacterial Identification

- ✓ **The Urgency of Timely Diagnosis:** Rapid and accurate identification of bacterial species is critical for effective treatment and improved patient outcomes. Delays in identification can lead to prolonged illness or the development of antibiotic resistance.
- ✓ **Limitations of Traditional Methods:**
- ✓ **Time-Consuming:** Conventional methods, which rely on visible colony growth and biochemical tests, often take several days to a week to yield a result.
- ✓ **Labor-Intensive:** These processes require skilled technicians for manual observation and a series of lab procedures, which increases human resource costs.
- ✓ **Subjective:** Colony morphology can be open to subjective interpretation, potentially leading to inconsistent results.



Early Bacterial Colony Identification through Time-Lapse Imaging

- ✓ **Our Proposed Solution:** To overcome these challenges, we propose a novel approach that combines time-lapse imaging with deep learning. This method aims to capture and analyze colony features from the earliest stages of growth, enabling a more rapid and objective identification of bacterial species.



Objectives

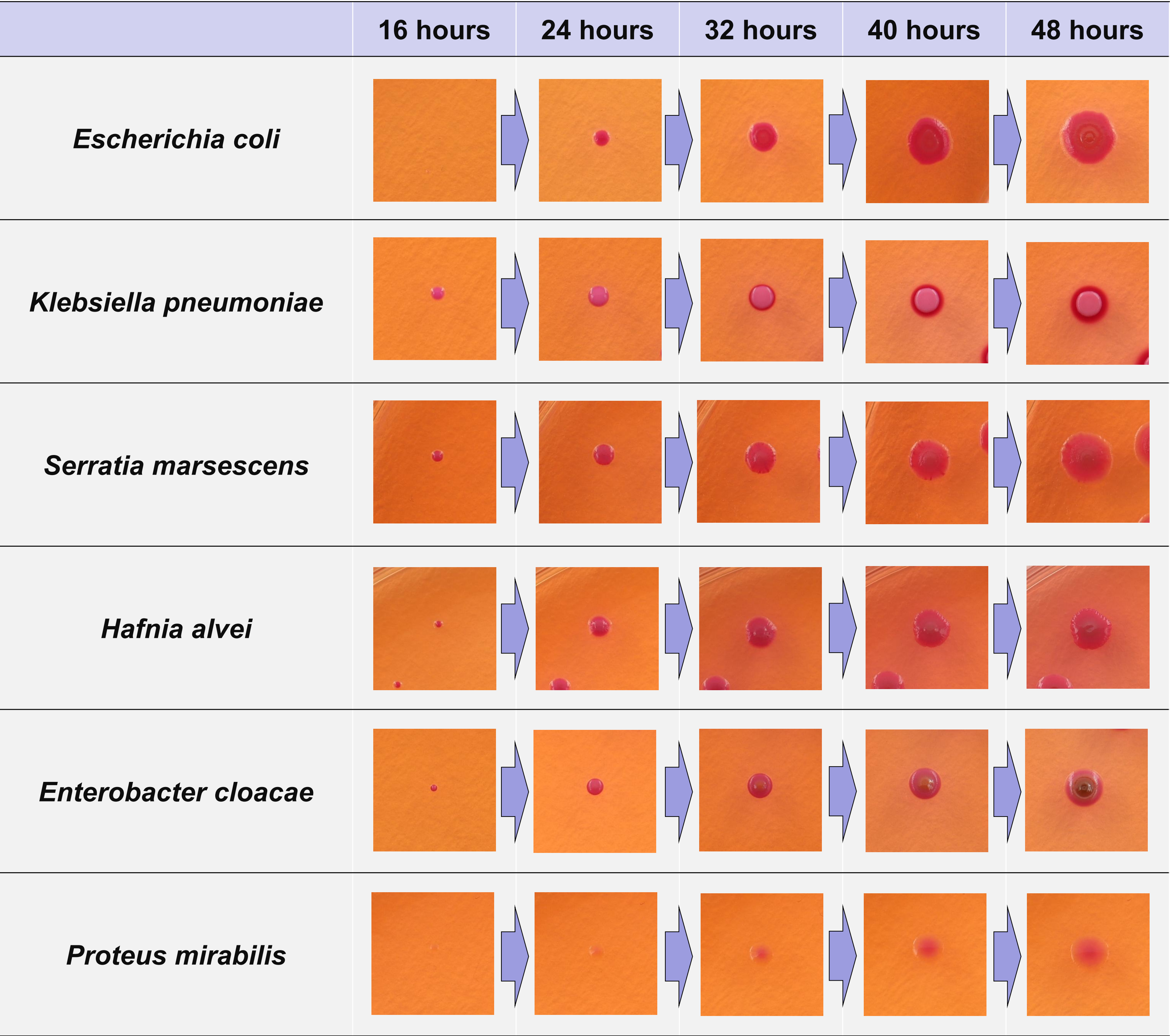
The primary goal of this study is to develop a novel AI model that uses a combination of time-lapse imaging and deep learning to enable rapid and accurate bacterial identification.

- ✓ **Achieve Rapid Identification:** Analyze colony growth at a much earlier stage than traditional methods to identify bacterial species faster.
- ✓ **Improve Objectivity and Accuracy:** Ensure objective and highly accurate identification using AI, reducing reliance on subjective human expertise.
- ✓ **Increase Efficiency:** Automate the culture process to save time and reduce labor in microbiology.
- ✓ **Contribute to Early Treatment:** Facilitate faster and more appropriate treatment for infectious diseases through rapid diagnosis.



Results

1. Time-lapse Macroscopic Imaging



Acknowledgement

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Conflict of Interest

- The authors have no financial conflicts of interest to disclose concerning the presentation.

Materials and Methods

1. Materials

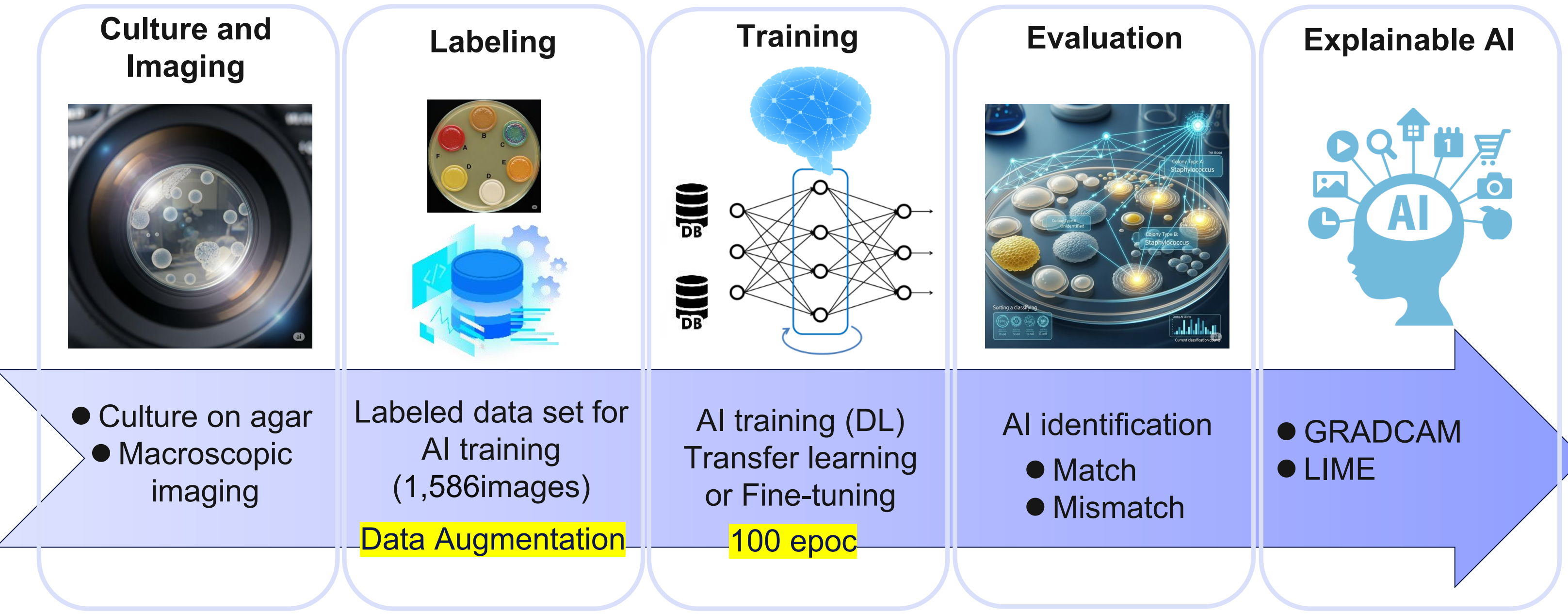
- American Type Culture Collection (ATCC) Strains:
- 6 Bacterial Species**
- *Escherichia coli*: 25922
  - *Klebsiella pneumoniae*: 13883
  - *Serratia marcescens*: 13880
  - *Hafnia alvei*: 51815
  - *Enterobacter cloacae*: 13047
  - *Proteus mirabilis*: 21100

2. Culture and imaging

- ① Culture at 35 °C for 5–6 hours in HI broth until McF reaches 0.5
- ② Spread 20 µL of a 10,000-fold diluted bacterial suspension onto DHL agar plates
- ③ Photograph colonies on plates cultured at 35 °C for 16, 24, 32, 40, and 48 hours
- ④ Photographed using a digital SLR camera (CANON INC. EOS 250D) at 90 degrees angle with a focal length of 260 mm.

AI modeling with Deep Learning

1. Study design -The process from AI model creation to evaluation-



2. Architecture and Configuration

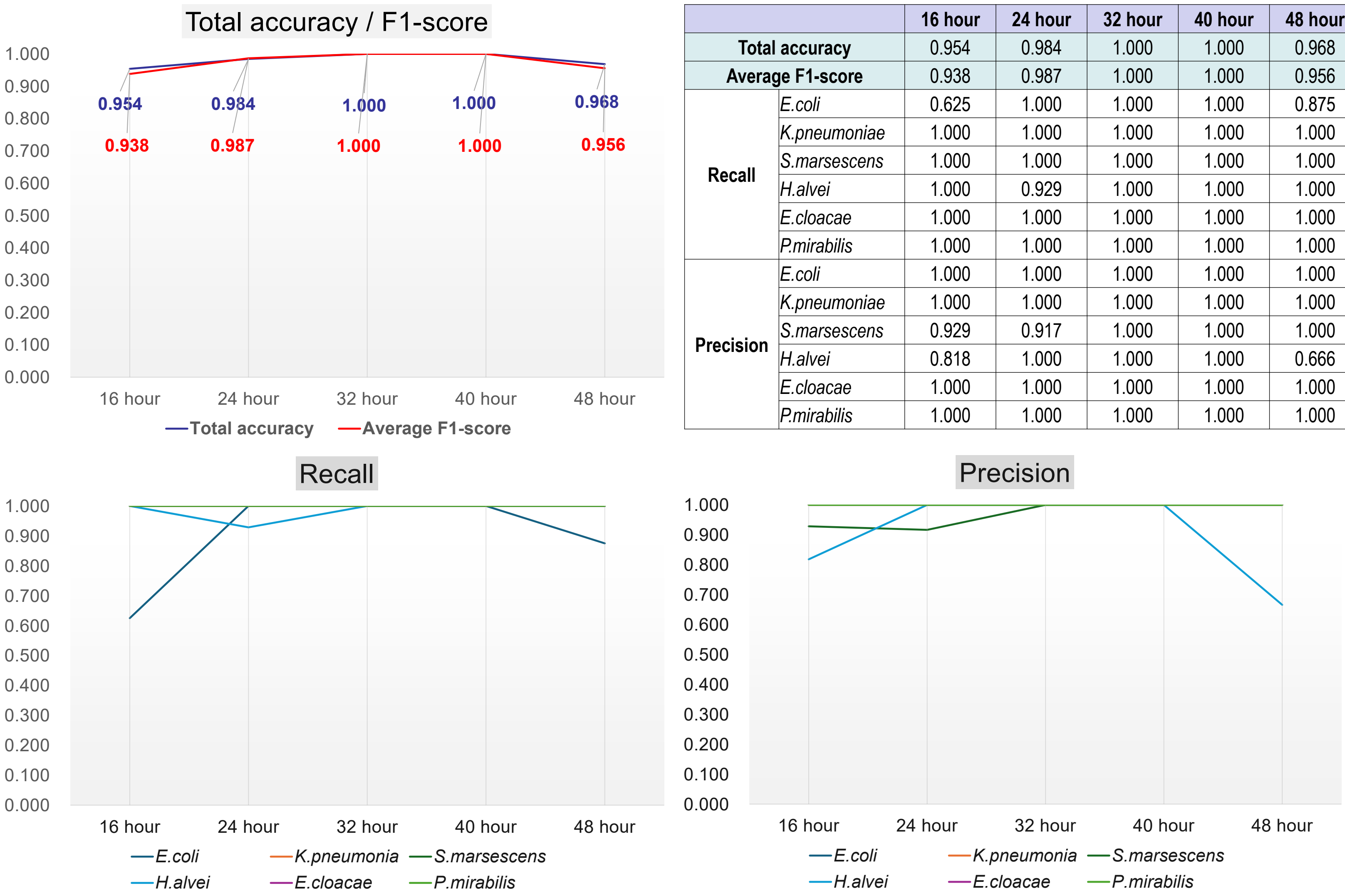
- Anaconda3.0 and Python3.5
- Libraries: Nnabla (SONY. INC)
- CPU: Intel(R) Core(TM) i7-12700 3.6GHz
- GPU: NVIDIA GeForce RTX 4090/24GB
- Architecture: ResNet-18 model

3. Training and validation data

- The AI training dataset consisted of 1,586 macroscopic images of bacterial colony.
- The dataset was divided into a training set (80%) and a validation set (20%).

Category (Bacterial species)	Number of images				
	16 hours	24 hours	32 hours	40 hours	48 hours
<i>Escherichia coli</i>	41	40	41	41	41
<i>Klebsiella pneumoniae</i>	65	59	59	59	59
<i>Serratia marsescens</i>	47	47	47	47	47
<i>Hafnia alvei</i>	59	59	59	59	55
<i>Enterobacter cloacae</i>	63	63	63	63	63
<i>Proteus mirabilis</i>	48	48	48	48	48
Total	323	316	317	317	313

2. Hold-out validation



Summary

- The AI model demonstrates high accuracy in identifying bacterial species from colonies growing on agar media.
- This AI model contributes to early-period bacterial species estimation.

Conclusion

- This deep learning-based approach offers a non-invasive, high-throughput solution for automated bacterial identification, potentially reducing turnaround time in clinical microbiology laboratories and improving patient outcomes.
- Further research will focus on expanding the dataset, validating the model with diverse strains, and integrating it into an automated diagnostic platform.