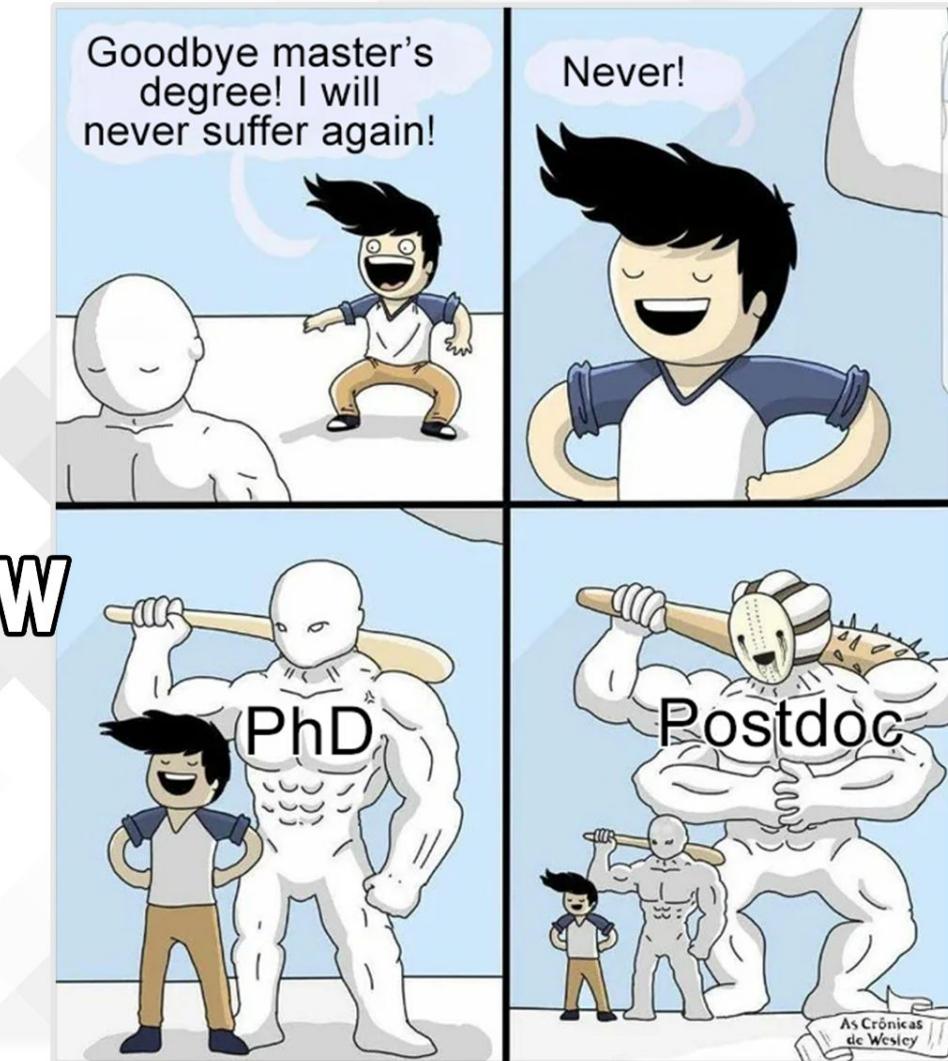


# Postdoc Interview

## Proposal presentation

Rafael Nozal Cañas

2024.04.23





# Introduction



dimensionality reduction

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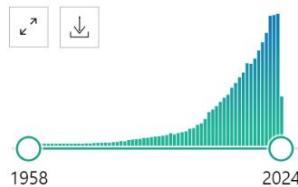
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RESULTS BY YEAR



TEXT AVAILABILITY

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- Full text

ARTICLE ATTRIBUTE

- Associated data

ARTICLE TYPE

- Books and Documents



### Dimensionality reduction for visualizing single-cell data using UMAP.

1 Becht E, McInnes L, Healy J, Dutertre CA, Kwok IWH, Ng LG, Ginhoux F, Newell EW.

Nat Biotechnol. 2018 Dec 3. doi: 10.1038/nbt.4314. Online ahead of print.

PMID: 30531897

Advances in single-cell technologies have enabled high-resolution dissection of tissue composition.

Several tools for **dimensionality reduction** are available to analyze the large number of parameters generated in single-cell studies. Recently, a nonlinear **dimensio ...**



### Dimensionality Reduction in Surrogate Modeling: A Review of Combined Methods.

2 Hou CKJ, Behdinan K.

Data Sci Eng. 2022;7(4):402-427. doi: 10.1007/s41019-022-00193-5. Epub 2022 Aug 21.

PMID: 36345394 [Free PMC article.](#) [Review.](#)

However, an ongoing challenge is to reduce execution and memory consumption of high-complexity processes, which often exhibit nonlinear phenomena. **Dimensionality reduction** algorithms have been employed for feature extraction, selection, and elimination for simplifyi ...



### Dimensionality reduction of calcium-imaged neuronal population activity.

3 Koh TH, Bishop WE, Kawashima T, Jeon BB, Srinivasan R, Mu Y, Wei Z, Kuhlman SJ, Ahrens MB, Chase SM,

Yu BM.

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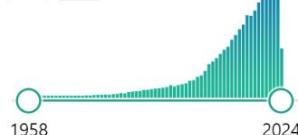
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34,057 results

  Page  of 3,406  

## RESULTS BY YEAR



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RESULTS BY YEAR



1958



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[Dimensionality reduction for visualizing single-cell data using t-SNE](#)

&gt;20.000 in the last ten years

Advances in single-cell technologies have enabled high-resolution dissection of tissue composition.

Several tools for **dimensionality reduction** are available to analyze the large number of parameters generated in single-cell studies. Recently, a nonlinear **dimensio** ...**Dimensionality Reduction in Surrogate Modeling: A Review of Combined Methods.**

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TEXT AVAILABILITY

 Abstract Free full text Full text

ARTICLE ATTRIBUTE

 Associated data

ARTICLE TYPE

 Books and Documents

2

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3

Cite



dimensionality reduction

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34,057 results

RESULTS BY YEAR



1958



2024

 Cite  
 Share[Dimensionality reduction for visualizing single-cell data using t-SNE](#)Advances in single-cell technology  
Several tools for dimensionality reduction have been developed and widely used. These methods generate a low-dimensional representation of the high-dimensional data, which can be used for various downstream analyses.[Dimensionality reduction for visualizing single-cell data using t-SNE](#)

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The main challenge is to reduce execution and memory consumption of high-complexity dimensionality reduction algorithms. These algorithms often exhibit nonlinear phenomena. Dimensionality reduction algorithms have been employed for feature extraction, selection, and elimination for simplifying the analysis ...

[Dimensionality reduction of calcium-imaged neuronal population activity.](#)

3

Koh TH, Bishop WE, Kawashima T, Jeon BB, Srinivasan R, Mu Y, Wei Z, Kuhlman SJ, Ahrens MB, Chase SM, Yu BM.

Cite

We need a dimensionality reduction of the dimensionality reduction methods !

# Multivariate Analysis

# Multivariate Analysis

Classical methods

Machine Learning

Tensors

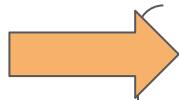
Multiset comparison

# Multivariate Analysis

Machine Learning

Tensors

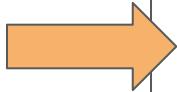
Multiset comparison



Classical methods

Dimensionality reduction (ie: PCA) + regression + ...

# Multivariate Analysis



Classical methods

Dimensionality reduction (ie: PCA) + regression + ...

Machine Learning

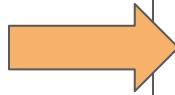
*"I have no idea what is happening but it is working"*

Explainability (SHAP, MDI, Boruta...)

Tensors

Multiset comparison

# Multivariate Analysis



Classical methods

Dimensionality reduction (ie: PCA) + regression + ...

Machine Learning

*"I have no idea what is happening but it is working"*

Explainability (SHAP, MDI, Boruta...)

Tensors

Multiset comparison

# Multivariate Analysis

Classical methods

Dimensionality reduction (ie: PCA) + regression + ...

Machine Learning

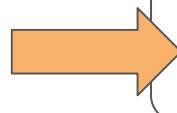
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Explainability (SHAP, MDI, Boruta...)

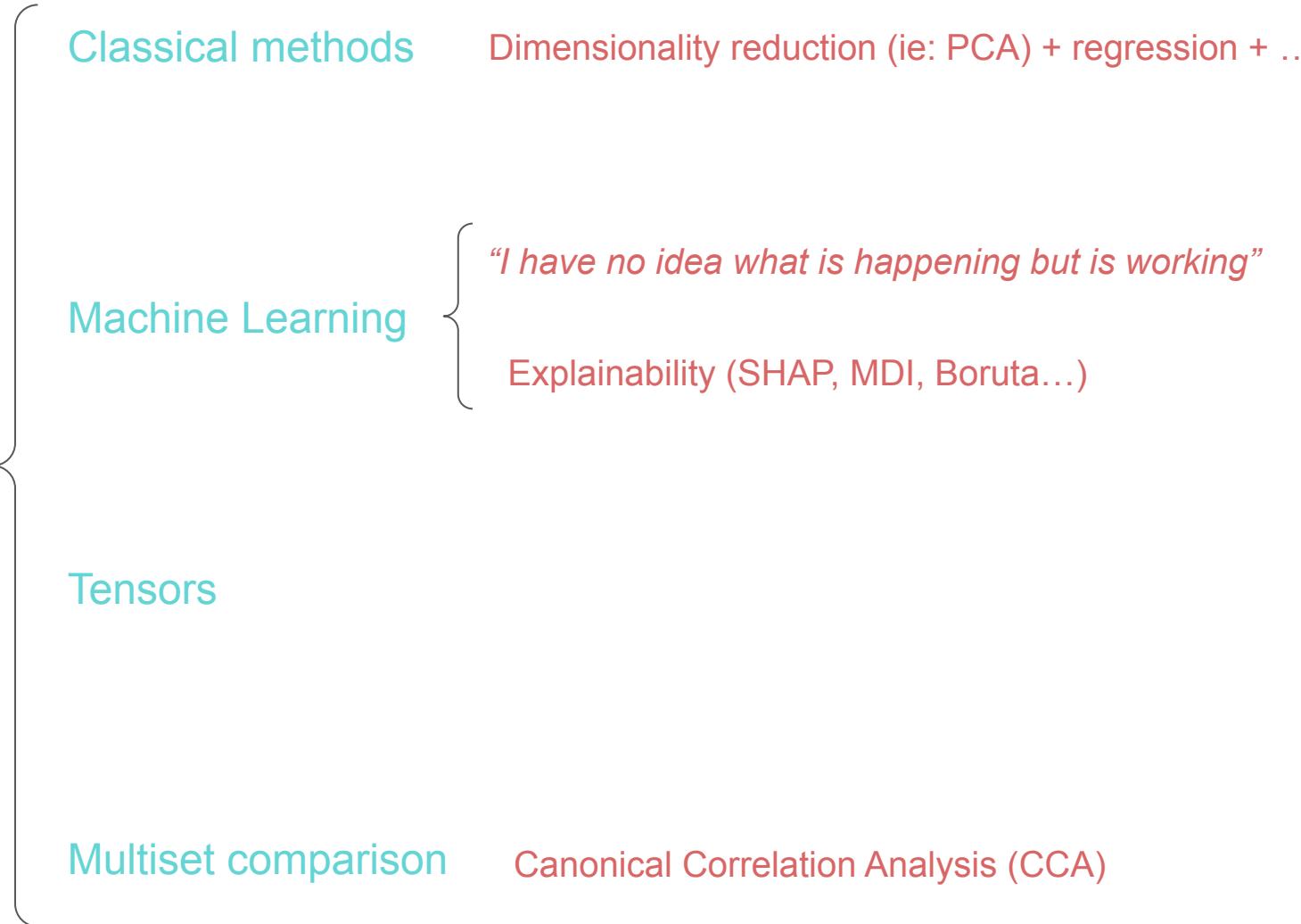
Tensors

Multiset comparison

Canonical Correlation Analysis (CCA)



# Multivariate Analysis



# Multivariate Analysis

Classical methods

Dimensionality reduction (ie: PCA) + regression + ..

Machine Learning

*"I have no idea what is happening but is working"*

Explainability (SHAP, MDI, Boruta...)

Working in the past and present

Tensors

Multiset comparison

Canonical Correlation Analysis (CCA)

# Multivariate Analysis

Classical methods

Dimensionality reduction (ie: PCA) + regression + ...

Machine Learning

*"I have no idea what is happening but is working"*

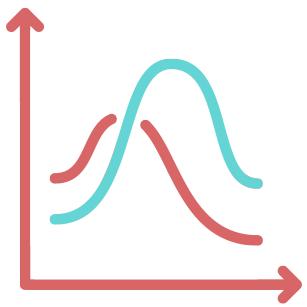
Explainability (SHAP, MDI, Boruta...)

Tensors

Planned work in the future

Multiset comparison

Canonical Correlation Analysis (CCA)



# Classical statistics

## Quality and Reliability Engineering International



CASE STUDY

Open Access

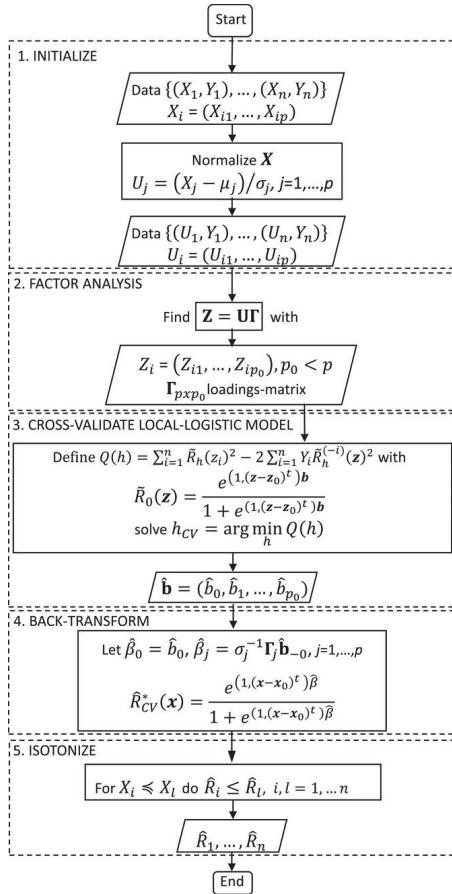


# Unsupervised and supervised learning for the reliability analysis of complex systems

Maria Luz Gámiz , Fernando Navas-Gómez, Rafael Nozal-Cañadas, Rocío Raya-Miranda

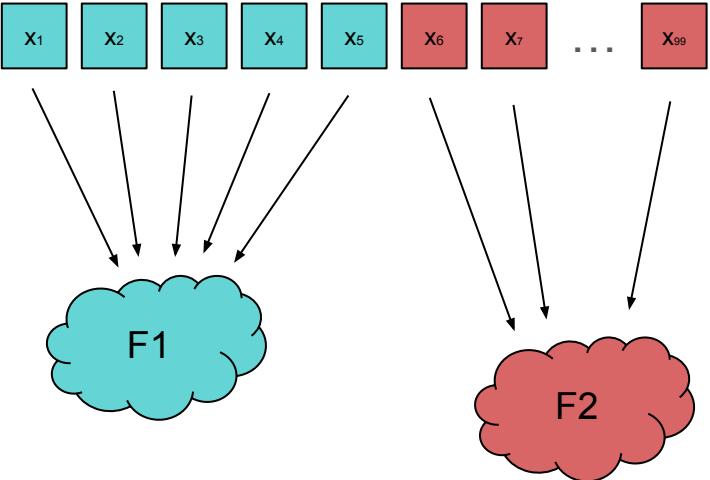
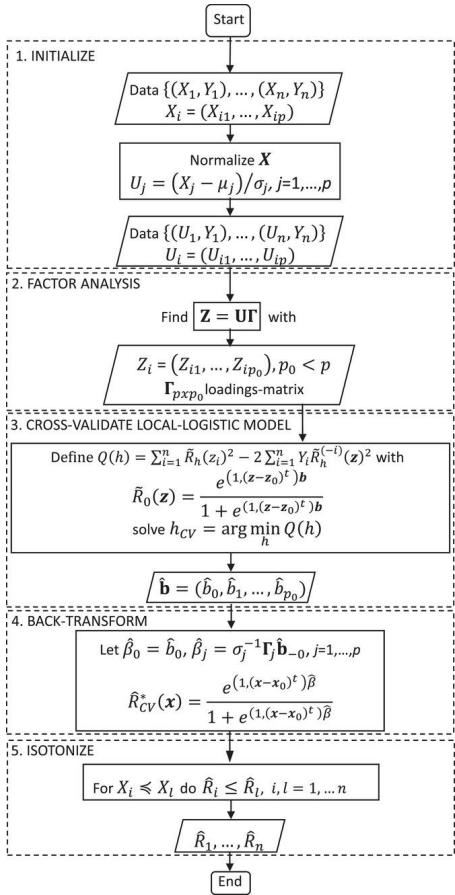
First published: 18 March 2023 | <https://doi.org/10.1002/qre.3311>

# Classical methods

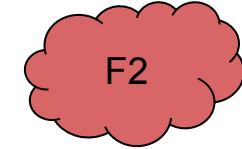
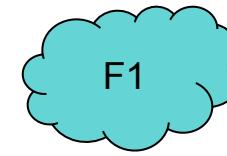
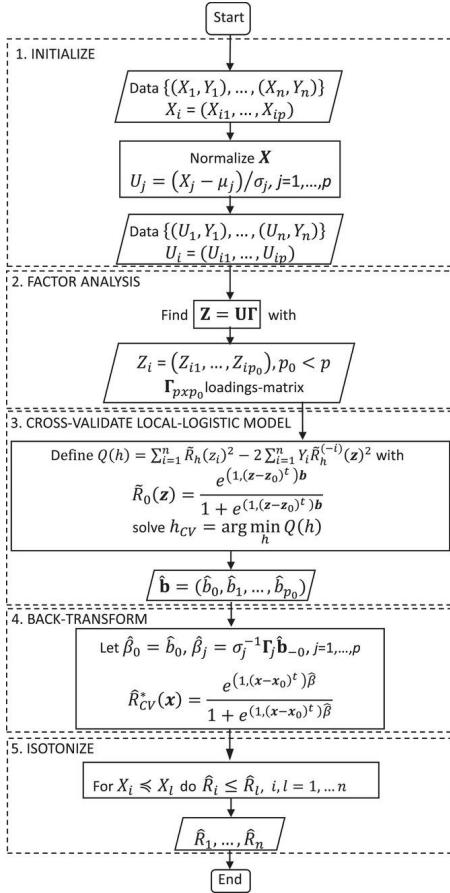


Data cleaning, normalization, etc...  
nothing weird or interesting in this step

# Classical methods



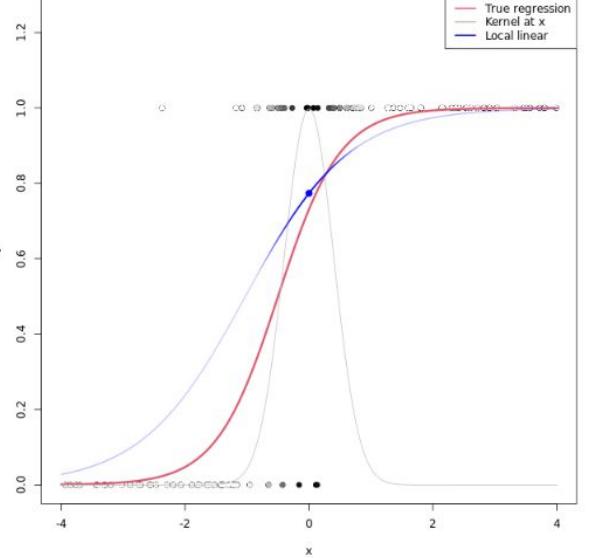
# Classical methods



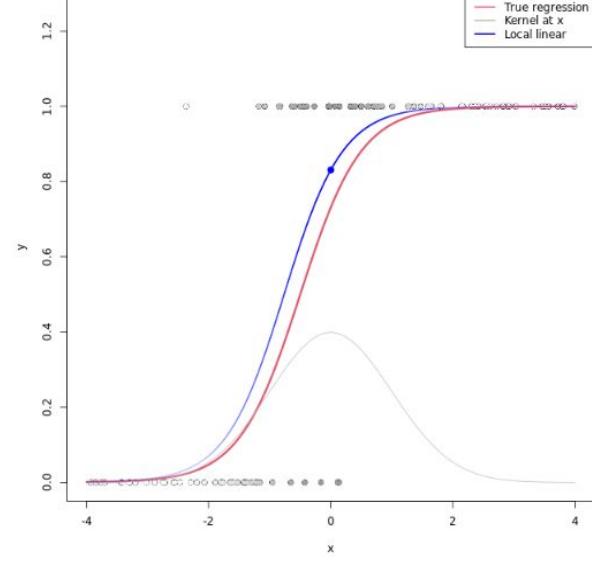
Factor analysis with:

- Isotonic regression
- Log-logistic local

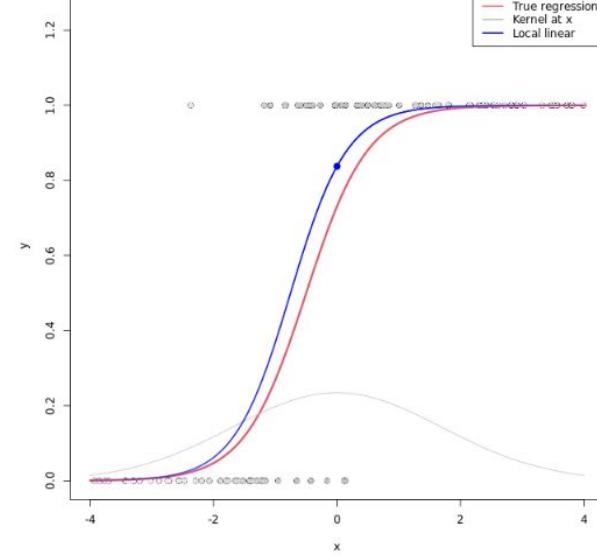
$h = 0.4$



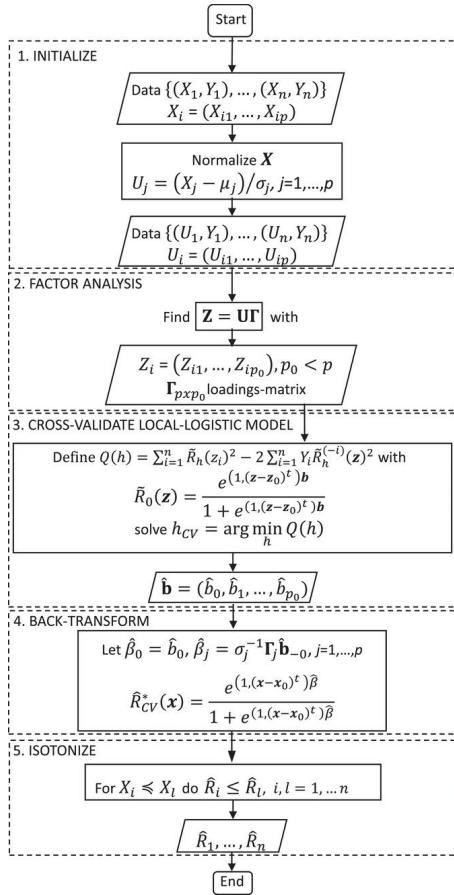
$h = 1$



$h = 1.4$

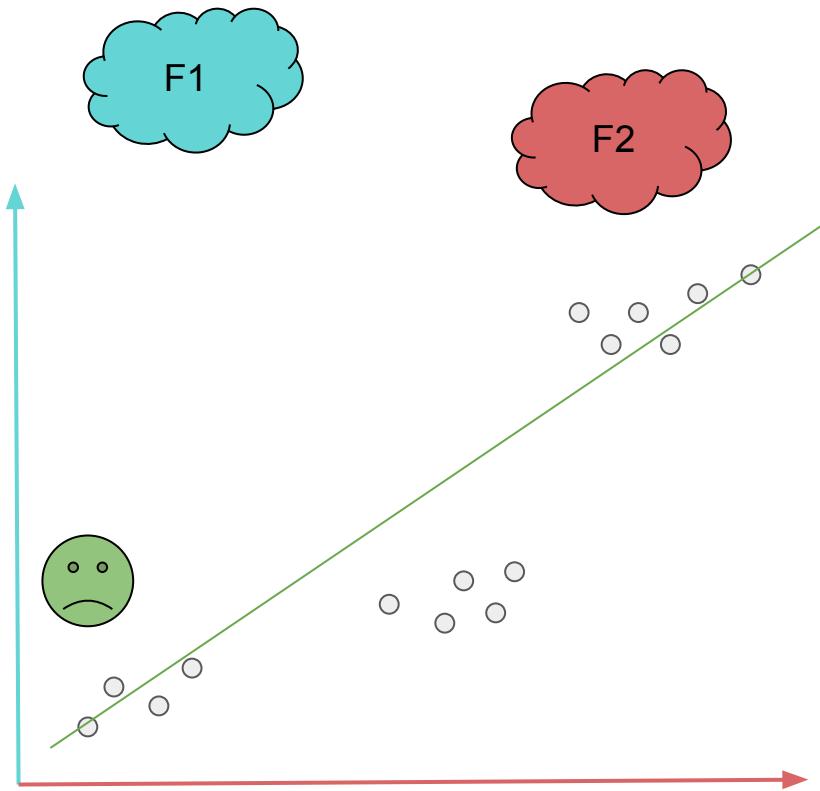


# Classical methods

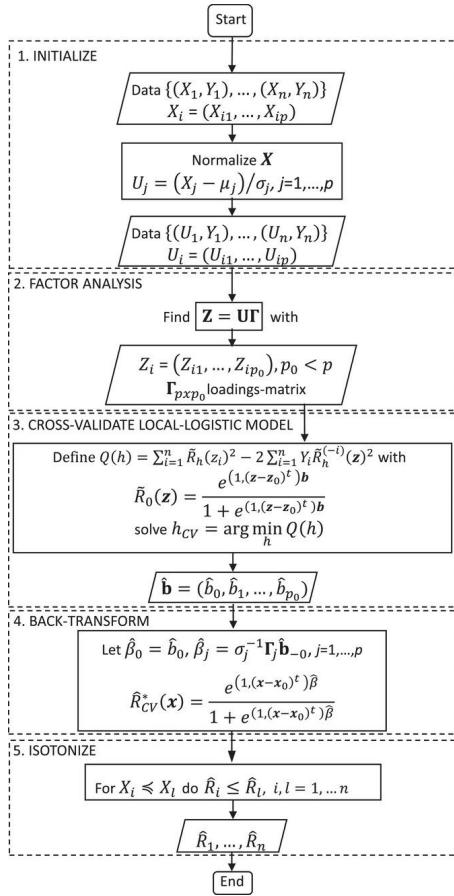


Factor analysis with:

- Isotonic regression
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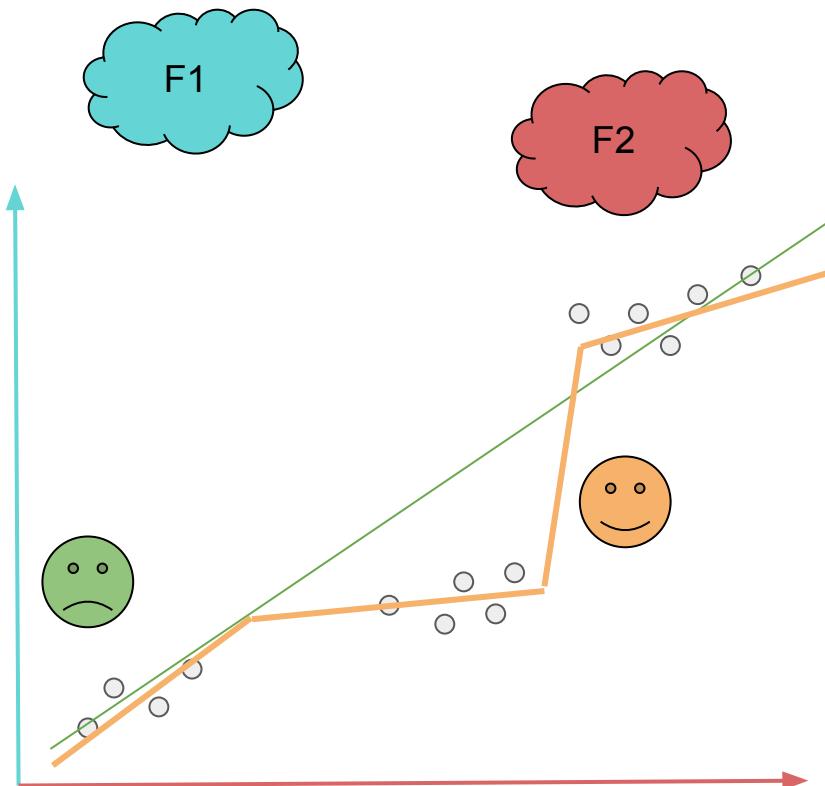


# Classical methods

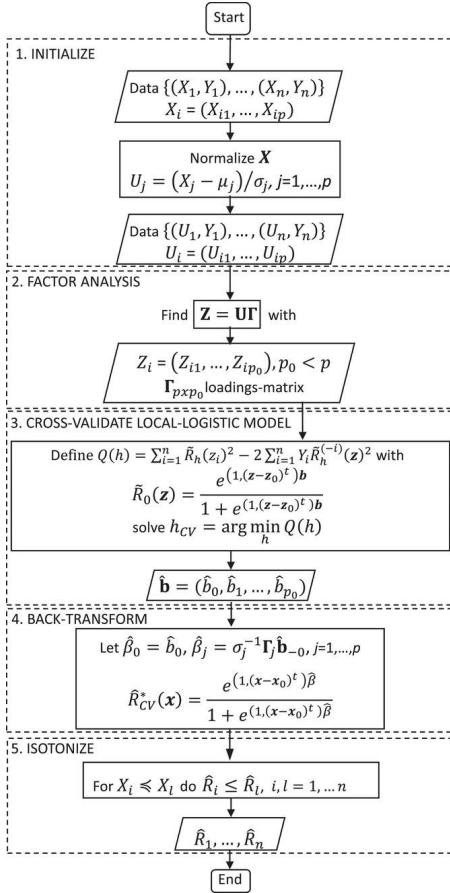


Factor analysis with:

- Isotonic regression
- Log-logistic local



# Classical methods

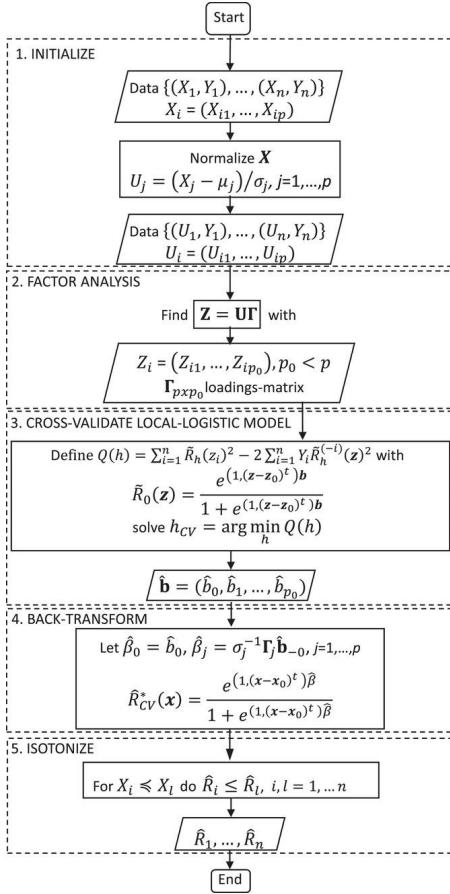


Factor analysis with:

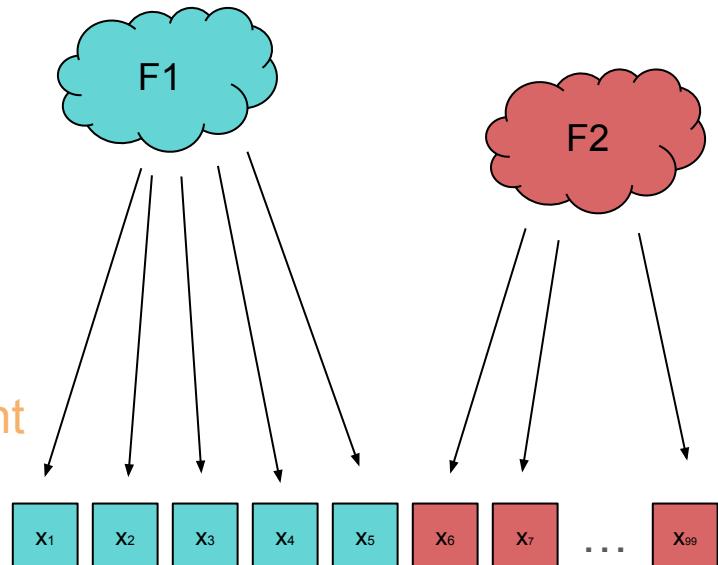
- Isotonic regression
- Log-logistic local

non-parametric

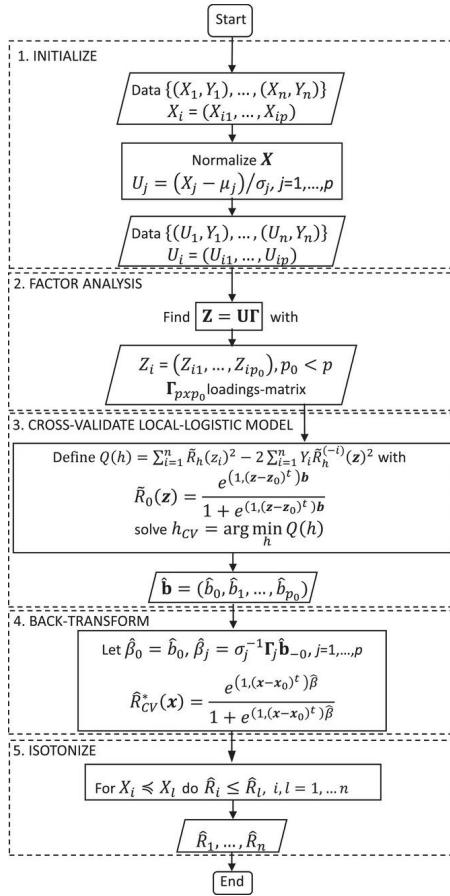
# Classical methods



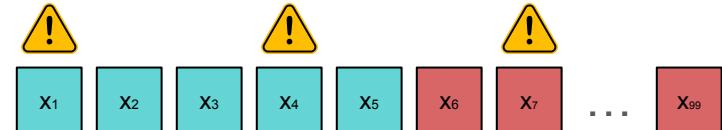
Brings back from the latent space into the real space

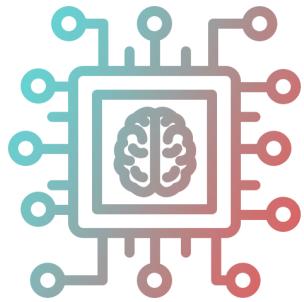


# Classical methods



Variable importance





# Machine Learning

# Machine learning



Predicted: Wolf  
True: Wolf



Predicted: Husky  
True: Husky



Predicted: Husky  
True: Husky



Predicted: Wolf  
True: Wolf



Predicted: Wolf  
True: Wolf



Predicted: Wolf  
True: Wolf



Predicted: Husky  
True: Wolf



Predicted: Wolf  
True: Wolf



Predicted: Wolf  
True: Husky

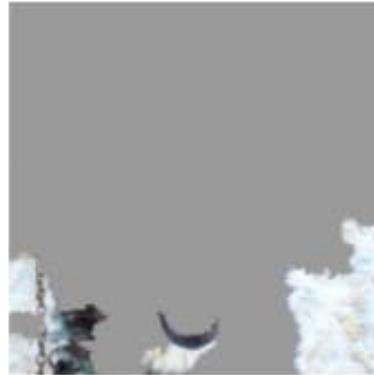


Predicted: Husky  
True: Husky

# Machine learning



(a) Husky classified as wolf



(b) Explanation

**Figure 11: Raw data and explanation of a bad model’s prediction in the “Husky vs Wolf” task.**

	Before	After
Trusted the bad model	10 out of 27	3 out of 27
Snow as a potential feature	12 out of 27	25 out of 27

**Table 2: “Husky vs Wolf” experiment results.**

# Machine learning

Can change  
multiple **test**  
predictions:



Orig (confidence): Dog (97%)

New (confidence): Fish (97%)

Analysis | [Open access](#) | Published: 15 March 2021

## Common pitfalls and recommendations for using machine learning to detect and prognosticate for COVID-19 using chest radiographs and CT scans

[Michael Roberts](#) , [Derek Driggs](#), [Matthew Thorpe](#), [Julian Gilbey](#), [Michael Yeung](#), [Stephan Ursprung](#), [Angelica I. Aviles-Rivero](#), [Christian Etmann](#), [Cathal McCague](#), [Lucian Beer](#), [Jonathan R. Weir-McCall](#), [Zhongzhao Teng](#), [Effrossyni Gkrania-Klotsas](#), [AIX-COVNET](#), [James H. F. Rudd](#), [Evis Sala](#) & [Carola-Bibiane Schönlieb](#)

[Nature Machine Intelligence](#) 3, 199–217 (2021) | [Cite this article](#)

**97k** Accesses | **560** Citations | **1193** Altmetric | [Metrics](#)

## Machine learning

- Source issues. Many papers (16/62) used the pneumonia dataset of Kermany et al.<sup>86</sup> as a control group. They commonly failed to mention that this consists of paediatric patients aged between one and five. Developing a model using adult patients with COVID-19 and very young patients with pneumonia is likely to overperform as it is merely detecting children versus adults. This dataset is also erroneously referred to as the Mooney dataset in many papers (being the Kermany dataset deployed on Kaggle<sup>91</sup>). It is also important to consider the sources of each image class, for example, if images for different diagnoses are from different sources. It is demonstrated by Maguolo et al.<sup>92</sup> that by excluding the lung region entirely, the authors could identify the source of the images in the Cohen et al.<sup>85</sup> and Kermany et al.<sup>86</sup> datasets with an AUC between 0.9210 and 0.9997, and 'diagnose' COVID-19 with an AUC = 0.68.

# Machine learning

## Deep learning papers

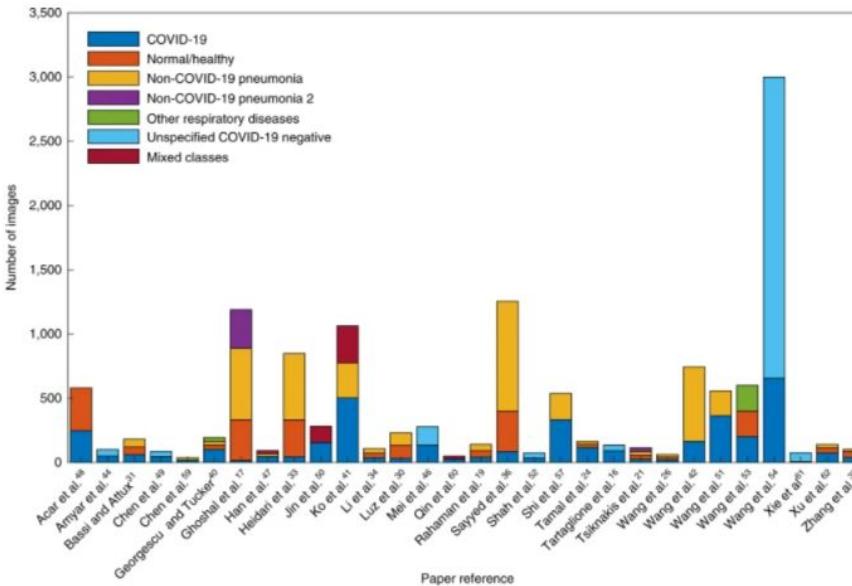
There were six non-mandatory CLAIM criteria not satisfied in at least half of the 37 papers.

- (1) 29 did not complete any external validation
- (2) 30 did not perform any robustness or sensitivity analysis of their model
- (3) 26 did not report the demographics of their data partitions
- (4) 25 did not report the statistical tests used to assess significance of results or determine confidence intervals
- (5) 23 did not report confidence intervals for the performance
- (6) 22 did not sufficiently report their limitations, biases or issues around generalizability

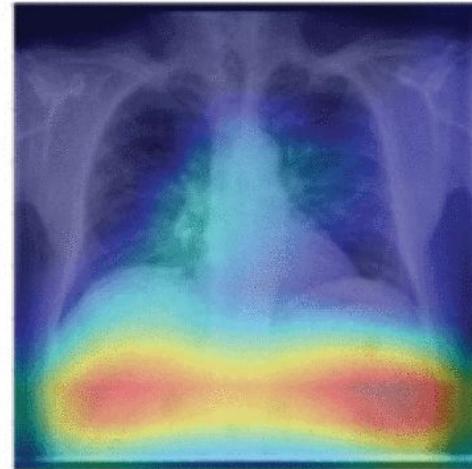
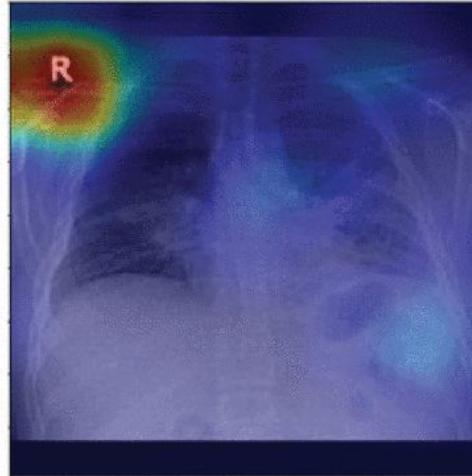
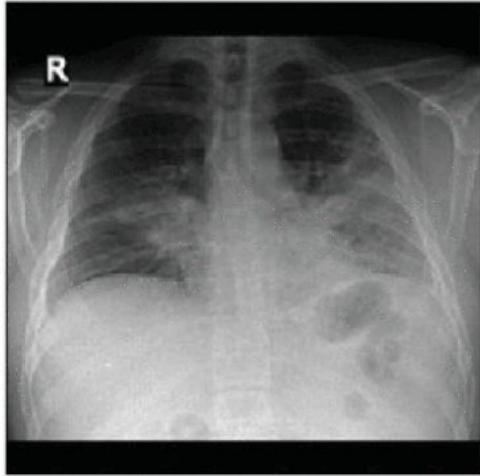
# Machine learning

Figure 3 shows the number of images of each class used in the holdout/test cohorts. We found that 6/32 papers had an imbalanced testing dataset<sup>17,24,33,36,37,61</sup>. Only 6/32 papers tested on more than 1,000 images<sup>17,27,36,41,54,81</sup>. Only 4/32 had both a large and balanced testing dataset<sup>27,41,54,81</sup>.

**Fig. 3: The number of images used for model testing split by image class.**



It is noted that we exclude Bai et al.<sup>81</sup> and Zhang et al.<sup>27</sup> from the figure as they used far more testing data (14,182 and 5,869 images respectively) than other papers. There were a large number of images (1,237) in the testing dataset in Wang et al.<sup>54</sup> that were unidentified in the paper (we include these in the unspecified COVID-19 negative).



Bias Analysis on Public X-Ray Image  
Datasets of Pneumonia and COVID-19  
Patients

Del Tejo Catalá et la.

ARTIFICIAL INTELLIGENCE

# Google's medical AI was super accurate in a lab. Real life was a different story.

If AI is really going to make a difference to patients we need to know how it works when real humans get their hands on it, in real situations.

By

Will Douglas Heaven

April 27, 2020



## Program CANS day; 23 February at Scandic Ishavshotel, PANORAMA

### TIME PROGRAM

08:30-08:45 "Welcome and introduction to the conference"

Camilla Brekke, Pro-Rector Research and Development, UiT  
Arnfinn Sundsfjord, Center leader

**Session 1 (Chair: Mona Johannessen)**

08:45-09:30 "Staphylococcal In host Adaption and Evolution" Annelies Zinkernagel,  
University of Zurich

**Session 2 (Chair: Klara Stensvåg)**

09:30-10:00 "Marine microbiomes and their role in the biodiscovery of new antibacterials",  
Teppo Räma, Marbio

10:00-10:30 "Including viruses of microbes as a resource for marine bioprospection".  
Gabriel Magno de Freitas Almeida, Marine Bioprospecting

10:30-10:45 BREAK

**Session 3 (Chair: Hanna-Kirsti Schröder Leiros)**

10:45-11:15 "Conjugation strategies for «new» antimicrobials and diagnostic tools" Marius  
M. Haugland, Haugland group

11:15-11:45 "Problems or opportunities in large biomedical data" Einar Holsbø, Health  
Data Lab

11:45 -12:30 LUNCH

**Session 4 (Poster group 1-6)**

12:45-14:45 Poster walk with short presentations of posters

14:45-15:00 BREAK

**Session 5 (Chair: Pål J. Johnsen)**

15:00-15:45 "The good, the bad and the ugly - how to rule the world of *E. coli*" Jukka  
Corander, Institute of Basic Medical Sciences, University of Oslo

**Session 6 (Chair: Johanna U. Ericson)**

15:45-16:15 "Human Microbiome in Pregnancy and Early Life" Veronika Pettersen, Host  
Microbe Interaction/Pediatric Infection

16:15-16:45 "Chemical Infection Biology – From identification of new enzymes to  
phenotypic profiling of single-cells" Christian Lentz, Host Microbe Interaction

16:45-17:00 Summary, Arnfinn Sundsfjord

17:00-17:15 Photo, Jan Fredrik Frantzen

17:15-17:30 BREAK

17:30-18:30 Session 7: Poster session

19:00 DINNER



## The Nordic AMR Research Centre Conference

When and where: 13-15 March 2024 at [Scandic Ishavshotel](#)

CANS invites researchers, PhD's and postdocs from all Nordic AMR Centres to a conference offering lectures, poster presentations and an exciting mixture of networking and cross-disciplinary discussions.

### 13 MARCH PROGRAM

13:00-14:00 LUNCH

14:00-14:15 Welcome and introduction: Professor Arne Smalås, Dean, Faculty of Science and Technology, and Chair board CANS, and professor Arnfinn Sundsfjord, CANS centre leader. UiT The Arctic University of Norway (UiT)

**Session 1: Clinical AMR and Diagnostics.** Chairs: Iren Löhr, Stavanger University Hospital (SUH) and Tone Tønje, University of Oslo (UiO)  
Genomics to enhance AMR control in clinical and public health settings. *Ben Howden, University of Melbourne (keynote)*

14:45-15:00 Clinical impact of the newly described *Staphylococcus borealis* in Norwegian hospitals. *Jorunn Pauline Cavanagh, UiT*  
Incubation of the blood cultures for up to 5 hours in a standard laboratory incubator is sufficient for the identification of sepsis-causing bacteria and ARGs using nanopore sequencing. *Jawad Ali, Inland Norway University of Applied Sciences (INN)*

15:00-15:15 Introducing a high-throughput single-cell approach that provides insights into growth variations in isogenic *Staphylococcus aureus* populations at single cell level. *Jonathan Hira, UiT*  
Novel technological solutions for rapid diagnostics of infection and antimicrobial resistance: A One Health approach. *Rafi Ahmad, INN/UiT*

15:45-16:00 Elucidating the biofilm genotype for successful and emerging sequence types in human pathogenic *Escherichia coli*. *Miriam Karlsen, UiT*  
General discussion

16:15-16:45 Break

**Session 2: Evolution of AMR.** Chairs: Teppo Hiltunen, University of Turku and Pål J. Johnsen (UiT)  
Using evolutionary approaches to understand the spread of antibiotic resistance. *Craig MacLean, University of Oxford (keynote)*

17:15-17:30 *Escherichia coli* plasmidome maps the game of clones. *Jukka Corander, UiO*  
Divergent genetic evolution employs the same molecular mechanisms. *Christopher Fröhlich, UiT*

17:30-17:45 Antibiotic-induced amino acid release (AIAAR): A bacterial emergency response to membrane-targeting antibiotics. *Margareth Siddartha, Chalmers University of Technology*

18:00-18:15 Hypercube inference to learn and predict the pathways of AMR evolution from data. *Iain Johnston, University of Bergen (UiB)*  
Using experimental evolution to study AMR in synthetic bacterial communities. *Teppo Hiltunen, University of Turku*

18:15-18:30 General discussion

18:30-18:45 Poster session

18:45-20:00 Poster session

## 14 MARCH PROGRAM

Session 3: Environmental AMR. Chairs: **Johan Bengstrøm Palme** (Chalmers University of Technology) and **Arnfinn Sundsfjord** (UiT)

09:00-09:30 On the environment's role in evolution, transmission, and surveillance of antibiotic resistance. **Joakim Larsson**, *University of Gothenburg* (keynote)

09:30-09:45 *Klebsiella pneumoniae* ecology in a genomic One Health perspective in Norway, 2001-2020. **Marit Hetland**, SUH

09:45-10:00 Transfer of antibiotic resistance in wastewater and environmental *Escherichia coli*, *Shewanella* spp. and *Vibrio* spp. strains. **Annie Justh de Neczpal**, *University of Gothenburg*

10:00-10:15 Circulation of enterotoxigenic *Escherichia coli* (ETEC) isolates expressing CS23 from the environment to clinical settings. **Enrique Joffré**, *University of Gothenburg*

10:15-10:30 Agree to Disagree? An Evaluation of Consistency Between Phenotypic and Genomic Methods for AMR Detection. **Markus Wenne**, *Chalmers University of Technology*

10:30-10:45 ResUrb: The urban resistome adaptation to climate change in an Anthropocene era. **Hilde Synnøve Volland**, *Norwegian Institute of Public Health*

10:45-11:00 General discussion

11:00-11:30 Break

11:30-13:00 Poster session

13:00-14:00 LUNCH

Session 4: New Antibiotics. Chairs: **Klara Stensvåg** (UiT) and **Dan Andersson**/ **Linus Sandegren** (Uppsala Antibiotic Center (UAC))

14:00-14:30 Current Ideas on How to Incentivise New Antibiotics R&D. **Francesco Ciabusci**, UAC (keynote)

14:30-14:45 Novel synthetic cationic antimicrobial peptides and their potential in combating antibiotic resistance. **Ataur Rahman**, UiT

14:45-15:00 Development of metallo- $\beta$ -lactamase inhibitors. **Kinga Virág Gulyás**, UAC

15:00-15:15 Bacterial extracellular vesicles (bEVs) as a ready to use model to study membrane interactions. **Maxim Brilkov**, UiT

15:15-15:30 Exploration of  $\beta$ -ketoacyl- [acyl-carrier protein] synthase I (FabB) inhibitors as lead structures for new antibiotics. **Vladyslav Yadykhinsky**, UiB

15:30-15:45 Novel Mycobacterial Tolerance Inhibitors (MTIs) against multidrug-resistant tuberculosis, **Tahira Riaz**, UiO

15:45-16:00 Rhodomyrtone nano-traps as a potent efflux pump inhibitor, **Gabriela Marinho Righetto**, Chalmers University of Technology

16:00-16:30 Break

Session 5: Alternative antimicrobial strategies/microbiome. Chairs: **Mona Johannessen** (UiT) and **Fredrik Almquist** (Umeå University)

16:30-17:00 Dynamics of early life gut resistome and mobilome: Meta-analysis. **Veronika K. Pettersen**, UiT (Keynote)

17:00-17:15 Cpx-signalling dependent silencing of urease in *Yersinia pseudotuberculosis*. **Dharmender Kumar Gahlot**, Umeå University

17:15-17:30 Phages in the North – the first two years. **Gabriel de Freitas Almeida**, UiT

17:30-17:45 Duration and dynamics of *Klebsiella pneumoniae* Species Complex gastrointestinal colonization. **Kenneth Lindstedt**, UiT

17:45-18:00 Chemoproteomic Identification of *Klebsiella pneumoniae* Serine Hydrolases with Potential Roles in Initial Fitness in Human-Derived Intestinal Organoids. **Md Jalal Uddin**, UiT

18:00-18:15 Differentiating Genome Content and Population Structure of *Enterococcus faecium* and *Enterococcus lactis*. **Theodor Ross**, UiT

18:15-18:30 The oral resistome in a population-based study of adults from Bergen, Melbourne and Tartu. **Bente Sved**, UiB

19:30 Conference dinner

## 15 MARCH PROGRAM

Session 6: Global challenges. Chairs: **Robert Leo Skov** (International Centre for Antimicrobial Resistance Solutions) and **Eva Garmendia** (UiC)

08:30-09:00 Mapping the sociological dimensions of AMR in Benin, West Africa for integrative data analysis, **Salla Sariola**, University of Helsinki (keynote)

09:00-09:15 A multisectoral partnership for the grand challenge of antibiotic resistance: cooperation and knowledge sharing, **Carla Sacchi**, Uppsala University

09:15-09:30 Global development indicators and the prevalence of antimicrobial resistance in low- and middle-income countries: Patterns and anomalies. **Gutu Wayessa**, University of Helsinki

09:30-10:00 Break

10:00-10:20 Edinburgh AMR Forum and the power of transdisciplinary networks to tackle AMR. **Till Bachmann**, University of Edinburgh

10:20-10:35 Application of network science to study drivers of antimicrobial resistance, **Luong Nguyen**, UAC

10:35-10:50 Machine/Deep Learning applications and challenges in Antimicrobial Resistance, **Belal Medhat**, UIT

10:50-11:30 Panel discussion

Closure

11:30-12:30 LUNCH



# Machine learning

**CANS**  
Centre for Antimicrobial Strategies

**UIT Norges arktiske universitet**

**Program CANS day; 23 February at Scandic Ishavshotel, PANORAMA**

TIME	PROGRAM	
08:30-08:45	"Welcome and introduction to the conference"	
08:45-09:30	Camilla Brekke, Pro-Rector Research and Development, UIT Arnefinn Sundsfjord, Center leader Session 1 (Chair: Monica Johansson): "Sepsis - from 'most Adoption and Evaluation' Annelies Zinkernagel, University of Zurich Session 2 (Chair: Klares Stenvig): "Marine microorganisms and their role in the biodescovery of new antibiotics", Teppo Räma, Marbi	
09:30-10:00	Break "Including viruses of bacteria as resources for marine bioprospecting". António Magno de Freitas Almeida, Marine Bioprospecting	
10:00-10:30	10:45-11:15	"Conjugation strategies for new antimicrobials and diagnostic tools" Marius M. Haugland, Haugland group "Predictions and opportunities in large biomedical data" Einar Holsbo, Health Data Lab
11:15-11:45	11:45-12:30	LUNCH Session 4 (Poster group 4)
12:45-14:00	Poster walk with short presentations of posters Break	
14:00-14:45	Session 5 (Chair: Pål J. Johnson): "The good, the bad and the ugly - how to rule the world of <i>E. coli</i> " Jukka Corander, Institute of Basic Medical Sciences, University of Oslo Session 6 (Chair: Johanna U. Ericson): "Human Microbiome in Pregnancy and Early Life" Veronika Pettersen, Host Microbe Interaction/Pediatric Infection	
14:45-15:15	15:45-16:15	"Chemical Infection Biology - From identification of new enzymes to phenotypic profiling of single-cell" Christian Lentz, Host-Microbe Interaction 16:45-17:00
15:15-15:45	17:00-17:15	Summary, Arnefinn Sundsfjord Photo, Jan Fredrik Frantzen
17:15-17:30	17:30-18:30	Break Session 7: Poster session 19:00 DINNER

**13 MARCH PROGRAM**

TIME	PROGRAM			
13:00-14:00	LUNCH			
14:00-14:15	Warming up and introduction: Professor Arne Smalås, Dean, Faculty of Science and Technology, and Chair board CANS, and professor Arnefinn Sundsfjord, CANS centre leader, UIT The Arctic University of Norway (UIT)			
14:15-14:45	Session 1: Clinical AMR and Diagnostics, Chairs: Ingvild Lühr, Stavanger University Hospital (SUH) and Tone Tamjum, University of Oslo (UDO) 14:45-15:15	"Clinical impact of the new rapid Staphylococcus aureus in Norwegian hospitals. Jørunn Pauline Øvretveit, University of Oslo (UDO) 15:15-15:45	"Incubation of the blood cultures for up to 5 hours in a standard laboratory incubator is sufficient for the identification of sepsis-causing bacteria and MRGs using nanopore sequencing." Jóseph Ali, Inland Norway University of Applied Sciences (INN) 15:45-16:15	"Introducing a high-throughput single-cell approach that provides insights into growth variations in isogenic <i>Staphylococcus aureus</i> populations at single cell level." Jonathan Hirn, UT
16:15-16:30	16:30-16:45	"Novel machine learning tools for rapid diagnostics of infection and antimicrobial resistance: A One Health approach." Rolf Ahmed, NTNU 16:45-16:50	"Evaluating the biofilm genotype for successful and emerging sequence types in human pathogenic <i>Escherichia coli</i> . Miriam Korsnes, UIT	
16:50-16:55	General discussion			
16:55-17:15	Poster session			
17:15-17:30	Break			
17:30-18:30	Session 8: Poster session 18:30-18:45	General discussion		
18:45-20:00	Poster session			

**14 MARCH PROGRAM**

TIME	PROGRAM	
09:00-09:30	Session 1: Alternative AMR, Chairs: Joshua Bengtsson Palme (Chalmers University of Technology) and Arnefinn Sundsfjord (UIT) On the environment's role in evolution, transmission, and surveillance of antibiotic resistance. Joakim Larsson, University of Gothenburg (keynote)	
09:30-09:45	Transfer of antibiotic resistance in wastewater and environmental <i>Escherichia coli</i> , <i>Shewanella</i> spp. and <i>Vibrio</i> spp. strains. Annie Justh de Nezpol, University of Gothenburg	
09:45-10:00	Circulation of enterotoxigenic <i>Escherichia coli</i> (ETEC) isolates expressing CS23 from the environment to clinical setting. Louise Joffe, University of Gothenburg	
10:00-10:15	Agree to disagree: the evaluation of machine learning Between Phenotypic and Genomic Methods for AMR Detection. Markus Wennig, Chalmers University of Technology	
10:15-10:30	ReSUlt: The urban resilience adaptation to climate change in an Anthropocene era. Hilde Sørvoll Vølle, Norwegian Institute of Public Health	
10:30-10:45	Break	
10:45-11:00	11:00-11:15	Poster session
11:15-11:30	11:30-11:45	LUNCH
11:45-12:00	Session 2: New Antibiotics, Chairs: Klara Stenvig (UIT) and Dan Andersson / Linus Sandgren (Uppsala Antibiotic Center (UAC))	
12:00-14:00	Current ideas on how to Inventive New Antibiotics R&D. Francesco Cisbani, IAC (keynote) Novel synthetic cationic antimicrobial peptides and their potential in combating antibiotic resistance. Attaur Rahman, IAC	
14:00-14:30	Development of metallo-β-lactamase inhibitors. Kinga Virág Gyulay, IAC	
14:45-15:00	Bacterial extracellular vesicles (EVs) as a ready to use model to study membrane interactions. Maxim Brilkov, IAC	
15:00-15:15	Exploration of β-ketetyl-β-lactam proteinase synthesis (FabB) inhibitors as lead structures for new antibiotics. Vlodyslav Yodkivskiy, IUB	
15:15-15:30	New Mycobacterial Tolerance Inhibitors (MTIs) against multidrug-resistant tuberculosis. Tohira Riaz, UIO	
15:30-15:45	Rhodomycin nano-traps as a potent efflux pump inhibitor. Gabriele Marinò Righetto, Chalmers University of Technology	
16:00-16:30	Break	
16:30-16:45	Session 5: Alternative antimicrobial strategies/microbiology. Chairs: Mona Johansson (UIT) and Fredrik Arnefinn Sundsfjord (UIT)	
16:45-17:00	Dynamics of early life gut metatome and metolizome: Meta-analysis. Veronika A. Pettersen, UIT (keynote)	
17:00-17:15	Cov-signalling dependent silencing of urease in <i>Yersinia pseudotuberculosis</i> . Ochander Kumar Gahlot, Umed University	
17:15-17:30	Phages in the North – the first two years. Gabriel de Freitas Almeida, UFT	
17:30-17:45	Duration and dynamics of <i>Klebsiella pneumoniae</i> Species Complex gastrointestinal colonization. Kenneth Lindstedt, UFT	
17:45-18:00	Chromoproteomic identification of <i>Klebsiella pneumoniae</i> Serine Hydrolases with Potential Roles in Initial Fitness Assessment of Bovine Intestinal Organoids. Md Jaber Uddin, UFT	
18:00-18:15	Differentiating Genome Content and Population Structure of <i>Enterococcus faecium</i> and <i>Enterococcus faecilli</i> . Theodor Ross, UFT	
18:15-18:30	The oral resistome in a population-based study of adults from Bergen, Melbourne and Tarta. Bente Sved, UFT	
19:30	Conference dinner	

**15 MARCH PROGRAM**

TIME	PROGRAM
08:30-09:00	Session 6: Machine learning challenges, Chairs: Robert Leo Skov (International Centre for Antimicrobial Resistance Skolteknikken) and Per Gummesson (IAC) Mapping the sociological dimensions of AMR in Benin, West Africa for integrative data analysis. Salla Sarjala, University of Helsinki (keynote)
09:00-09:15	A multistakeholder partnership for the grand challenge of antibiotic resistance: cooperation and knowledge sharing. Carlo Scachetti, Upsala University
09:15-09:30	Global development indicators and the prevalence of antimicrobial resistance in low- and middle-income countries: Patterns and anomalies. Gutu Woyessa, University of Helsinki
09:30-10:00	Break
10:00-10:20	Edinburgh AMR Forum and the power of transdisciplinary networks to tackle AMR. Till Bechemann, University of Edinburgh
10:20-10:35	Application of network science to study drivers of antimicrobial resistance. Luong Nguyen, UAC
10:35-10:50	Machine/Deep Learning applications and challenges in Antimicrobial Resistance. Béatrice Medhat, UFT
10:50-11:30	Panel discussion Closure LUNCH
11:30-12:30	



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# Machine learning

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**Program CANS day; 23 February at Scandic Ishavshotel, PANORAMA**

TIME	PROGRAM
08:30-08:45	"Welcome and introduction to the conference"
08:45-09:30	Camilla Brekke, Pro-Rector Research and Development, UIT Arinfinn Sundsfjord, Center leader <b>Session 1 (Chair: Monja Johannessen):</b> "Society - people - planet Adoption and Evolution" Annelies Zinkernagel, University of Zurich <b>Session 2 (Chair: Klaas Stenvinkel)</b> "Marine microorganisms and their role in the biosynthesis of new antibiotics", Teppo Räma, Marbio
09:30-10:00	<b>BREAK</b> "Including viruses of bacteria as resources for marine bioprospecting". António Magno de Freitas Almeida, Marine Bioprospecting
10:30-10:45	<b>BREAK</b>
10:45-11:15	<b>Session 3 (Chair: Hanna-Kirsti Schrader Læren)</b> "Conjugation strategies for new antimicrobials and diagnostic tools" Marius M. Haugland, Haugland group
11:15-11:45	"Innovations and opportunities in large biomedical data" Einar Holsbo, Health Data Lab
11:45-12:30	<b>LUNCH</b>
12:45-14:00	<b>Session 4 (Poster group 1-4)</b> Poster walk with short presentations of posters
14:45-15:00	<b>BREAK</b>
15:00-15:45	<b>Session 5 (Chair: Pål J. Johnsen)</b> "The point, the line and the sky - how to rule the world of <i>E. coli</i> " Jukka Corander, Institute of Basic Medical Sciences, University of Oslo <b>Session 6 (Chair: Johanna U. Ericson)</b> "Human Microbiome in Pregnancy and Early Life" Veronika Pettersen, Host Microbe Interaction/Pediatric infection
15:45-16:15	"Chemical Infection Biology - From identification of new enzymes to phenotypic profiling of single-cell" Christian Lentz, Host-Microbe Interaction
16:45-17:00	<b>BREAK</b>
17:00-17:15	Photo, Jan Fredrik Frantzen
17:15-17:30	<b>BREAK</b>
17:30-18:30	<b>Session 7: Poster session</b>
19:00	<b>DINNER</b>

**13 MARCH PROGRAM**

TIME	PROGRAM
13:00-14:00	<b>LUNCH</b>
14:00-14:15	Warming up and introduction: Professor Arne Smalås, Dean, Faculty of Science and Technology, and Chair board CANS, and professor Arinfinn Sundsfjord, CANS centre leader. <b>UIT The Arctic University of Norway (UIT)</b>
14:15-14:45	<b>Session 1: Clinical AMR and Diagnostics</b> , Chairs: Iren Lühr, Stavanger University Hospital (SUH) and Tone Tønjeum, University of Oslo (UiO)
14:45-15:00	Workshop to enhance AMR control in clinical and public health settings. <b>Ben Howlett, University of Melbourne (keynote)</b>
15:00-15:15	Clinical impact of the newly described <i>Staphylococcus borealis</i> in Norwegian hospitals. <b>Jørunn Pauline Åberg, University of Oslo (UiO)</b>
15:15-15:30	Incubation of the blood cultures for up to 5 hours in a standard laboratory incubator is sufficient for the identification of sepsis-causing bacteria and MRGs using nanopore sequencing. <b>Jøewald Ali, Inland Norway University Hospital (INN)</b>
15:30-15:45	Introducing a high-throughput single-cell approach that provides insights into growth variations in <i>legionella</i> <i>Staphylococcus aureus</i> populations at single cell level. <b>Jonathan Hirn, UT</b>
15:45-16:00	Novel technological solutions for rapid diagnostics of infection and antimicrobial resistance. <b>A One Health collaboration. Miriam Kovacs, UT</b>
16:00-16:15	Establishing the better genotype for successful and emerging sequence types in human pathogenic <i>Escherichia coli</i> . <b>Miriam Kovacs, UT</b>
16:15-16:45	<b>Break</b>
16:45-17:15	<b>Session 2: Evolution of AMR</b> , Chairs: Teppo Hiltunen, University of Turku and Pål J. Johnsen (UiT) "Evolutionary approaches to understand the spread of antibiotic resistance. <b>Craig MacLean, University of Oxford (keynote)</b>
17:15-17:30	<i>Escherichia coli</i> plasmidome maps the game of clones. <b>Jukka Corander, UIO</b>
17:30-17:45	Divergent genetic evolution employs the same molecular mechanisms. <b>Christopher Fröhlich, UT</b>
17:45-18:00	Antibiotic-induced amino acid release (AAM) A bacterial emergency response to membrane-targeting antibiotics. <b>Göran Sandström, Chalmers University of Technology</b>
18:00-18:15	Experimental inference to learn and predict the pathways of AMR evolution from data. <b>Iain Johnston, University of Bergen (UBG)</b>
18:15-18:30	Using experimental evolution to study AMR in synthetic bacterial communities. <b>Teppo Hiltunen, University of Turku (UT)</b>
18:30-18:45	General discussion
18:45-20:00	<b>Poster session</b>

**CANS**  
Centre for Antimicrobial Strategies

**UIT The Arctic University of Norway**

**The Nordic AMR Research Centre Conference**

When and where: 13-15 March 2024 at [Scandic Ishavshotel](#)

CANS invites researchers, PhDs and postdocs from all Nordic AMR Centres to a conference offering lectures, poster presentations and an exciting mixture of networking and cross-disciplinary discussions.

**13 MARCH PROGRAM**

TIME	PROGRAM
13:00-14:00	<b>LUNCH</b>
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18:30-18:45	General discussion
18:45-20:00	<b>Poster session</b>

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**14 MARCH PROGRAM**

TIME	PROGRAM
09:00-09:30	<b>Session 3: Epidemiology of AMR</b> , Chairs: Jóhanna Bengtsson Palme (Chalmers University of Technology) and Arinfinn Sundsfjord (UiT)
09:30-09:45	On the environment's role in evolution, transmission, and surveillance of antibiotic resistance. <b>Joséphin Larsson, University of Gothenburg (keynote)</b>
09:45-10:00	Transfer of antibiotic resistance in wastewater and environmental <i>Escherichia coli</i> , <i>Shewanella</i> spp. and <i>Vibrio</i> spp. strains. <b>Annie Justh de Nezpoli, University of Gothenburg</b>
10:00-10:15	Circulation of enterotrophoblasts ( <i>ETEC</i> ) isolates expressing CS23 from the environment to clinical setting. <b>Christophe Joffre, University of Gothenburg</b>
10:15-10:30	Agree to disagree: the evaluation of agreement between Phenotypic and Genomic Methods for AMR Detection. <b>Marius Wenni, Chalmers University of Technology</b>
10:30-10:45	ReSUltB: The urban resilience adaptation to climate change in an Anthropocene era. <b>Hilde Sørvoll Vøllebø, Norwegian Institute of Public Health</b>
10:45-11:00	<b>Break</b>
11:00-11:30	<b>Poster session</b>
11:30-11:45	<b>LUNCH</b>
11:45-12:30	<b>Session 4: New Antibiotics</b> , Chairs: Klara Stenvinkel (UiT) and Dan Andersson / Linus Sandgren (Uppsala Antimic Center (UAC))
14:00-14:30	Current ideas on how to incentivize New Antibiotics R&D. <b>Francesco Cisbani, UAC (keynote)</b>
14:30-14:45	Novel synthetic cationic antimicrobial peptides and their potential in combating antibiotic resistance. <b>Attaur Rahman, UAC</b>
14:45-15:00	Development of metallo-β-lactamase inhibitors. <b>Kingshuk Ganguly, UAC</b>
15:00-15:15	Bacterial extracellular vesicles (EVs) as a ready to use model to study membrane interactions. <b>Maxim Brilkov, UAC</b>
15:15-15:30	Exploration of β-ketetyl (acyl-carrier protein) synthase (FabB) inhibitors as lead structures for new antibiotics. <b>Vladislav Yudkowsky, UAC</b>
15:30-15:45	New Mycobacterial Tolerance Inhibitors (MTIs) against multidrug-resistant tuberculosis. <b>Tohira Riaz, UIO</b>
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16:00-16:15	<b>Session 5: Alternative antimicrobial strategies/microbiology</b> , Chairs: Monja Johannessen (UiT) and Fredrik Andersson (Umeå University)
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19:30	<b>Conference dinner</b>

**15 MARCH PROGRAM**

TIME	PROGRAM
08:30-09:00	<b>Session 6: Global challenges</b> , Chairs: Robert Leo Söderström (International Centre for Antimicrobial Resistance Söderström) and Per Gummesson (UIC)
09:00-09:15	Mapping the sociological dimensions of AMR in Benin, West Africa for integrative data analysis. <b>Salla Sarjala, University of Helsinki (keynote)</b>
09:15-09:30	A multistakeholder partnership for the grand challenge of antibiotic resistance: cooperation and knowledge sharing. <b>Carlo Scachetti, Uppsala University</b>
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09:45-10:00	<b>Break</b>
10:00-10:20	Edinburgh AMR Forum and the power of transdisciplinary networks to tackle AMR. <b>Till Bechmann, University of Edinburgh</b>
10:20-10:35	Application of network science to study drivers of antimicrobial resistance. <b>Luong Nguyen, UAC</b>
10:35-10:50	Machine/Deep Learning applications and challenges in Antimicrobial Resistance. <b>Béatrice Medhat, UIC</b>
10:50-11:30	<b>Panel discussion</b> <b>Closure</b> <b>LUNCH</b>
11:30-12:30	



## Quality and Reliability Engineering International



CASE STUDY

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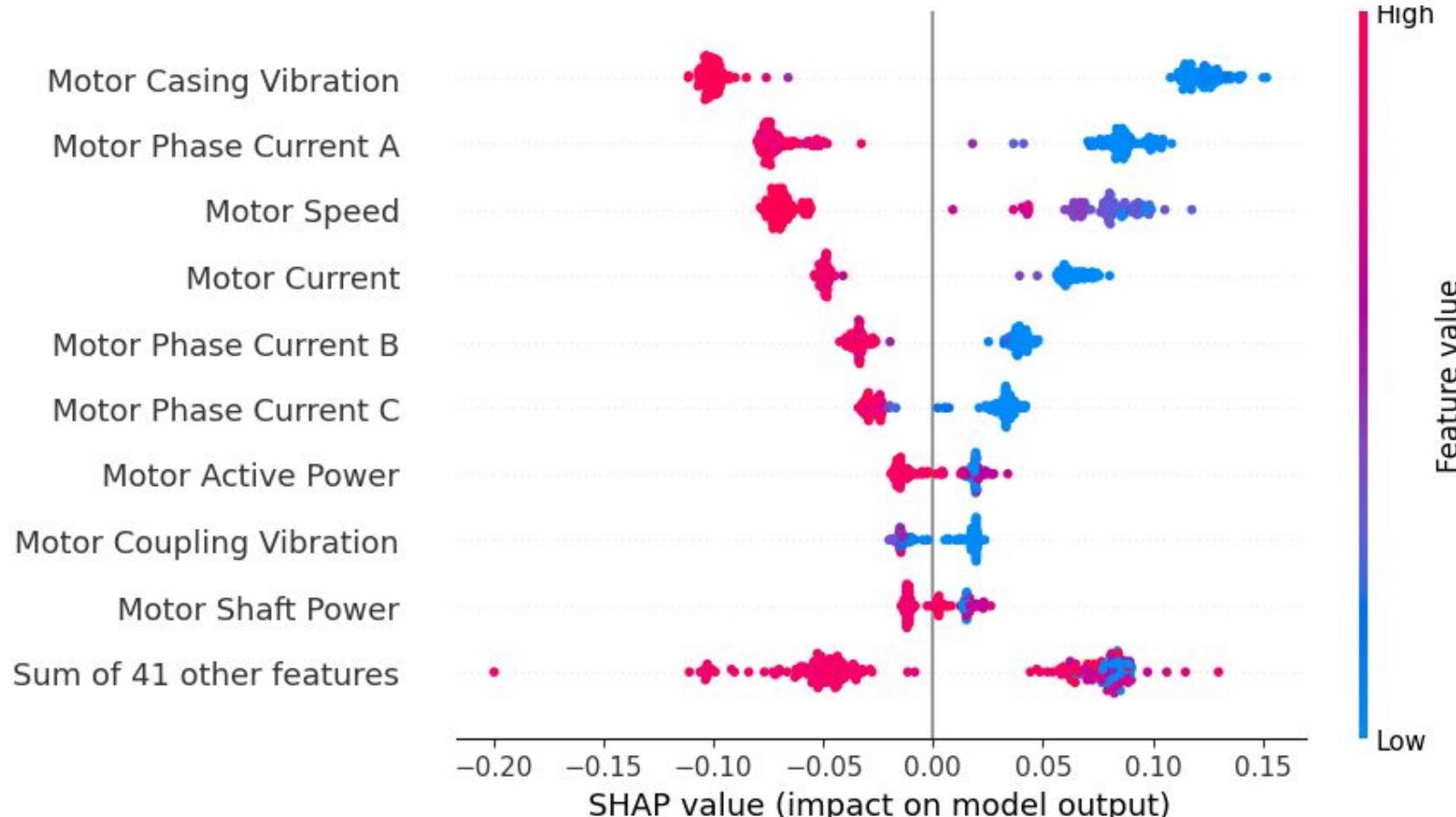


# Unsupervised and supervised learning for the reliability analysis of complex systems

Maria Luz Gámiz , Fernando Navas-Gómez, Rafael Nozal-Cañadas, Rocío Raya-Miranda

First published: 18 March 2023 | <https://doi.org/10.1002/qre.3311>

# Machine learning



# Machine learning

	ANN_SHAP	KNN_SHAP	RandomForest_SHAP	RandomForest_MDI	PLS	AF-RL
Motor Casing Vibration – 0.01	0.00	1.00	1.00	1.00	0.85	
Motor Frequency A – 0.01	0.00	0.05	0.02	0.22	0.21	
Motor Frequency B – 0.01	0.00	0.03	0.07	0.02	0.02	
Motor Frequency C – 0.01	0.00	0.00	0.00	0.17	0.08	
Motor Speed –	1.00	1.00	0.65	0.60	0.83	0.68
Motor Current –	0.10	0.01	0.51	0.50	0.95	0.80
Motor Active Power –	0.01	0.00	0.14	0.19	0.16	0.12
Motor Apparent Power –	0.01	0.00	0.07	0.08	0.06	0.28
Motor Reactive Power –	0.01	0.00	0.08	0.18	0.06	0.31
Motor Shaft Power –	0.01	0.00	0.11	0.20	0.05	0.32
Motor Phase Current A –	0.06	0.00	0.70	0.98	0.83	0.82
Motor Phase Current B –	0.07	0.00	0.33	0.46	0.81	0.84
Motor Phase Current C –	0.01	0.00	0.27	0.37	0.77	0.78
Motor Coupling Vibration –	0.01	0.00	0.14	0.17	0.08	0.30
Motor Phase Voltage AB –	0.01	0.00	0.00	0.00	0.03	1.00

# Machine learning

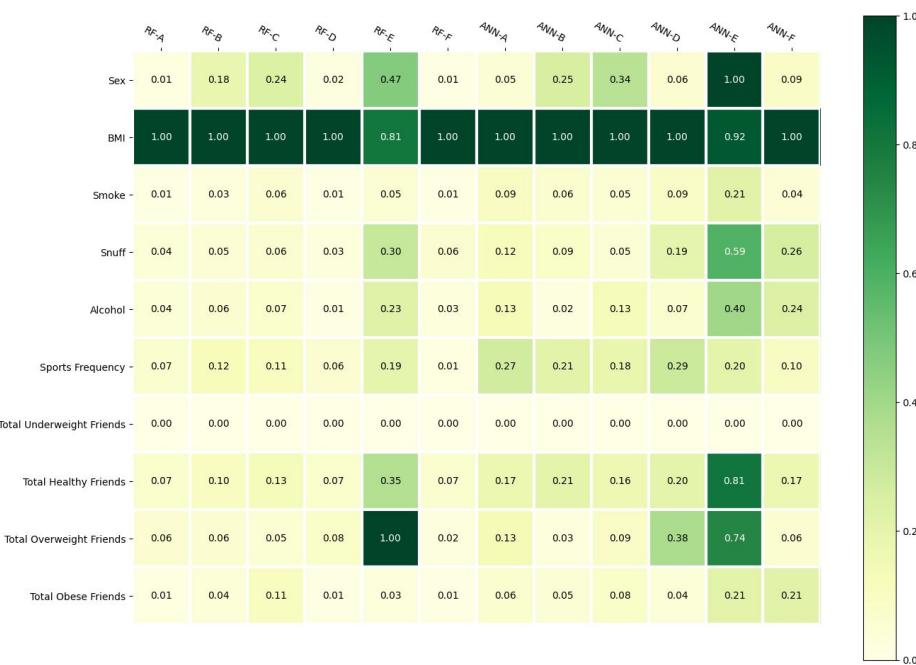
## Polar Peers: A Machine Learning Approach to Assessing BMI Influence in the Arctic Youth.

v: ARXIV

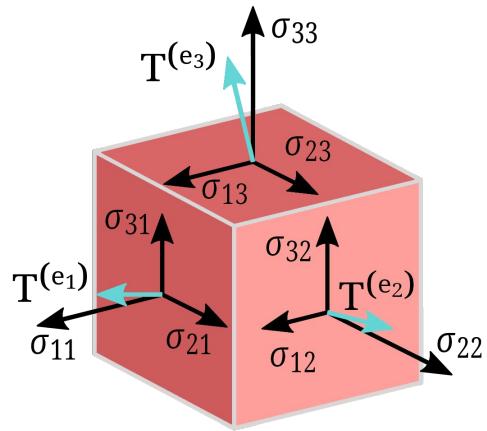
**Table 2:** Model performance summary.

ID	Name	Samples	MAE		Mean BMI	
			RF	ANN	FF1	FF2
A	Healthy or worse to Overweight or worse	168	1.71	1.81	26.88	29.07
B	Healthy or worse to Healthy or better	440	0.99	1.00	21.43	21.98
C	Healthy to Healthy	420	1.05	1.07	21.12	21.81
D	Overweight or worse to lower BMI	44	0.96	1.39	28.69	26.79
E	Healthy to Overweight or worse BMI	63	0.90	1.60	23.32	26.52
F	Overweight or worse to higher BMI	80	1.86	1.95	28.99	31.46

Summary of all models and datasets used. From left to right, the ID of each dataset is represented by a letter, the short name of the dataset, the total samples in the dataset, the Mean Absolute Error (MAE) for each model (RF and ANN) performing in this dataset, mean BMI in FF1 and mean BMI in FF2 in this dataset.



**Figure 2:** Heatmap with the normalized mean |SHAP values| for the models with respect to each dataset (top names) against each variable (left names). Values closer to 1 indicate strong importance in the model.



# Tensors

$$R_{\mu\nu} - \frac{1}{2} R \; g_{\mu\nu} + \Lambda \; g_{\mu\nu} = \frac{8\pi G}{c^4} \; T_{\mu\nu}$$

# Einstein Field Equation (1915)

$$R_{\mu\nu} - \frac{1}{2} R g_{\mu\nu} + \Lambda g_{\mu\nu} = \frac{8\pi G}{c^4} T_{\mu\nu}$$

How energy/mass curve space

How energy/mass move throughout curved space

$$R_{\mu\nu} - \frac{1}{2} R g_{\mu\nu} + \Lambda g_{\mu\nu} = \frac{8\pi G}{c^4} T_{\mu\nu}$$

$$R_{\mu\nu} - \frac{1}{2} R g_{\mu\nu} + \Lambda g_{\mu\nu} = \frac{8\pi G}{c^4} T_{\mu\nu}$$

Cosmological constant

Newton's gravitational constant

Light speed constant

Ricci tensor

Metric tensors

Energy tensor

## Tensors

Einstein Field Equation (1915)

# PLOS COMPUTATIONAL BIOLOGY



OPEN ACCESS



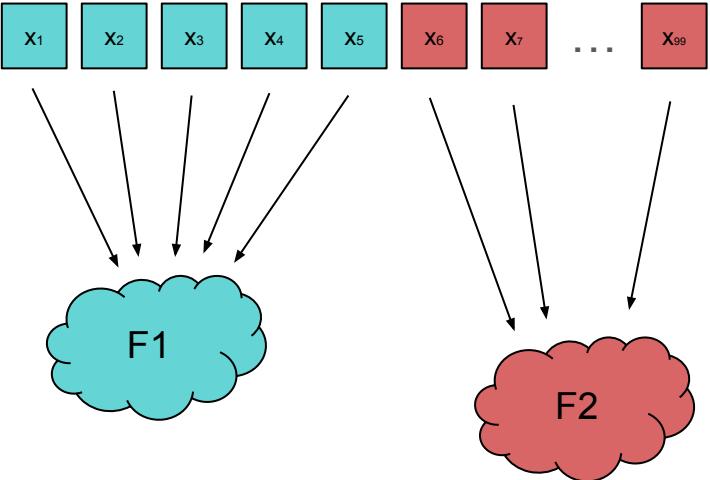
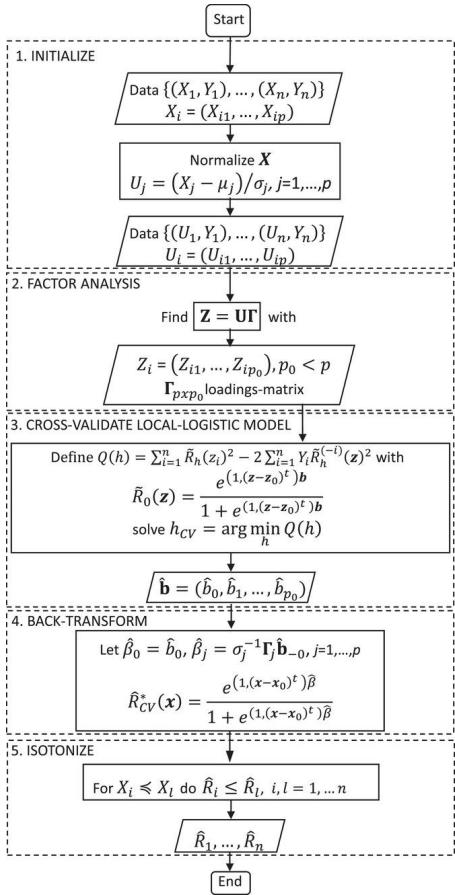
PEER-REVIEWED

RESEARCH ARTICLE

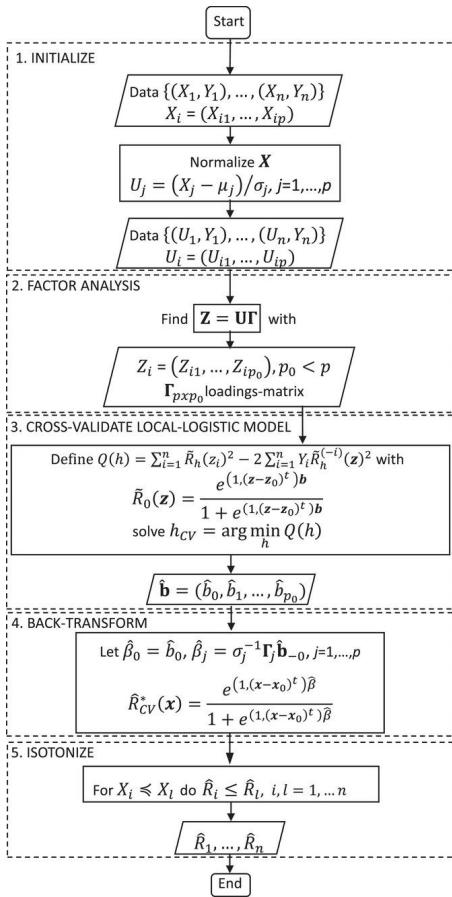
## Dimensionality reduction of longitudinal 'omics data using modern tensor factorizations

Uria Mor , Yotam Cohen , Rafael Valdés-Mas , Denise Kviatcovsky, Eran Elinav , Haim Avron

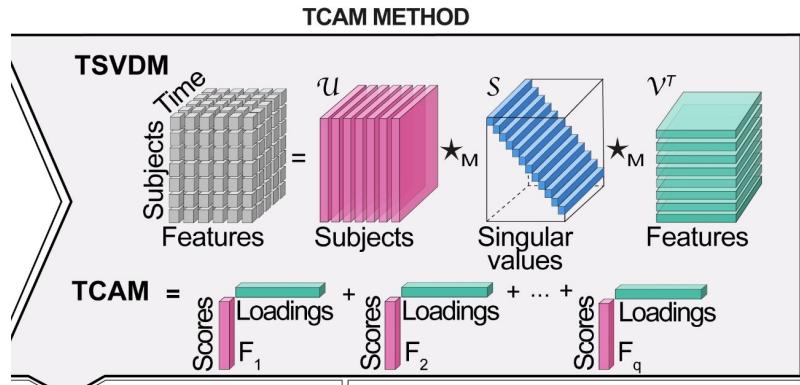
# Classical methods

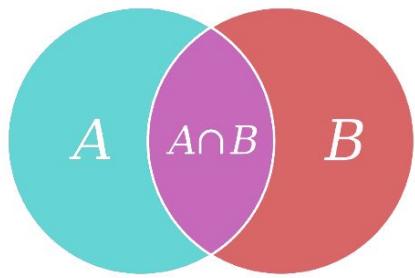


# Classical methods with TENSORS! :D



Brings a lot of variable into the latent space





# Multiset comparison

# Multiset comparison

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## Supervised dimensionality reduction for big data

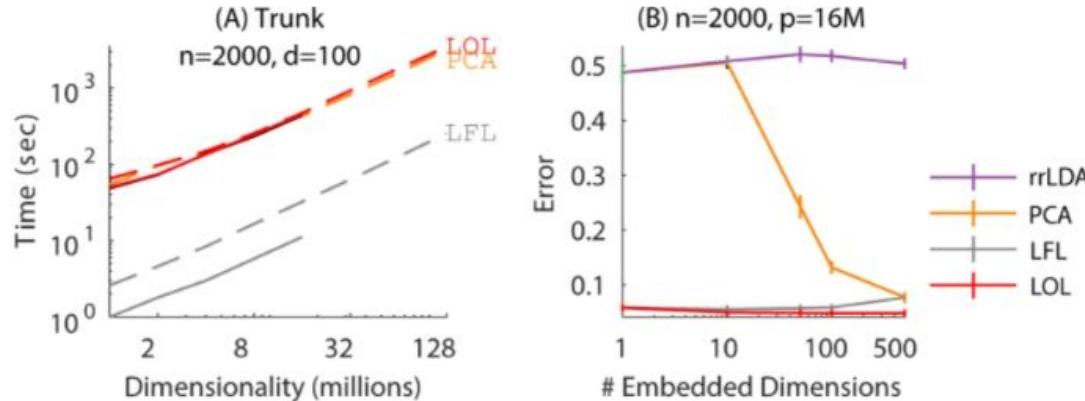
[Joshua T. Vogelstein](#)  , [Eric W. Bridgeford](#), [Minh Tang](#), [Da Zheng](#), [Christopher Douville](#), [Randal Burns](#) & [Mauro Maggioni](#)

[Nature Communications](#) **12**, Article number: 2872 (2021) | [Cite this article](#)

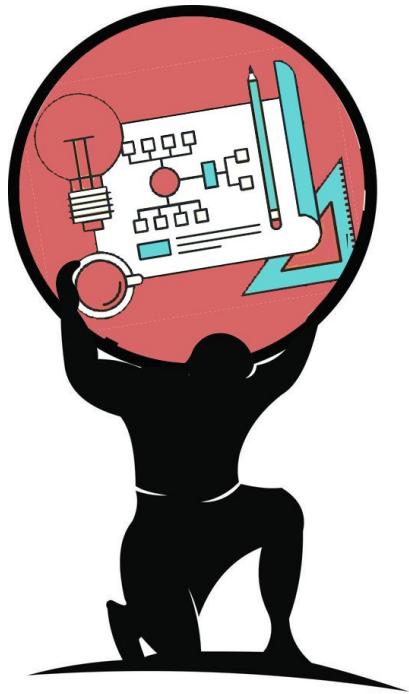
**13k** Accesses | **22** Citations | **1** Altmetric | [Metrics](#)

# Multiset comparison

**Fig. 2: Computational efficiency and scalability of LOL using  $n = 2000$  samples from spherically symmetric Gaussian data (see Supplementary Note 3 for details).**



**A** LOL exhibits optimal (linear) scale up, requiring only 46 min to find the projection on a 500 gigabyte dataset, and only 3 min using LFL (dashed lines show semi-external memory performance). **B** Error for LFL is the same as LOL in this setting, and both are significantly better than PCA and rrLDA for all choices of projection dimension, regardless of whether a randomized approach is used to compute the projection dimensions. Note that while similar scalability enhancements can be made to PCA in (A), our focus is to highlight that LFL maintains the high performance of LOL in comparison to PCA in (B) despite the randomization technique.



# Results Atlas

# Multivariate Analysis

Classical methods

Machine Learning

Tensors

Multiset comparison

# Multivariate Analysis

Classical methods

Machine Learning

Tensors

Multiset comparison



Fit Futures

Tromsø study

Norwegian prescription  
database

Microbial genomes atlas

Bacmap genomes atlas

Human gut  
microbiome atlas

...and more (Card github)



**GDPR  
COMPLIANT**

## GDPR issues

### Automated Decision-Making or Human Intervention

Individuals have the right not to be subject to a decision based solely on automated processing, including profiling, which produces legal effects concerning them or similarly significantly affects them. This means that there must be an option for human intervention in decisions made by AI systems in healthcare.

## GDPR issues

### Cross-Border Data Transfers

There are restrictions on the transfer of personal data outside the EU, ensuring that the level of protection guaranteed by the GDPR is not undermined.

## GDPR issues

### Data minimization

Only the data necessary for the specific purposes of processing should be collected and processed.

[...] to be continue (during the postdoc)