Imperial College London

Data-driven web-based intelligent decision support systems for infection management at the point of care

"Revolutionizing Antimicrobial Decision-Making: Harnessing the Potential of AI and Machine Learning in Integrated Clinical Decision Support Systems" - ChatGPT

Bernard Hernandez
b.hernandez-perez@imperial.ac.uk
Department of Medicine
Imperial College London
https://bahp.github.io/portfolio-academic/

21th of June 2023

camo centre for antimicrobial optimisation

epic impoc enhanced, personalized and integrated care for infection management at point of care

BACKGROUND

- **Rey Juan Carlos University (URJC), Madrid, Spain**
  - B.Sc. in Telecommunications
  - B.Sc. in Computer Science
- **Royal Institute of Technology (KTH), Stockholm, Sweden**
  - M.Sc. in Machine Learning
- **Imperial College London (ICL), London, United Kingdom**
  - Ph.D. in Computer Science and Healthcare

AREAS OF RESEARCH FOR CDSS

Areas of research to leverage healthcare through clinical decision support systems

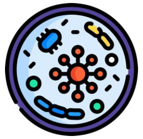
Management to facilitate access to records, laboratory results, and communication.

Facilitate **data collection** to enhance decisions, send **reminders** or clinical **alerts**

Patient engagement to improve understanding and shape future patient behaviour

Assess or predict complications using machine learning methods on tabular patient data

Review of **past similar cases** to improve decisions matching clinicians' reasoning process



AMR surveillance to strengthen knowledge for action in support of strategies to improve guidelines

Support **medication** from allergy checking, and therapy selection to adjusting antimicrobial doses

Using **NLP** to extract medical information from free-text clinical notes

Image processing to extract useful information from medical imaging (X-ray, CT, MRI)

+ more!

Imperial College London

SUPERVISED LEARNING

6, 5, 4

Infection

>500.000 daily profiles
2.7% prevalence

6 biomarkers
CRP, WBC, BIL, CRE, ALT, ALP

SVM
AUC ROC 0.85 (95% CI:0.84 - 0.86)
SENS 0.75 | SPEC 0.91

104 patients
35% prevalence at 72h
42% had microbiological tests

AUC ROC 0.84 (95% CI:0.76 - 0.91)
SENS 0.89 | SPEC 0.63 at 0.81

3

SARS-CoV-2

1186 patients
65% prevalence
14% had microbiological tests

21 biomarkers
Full Blood Count (FBC)

SVM
AUC ROC 0.91 (95% CI:0.76 - 0.91)
SENS 0.80 | SPEC 0.89

54 patients
52% prevalence

AUC ROC (0.96% CI: 0.90 – 1.00)
SENS 0.75 | SPEC 0.90

2

Dengue

8100 patients
27.7% prevalence

Age, Gender, Day + 4 biomarkers
HCT, PLT, WBC, LYMPH

XGB
AUC ROC 0.86 (95% CI:0.84 - 0.86)
SENS 0.92 | SPEC 0.56
PPV 0.73 | NPV 0.84

+ seasonality!

1

Dengue Shock Syndrome

4131 patients
5.4% prevalence

Age, Gender, Weight, Day + 2
biomarkers first 48h
HCT, PLT

ANN
AUC ROC 0.83 (95% CI:0.76 - 0.85)
SENS 0.66 | SPEC 0.84
PPV 0.18 | NPV 0.98

Bloodstream Infection
using temporal dynamics trough LSTM

1. Damien et al – *The diagnosis of dengue in patients presenting with acute febrile illness using supervised machine learning and impact of seasonality* – Frontiers in Digital Health (2022)
2. Damien et al – *Applied machine learning for the risk-stratification and clinical decision support of hospitalised patients with dengue in Vietnam* – PLOS Digital Health (2022)
3. TM Rawson et al – *Supervised machine learning to support the diagnosis of bacterial infection in the context of COVID-19* – JAC Antimicrobial Resistance – BMC Medicine (2021)
4. B Hernandez et al – *Data-driven web based intelligent CDSS for infection management at the point of care* – PhD Thesis Imperial College London (2019)
5. TM Rawson et al – *Supervised machine learning for the prediction of infection on admission to hospital: a prospective observational cohort study* – JAC (2018)
6. B Hernandez et al – *Supervised learning for infection risk inference using pathology data* – BMC Medical Informatics and Decision Making (2017)

CASE-BASED REASONING

In clinical environments, physician reasoning is based on **knowledge acquired from past** cases personally experienced which is exactly what CBR does! The aim of CBR is to solve new problems based on the solutions of similar past problems in the form of cases

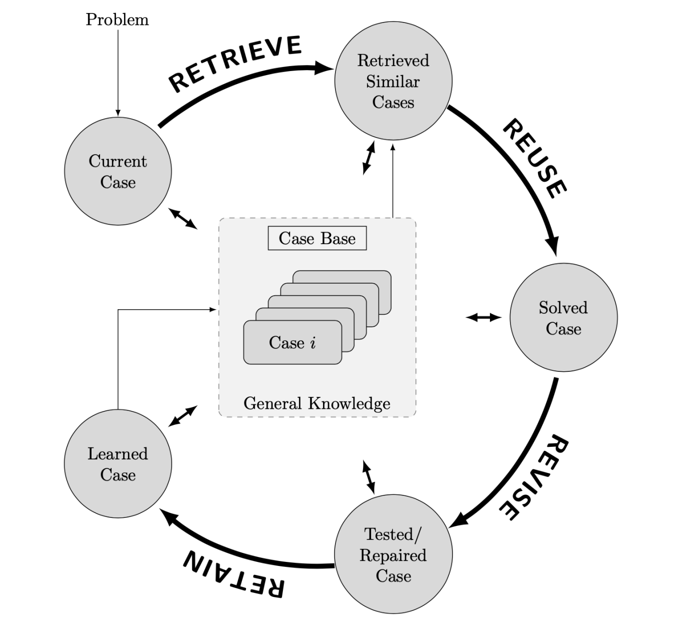
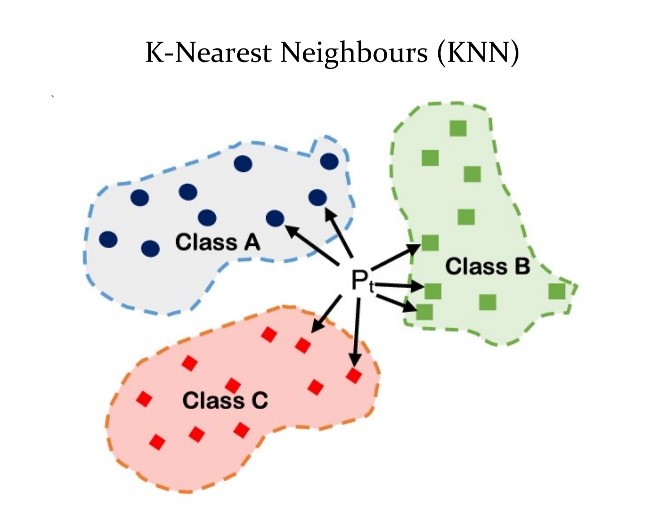
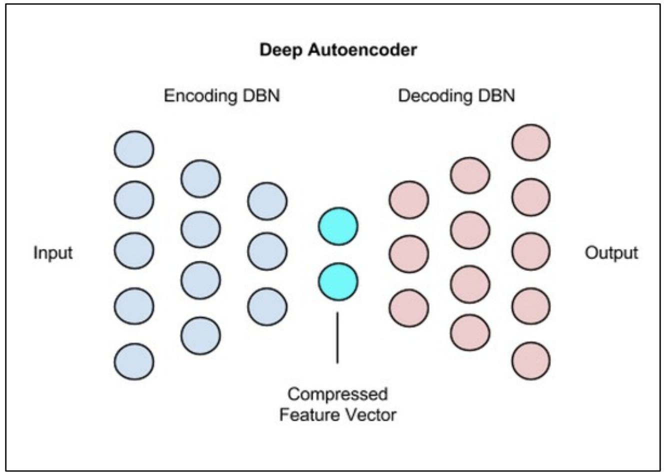
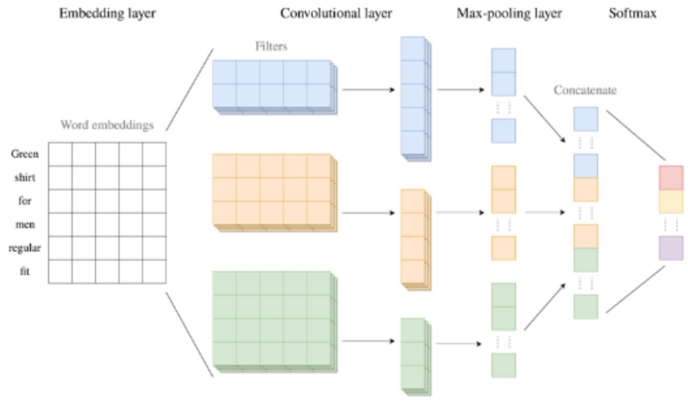


Figure 5.1: The CBR cycle. Diagram showing the different phases for a cycle within the case-based reasoning methodology as outlined by Aamodt and Plaza [7].







1. TM Rawson et al – *A real-world evaluation of a CBR to support antimicrobial prescribing decisions in acute care - CID* (2020)
2. B Hernandez et al – *Data-driven web-based intelligent CDSS: CBR benefits and limitations* – Health informatics (2017)

CASE-BASED REASONING - DENGUE

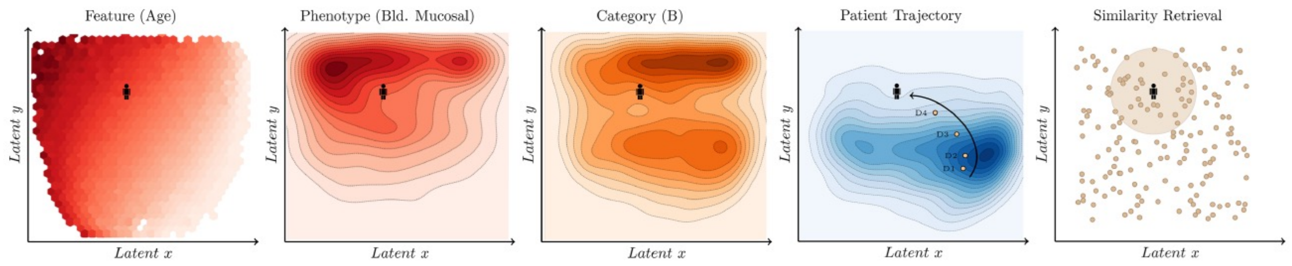


FIGURE 2
Latent space analysis. From left to right, the latent space produced can be described in terms of features using the average value (e.g. age) and phenotypes (e.g. mucosal bleeding) or categories (e.g. category which is associated with the warning signs defined in the WHO 2009 dengue guidelines) using the density distribution. In addition, it is possible to visualise the evolution of the patient over time (patient trajectory) and retrieve previous past similar patients to support decision making (similarity retrieval).

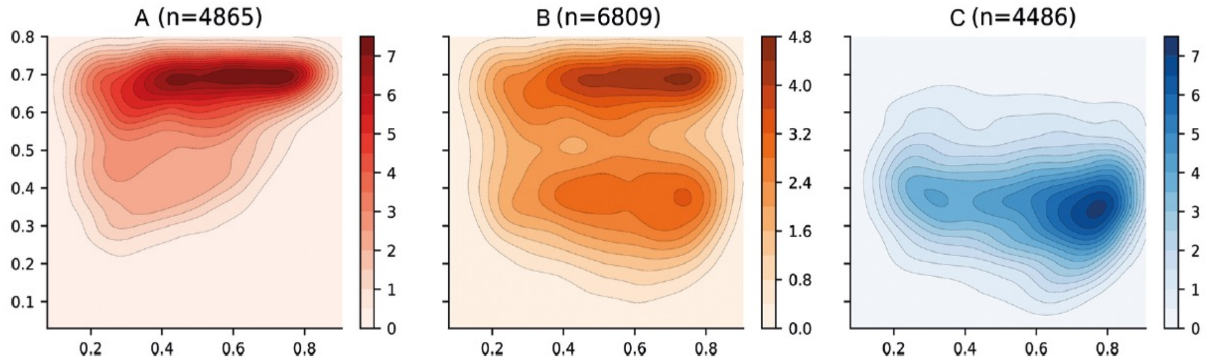


FIGURE 6
Latent space description: Categories. The graphs represent the density distribution over the latent space for three categories (A, B and C) estimated using a Gaussian kernel. These categories are defined as a compendium of various phenotypes (see Table 2) and therefore the value on each bin (pixel) described in the colorbar represents the estimated density on that bin for which one or more of the conditions associated to the category occurs.

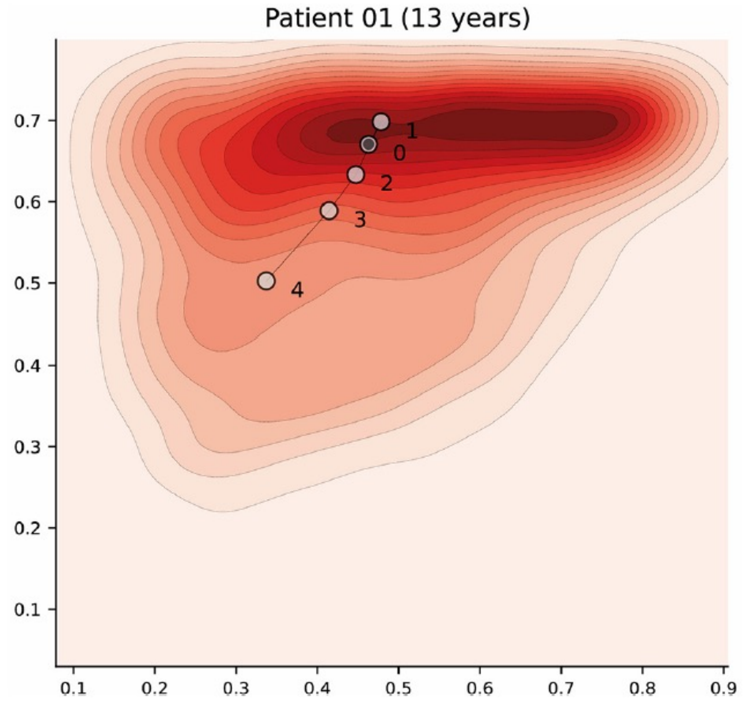


FIGURE 7
Latent space description: Trajectories. The graph represents the trajectory of a patient over the latent space using the density distribution for *Category A*, which associated with severe disease, as a background reference. Each marker represents a daily profile where the number indicates the day from admission. Filled markers indicate days in which the patient suffered an episode of shock. Further examples have been included in Figure A3 (Appendix).

Imperial College London

AMR SURVEILLANCE

Rates

The proportion of resistant isolates

Trends

Ratio of change of resistance rates over time

Multiple

Ratio of antimicrobials tested to which a pathogen is resistant

Spectrum

#microorganisms that can be treated with an antimicrobial

Concurrence

Whether resistance to one drug is associated to resistance to another

DRI

Ratio of resistant isolates to drugs used to treat them

Table 4.8: AMR summary for *Escherichia coli* in urine samples.

Antimicrobial	R(%) (95% CI)	References	T_M(%) (95% CI)	References	T_Y(%)	Pearson	Isolates
Cephalexin (CELX)	**11.1** (10.9, 11.3)		**0.055** (0.045, 0.065)		0.7 ↑	-0.25	79090
Ciprofloxacin (CIP)	**16.3** (16.0, 16.5)	[37, 39]	**0.046** (0.031, 0.062)	[14, 39]	0.6 ↑	-0.46	79239
Ampicillin (AMPC)	**69.6** (68.2, 70.9)	[39]	**0.038** (-0.058, 0.134)		0.5 ↔	-0.18	4729
Trimethoprim (TRI)	**37.8** (37.4, 38.1)	[12][37][38][39]	**0.033** (0.020, 0.046)	[39]	0.4 ↑	-0.14	79133
Amoxicillin-Clavulanate (AUG)	**10.9** (10.7, 11.2)		**0.018** (-0.022, 0.059)		0.2 ↔	-0.42	79093
Meropenem (MER)	**0.2** (0.1, 0.3)		**0.002** (-0.002, 0.006)		0.0 ↔	0.02	9875
Nitrofurantoin (NIT)	**2.7** (2.6, 2.8)	[12][37][38][39]	**-0.006** (-0.013, 0.001)		-0.1 ↔	-0.18	79108
Amikacin (AMI)	**1.1** (0.9, 1.2)		**-0.011** (-0.022, 0.000)		-0.1 ↔	-0.23	9786
Cefotaxime (CTX)	**60.8** (59.9, 61.8)		**-0.012** (-0.083, 0.059)		-0.1 ↔	0.01	9803
Tazocin (TAZ)	**24.2** (23.3, 25.0)	[37]	**-0.023** (-0.078, 0.032)		-0.3 ↔	0.01	9878
Gentamicin (GEN)	**9.3** (9.1, 9.5)	[38]	**-0.033** (-0.061, -0.005)		-0.4 ↓	-0.62	63399
Ertapenem (ERT)	**2.0** (1.7, 2.3)		**-0.033** (-0.050, -0.017)		-0.4 ↓	-0.31	8882
Ceftazidime (CAZ)	**57.3** (53.3, 58.2)		**-0.038** (-0.113, 0.037)		-0.5 ↔	-0.04	9810
Mecillinam (MEC)	**5.4** (4.9, 5.8)		**-0.048** (-0.071, -0.024)		-0.6 ↓	-0.29	9083
Cefoxitin (CXT)	**26.0** (25.1, 26.8)		**-0.069** (-0.123, -0.016)		-0.8 ↓	0.15	9798

Keys: CI=confidence interval; R=resistance; T_M=monthly trend; T_Y=yearly trend; ↑=significant increase; ↓=significant decrease.
Significance: A trend is significant if the CI does not include 0.

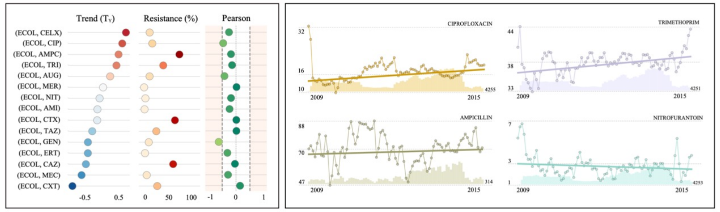
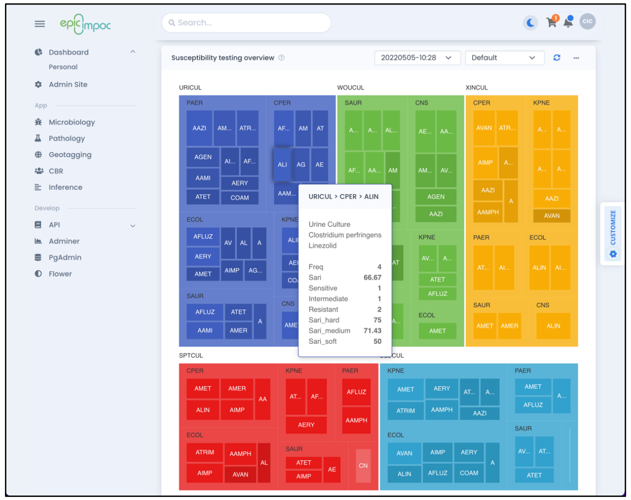


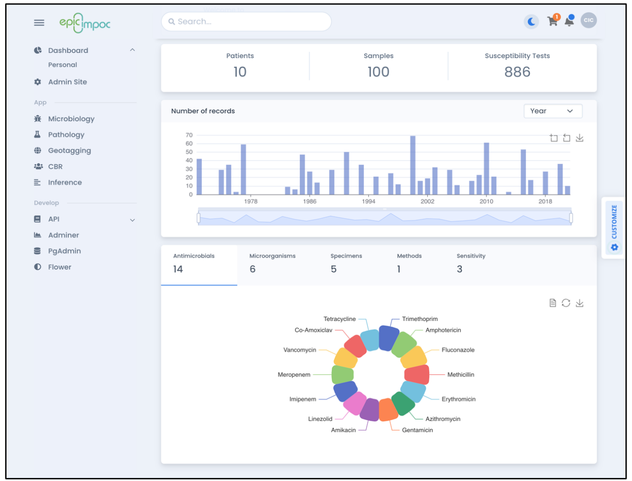
Figure 4.9: AMR summary for *Escherichia coli* in urine samples.

Table 4.7: Antimicrobial spectrum of activity (ASAI) summary in urine cultures.

Antimicrobial	$ASAI_N$ (N_{gn}–N_{sp})	$ASAI_P$ (N_{gn}–N_{sp})	Category	$ASAI_N$ $ASAI_P$
Tazocin (TAZ)	**71.4** (7–22)	**100.0** (3–4)	Broad	
Meropenem (MER)	**83.9** (7–22)	**75.0** (4–5)	Broad	
Amikacin (AMI)	**75.0** (8–23)	**66.7** (3–4)	Broad	
Ceftazidime (CAZ)	**64.0** (7–22)	**66.7** (3–4)	Broad	
Ertapenem (ERT)	**56.7** (6–18)	**75.0** (4–5)	Broad	
Amoxicillin (AMO)	**50.0** (4–5)	**73.8** (5–27)	Intermediate	
Gentamicin (GEN)	**63.7** (9–24)	**54.0** (6–27)	Intermediate	
Tigecycline (TIG)	**33.3** (3–5)	**100.0** (2–4)	Intermediate	
Amoxicillin-Clavunalate (AUG)	**38.1** (7–18)	**86.3** (6–31)	Intermediate	
Nitrofurantoin (NIT)	**36.2** (7–17)	**66.7** (6–32)	Intermediate	
Cefotaxime (CTX)	**24.7** (5–18)	**75.0** (4–5)	Intermediate	
Cephalexin (CELX)	**33.3** (6–14)	**54.2** (6–29)	Intermediate	
Ciprofloxacin (CIP)	**34.9** (9–25)	**27.0** (6–26)	Intermediate	
Mecillinam (MEC)	**17.5** (6–18)	**50.0** (2–3)	Intermediate	
Cefoxitin (CXT)	**11.7** (5–16)	**68.6** (4–8)	Intermediate	
Trimethoprim (TRI)	**20.1** (8–20)	**13.8** (5–29)	Intermediate	
Vancomycin (VAN)	**100.0** (1–1)†	**75.0** (5–25)	Narrow	
Aztreonam (AZT)	**41.5** (7–10)	–	Narrow	
Clindamycin (CLI)	**100.0** (1–1)†	**36.0** (5–27)	Narrow	
Erythromycin (ERY)	**100.0** (1–1)†	**34.0** (5–26)	Narrow	

† represents insufficient number of species not displayed in graphical summary.
Note: The effective threshold was set at 0.05.
Note: The antimicrobials have been sorted using the geometric mean of the indexes.
N_{gn}=number of genera; N_{sp}=number of species;





B Hernandez – pyAMR Python library (2023) - https://bahp.github.io/pyAMR
B Hernandez –PhD Thesis Imperial College London (2019) – http://spiral.imperial.ac.uk/handle/10044/1/73000
B Hernandez et al - *Resistance trend estimation using regression analysis to enhance antimicrobial surveillance: A multi-centre study in London 2009-2016* – Antibiotics (2021)

QUESTIONS

?

Bernard Hernandez
b.hernandez-perez@imperial.ac.uk
Department of Medicine
Imperial College London
https://bahp.github.io/portfolio-academic/

18th of May 2023