IPCPREDICT

Colonization prediction

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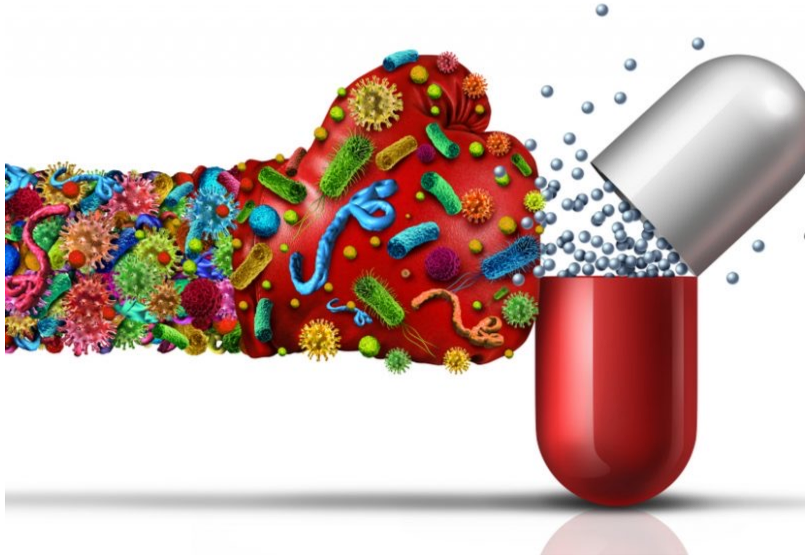
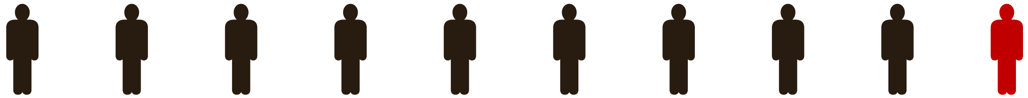
Background - HAI



- 1 in every 10 inpatients develop a HAI*.
- Healthcare units are one of the biggest reservoirs of Carbapenem-resistant Enterobacteriaceae (CRE).
- 1.7 million infections and 99,000 associated deaths from AMR bacteria every year.
- HAIs result in unnecessary death and prolong hospital stays.



* World Health Organization (2016) Health care without avoidable infections - The critical role of infection prevention and control. World Health Organization, Geneva, Switzerland

Background - IPC

- The major goal of an IPC program is to decrease the incidence of healthcare associated infections (HAI), ideally to zero.

- World Health Organization (WHO) data demonstrates that
  - Effective IPC programs Reduce HAI rates by at least 30%
  - Surveillance contributes to a up to 57% reduction in HAIs

- WHO calls for
  - Better hand hygiene
  - Adequate environmental cleaning and disinfection
  - Adequate ventilation

- IPC strategies and measures are required to prevent or limit pathogens transmission

- High risk an inpatient faces of being colonized or infected by HCW, caregivers, other patients or visitors

Objective

- *Develop new systems as alternative solution to fight infection within the healthcare.*

- *Develop a machine learning model-based graph that predict inpatients colonization risks.*

MIMIC III

- Medical Information Mart for Intensive Care
- Data associated with 53,423 distinct hospital admissions between 2001 and 2012
- Consist of 22 tables
- Tables are linked by identifiers

The admissions table

Table source: Hospital database.

Table purpose: Define a patient's hospital admission, HADM_ID

The patients table

Table source: CareVue and Metavision ICU databases.

Table purpose: Defines each SUBJECT_ID in the database, i.e. defines a single patient.

The microbiologyevents table

Table source: Hospital database.

Table purpose: Contains microbiology information, including cultures acquired and associated sensitivities.

Number of rows: 631,726

MIMIC III - Deidentification

- Data removal :
  - Patient name
  - Telephone number
  - Address

HIPAA
Health Insurance Portability and Accountability Act

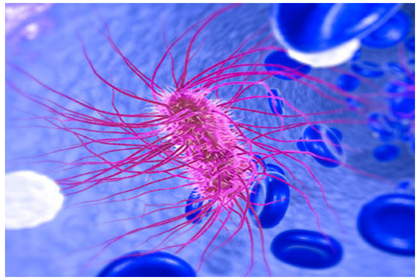
- Data shifting: From 2001-2012 to 2100 - 2200
  - Dates : shifted into the future preserving intervals
  - Time of day, day of the week, and approximate seasonality were conserved during date shifting.

State of art using MIMIC

- Prediction:
  - Mortality[1]
  - Length-of-Stay (LOS) [2]
  - Phenotyping (ICD code) [3]
  - Acute Respiratory Failure (ARF) [4]

[1] Huang B, Liang D, Zou R, Yu X, Dan G, Huang H, Liu H, Liu Y. Mortality prediction for patients with acute respiratory distress syndrome based on machine learning: a population-based study. Annals of Translational Medicine. 2021.
[2] T. Gentimis, A. J. Alnaser, A. Durante, K. Cook and R. Steele. Predicting Hospital Length of Stay Using Neural Networks on MIMIC III Data," 2017 IEEE 15th Intl Conf on Dependable, Autonomic and Secure Computing
[3] Gehrmann, Sebastian, et al. "Comparing rule-based and deep learning models for patient phenotyping." arXiv preprint arXiv:1703.08705 (2017)
[4] Wong, An-Kwok Ian, et al. "Machine learning methods to predict acute respiratory failure and acute respiratory distress syndrome." Frontiers in big Data 3 (2020): 39.

Enterobacteriaceae



Escherichia coli

Klebsiella pneumoniae

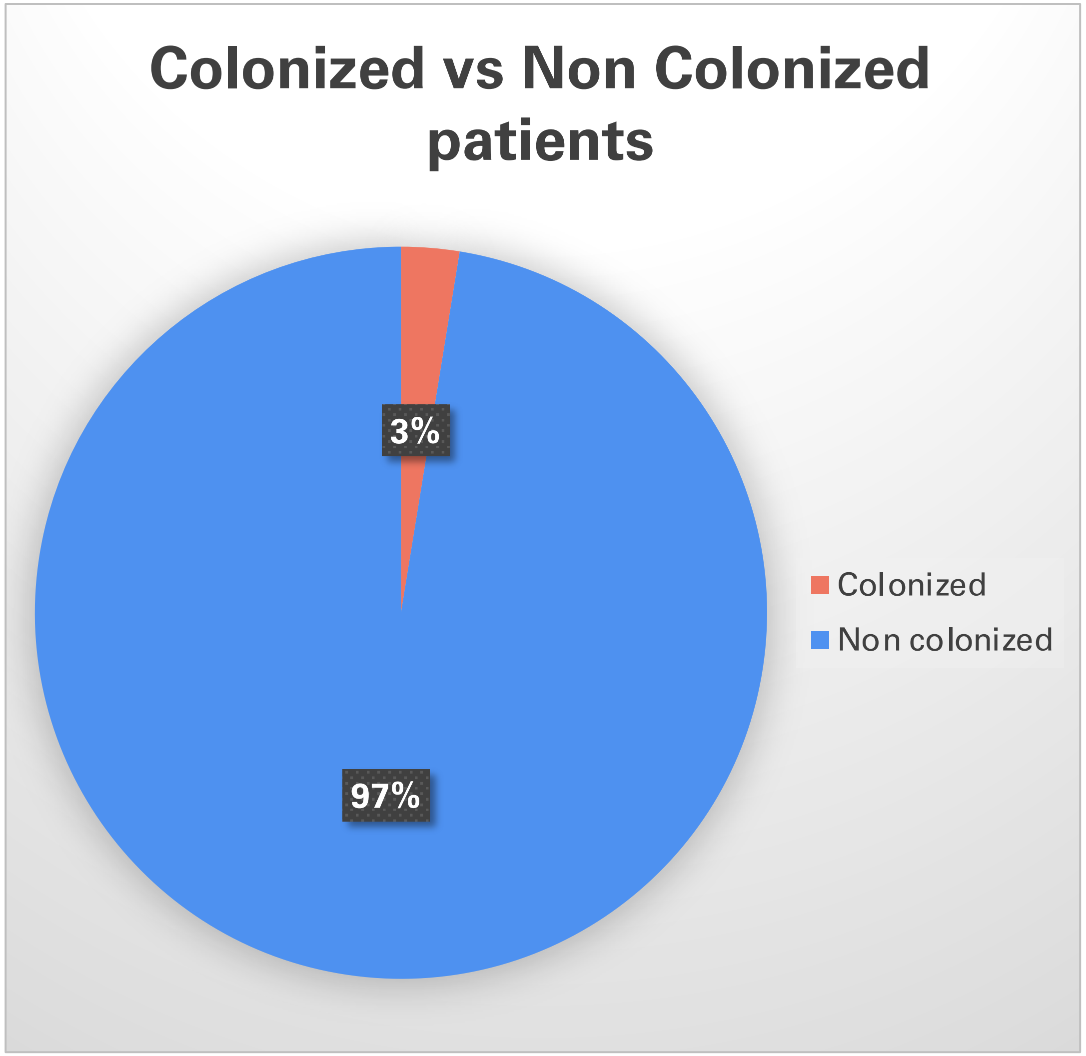
- Enterobacteriaceae are a large family of Gram-negative bacteria that includes E.coli and are a normal part of the gut flora.
- These pathogens can spread to the bloodstream resulting in life-threatening complications.
- Carbapenem-resistant *Enterobacteriaceae* (CRE) are *Enterobacteriaceae* that develop resistance to a group of antibiotics called carbapenems.

Example of specimens

Specimen	Flag	Category
SPUTUM	1	Respiratory
BLOOD CULTURE	**1**	**Blood**
URINE	**1**	**Urine**
BLOOD CULTURE	1	Blood
MRSA SCREEN	0	Other
SEROLOGY/BLOOD	1	Blood
EYE	1	Other
PLEURAL FLUID	1	Respiratory
STOOL	**0**	**Gastro**
SWAB	1	Other

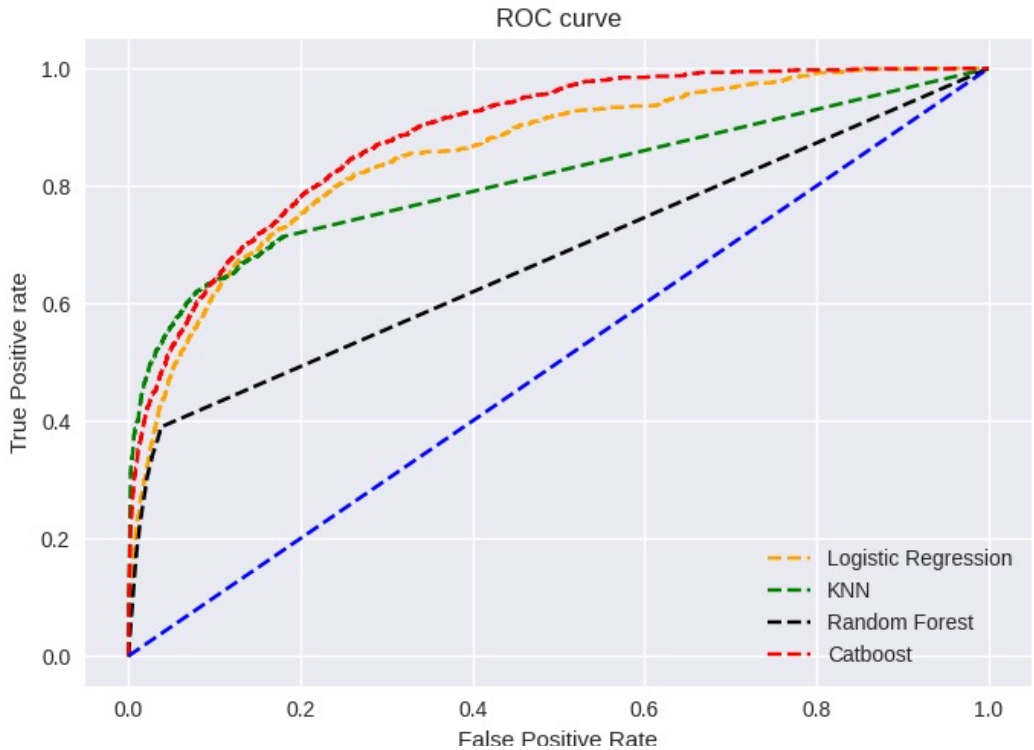
Data preprocessing

- Filter the data
- Link between tables
- Define relevant features
- Create new features



Results – Imbalanced (RWD)

	Accuracy (%)	**Precision (%)**	**Recall (%)**	**F1-score (%)**	**AUC (%)**
Logistic regression	82.2	10.2	**72.8**	17.9	85.4
KNN	**97.8**	**72.5**	33.5	**45.9**	80.9
Random forest	94.4	21.3	41	28	68.6
Catboost	**97.8**	69.1	31.5	43.2	**88.5**



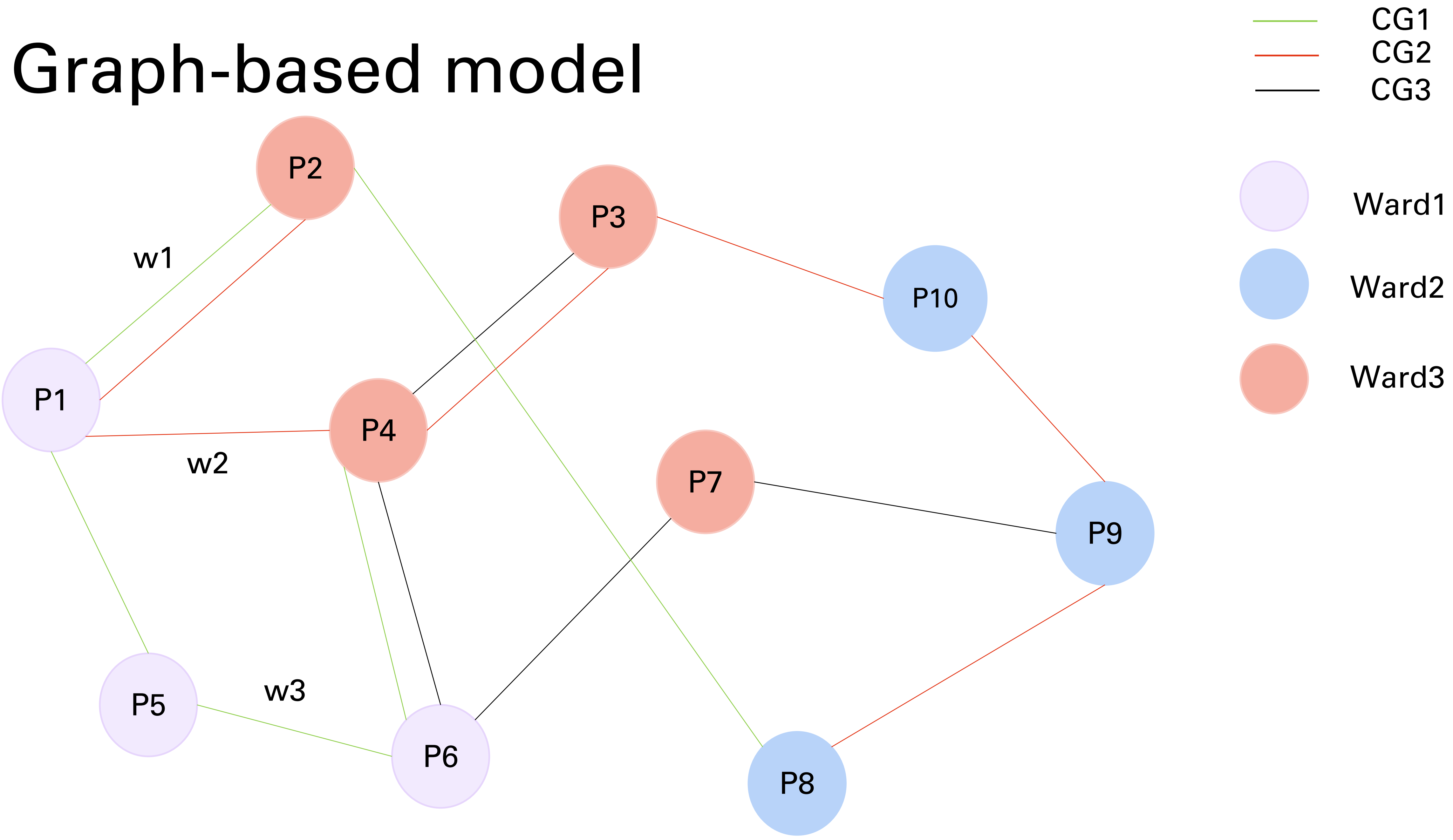
Results – Balanced (Optimal)

	Accuracy (%)	**Precision (%)**	**Recall (%)**	**F1-score (%)**	**AUC (%)**
Logistic regression	75.64	76.78	72.06	74.35	75.57
KNN	78.94	78.14	79.13	78.63	78.94
Random forest	73.08	72.25	73.12	72.68	73.08
Catboost	**80.67**	**79.15**	**82.17**	**80.63**	**80.70**

Next step and future work

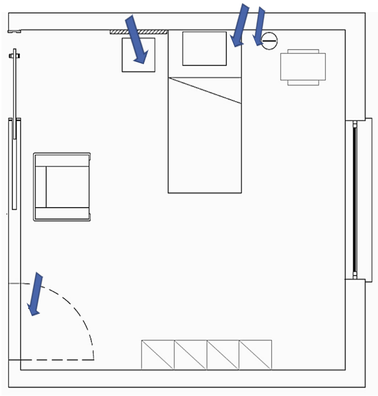
- Graph based-model
- Apply our model to long-term healthcare unit (LTHU) dataset
- Predict risk of infection in addition to the risk of colonization

Graph-based model

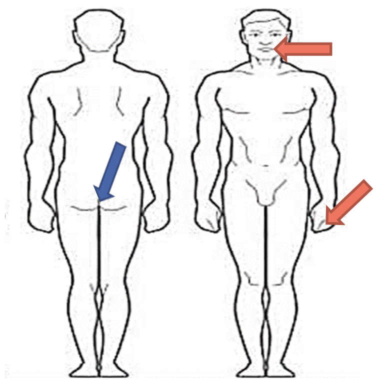


LTHU data

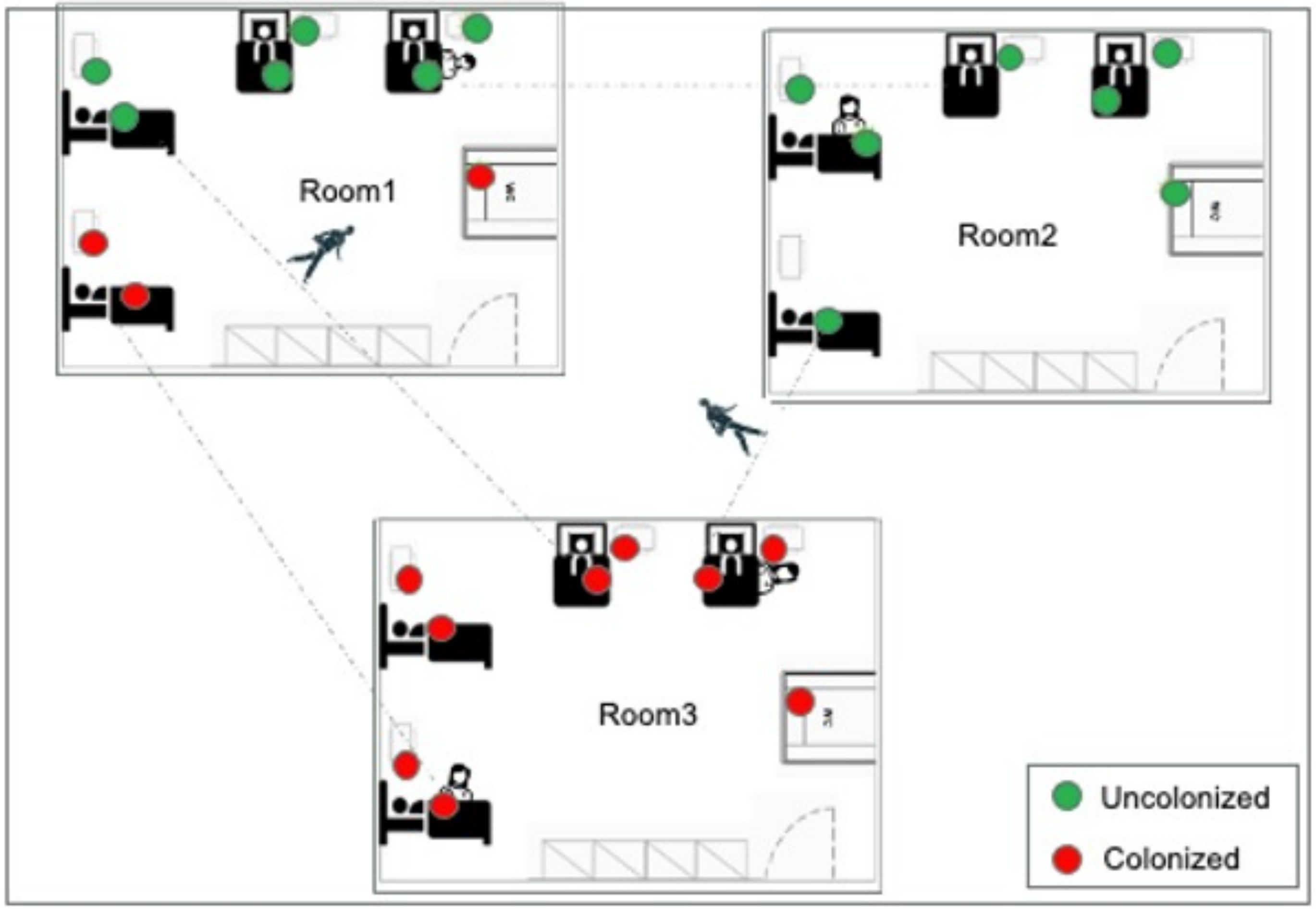
- Environmental samples
- Clinical samples
- Long-term healthcare unit (LTHU)



Environmental sampling



Clinical sampling



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THANK YOU