

Centre for Computational Personalised Medicine International Research Foundation

We create computational technologies for optimised healthcare

# Overview of Achievements in Computational Medicine at the Sano Centre

M. Bubak, M. Malawski, A. Crimi, A.A. Hamed, P. Korzeniowski, P. Nowakowski, and J. Sousa

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CompBioMed, 12-14 September 2023, Garching, DE





- Funding and partnership
- Main objectives of Sano
- Sano research teams
- Examples of research at Sano
- Sano in numbers
- Summary collaboration opportunities

### **Funding and partners**

- H2020-WIDESPREAD-2016-2017 TEAMING PHASE 2 programme (grant 857533) (15 M €)
- International Research Agendas Programme (IRAP) of the Foundation for Polish Science, co-funded by the EU in the scope of the European Regional Development Fund (10 M €) Strategic Partner: University of Sheffield Applicants: Marco Viceconti, University of Bologna (ISC Chair), Marian Bubak, AGH University Krakow (Scientific Affairs Director) Director of Sano and IRAP Part 2 Manager: Arkadiusz Sitek (since 15.02.2021), Maciej Malawski (since 1.08.2022)
- Polish Ministry of Science and Higher Education (after 2023, 5 M €)



### Teaming Partners:





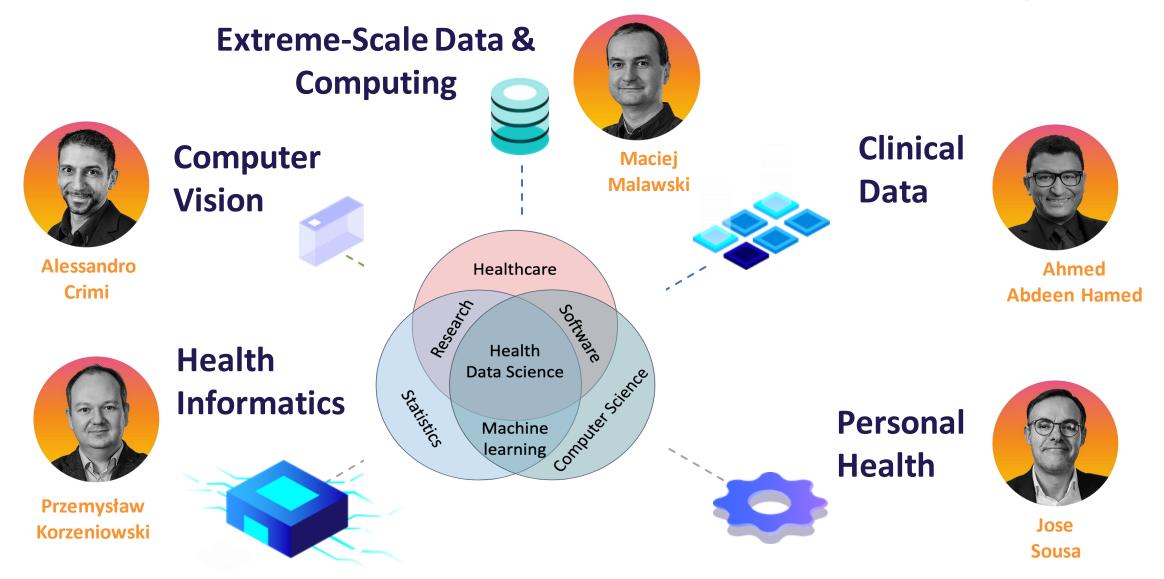
### Main objectives of Sano



Science	<ul><li>Scientific leadership</li><li>Enhancing scientific reputation</li></ul>	
Education	<ul><li>Training &amp; personnel development</li><li>Unique set of skills</li></ul>	Create world-class
Clinical	<ul><li>Clear links with healthcare needs</li><li>Close collaboration with clinicians</li></ul>	research institute in computational
Translation	<ul> <li>Combining scientific, clinical &amp; industrial perspective</li> </ul>	medicine
Entrepreneurship	<ul><li>Entrepreneurial mindset</li><li>Building IP awareness</li></ul>	

### **Sano Research Teams**





# **Healthcare Informatics Team**



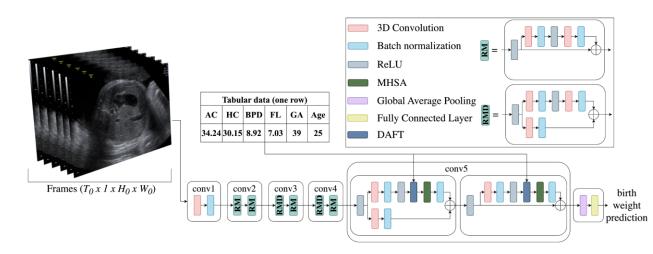
Leader: Przemyslaw Korzeniowski

- We develop new diagnostic and therapeutic processes based on patient data to extract insights that can be used to improve patient care and prevention
- We work on a new generation of medical communication and incorporation of artificial intelligence (AI), virtual and augmented reality (VR/AR) and robotics in existing and new medical workflows

#### 7

### Fetal Birth Weight Prediction using Multimodal Data

- Goal: Accurate prediction of fetal weight at birth is essential for determining the timing and mode of delivery.
- Performing a prenatal ultrasound 24 hours prior to delivery presents challenges as it requires acquiring high-quality images, which becomes difficult during advanced pregnancy due to the lack of amniotic fluid.
- We present a novel method that automatically predicts fetal birth weight by using fetal ultrasound video scans and clinical data.
- Our results show that our method outperforms several state-of-the-art methods and estimates fetal birth weight with an accuracy comparable to human experts and can minimize the risk of errors inherent in manual measurements.
- Next steps: Add more data from multi-centers and deploy them as support tool for clinicians.





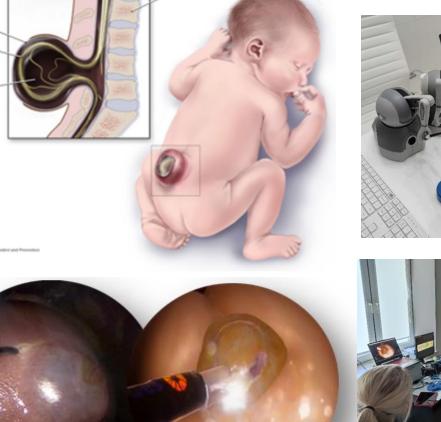


# Virtual Reality Surgical Simulators

Dura Mate

Spinal Cor

- Goal: Spina Bifida (SB) is a defect during the early stage of pregnancy - an incomplete closing of the spine around the spinal cord. The learning curve is steep and requires excellent procedural skills.
- Computer-based virtual reality (VR) simulation systems offer a safe, cost-effective, and configurable training environment free from ethical and safety issues.
- An initial simulation realism validation study was carri ed out by obtaining subjective feedback (face and content validity) from 14 clinicians. The overall simulation realism was on average marked 4.07 on a 5-point Likert scale (1 -'very unrealistic', 5 -'very realistic'). Its usefulness as a training tool for SB-repair as well as in learning fundamental laparoscopic skills was marked 4.63 and 4.80, respectively.
- Next steps: to develop the simulator further based on clinicians' feedback and follow it up with wider and more through clinical studies such as construct validity and/or transfer of skills.









### **Sim2Real with Generative Al**

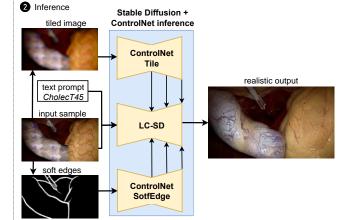
**Goal**: Developing an unsupervised Image-to-Image translation approach that could generate fully labeled and realistic-looking datasets based on surgical simulators. This is particularly effective with minimal real data requirements.

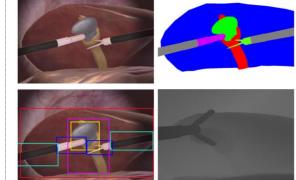
#### **Research Results:**

- Method which uses fewer than 100 actual images of laparoscopic cholecystectomy for training was created and evaluated on simplified abdomen simulator data.
- The approach consists of Stable Diffusion for image generation, ControlNets to maintain the consistency of generated samples, and Dreambooth for a minimal data training scheme. All techniques are novel and not widely employed in the medical Sim2Real field.
- The quality of the generated dataset was tested and compared with a GAN-based baseline.

#### Possible extensions of this approach:

- apply to a more realistic laparoscopic cholecystectomy simulation, including real tool-tissue interactions and temporal consistency between frames,
- reduce the dependency on input images and exploring multiregion approaches,
- explore lightweight techniques for training.











# **Computer Vision Team / Brain and More Lab** Leader: Alessandro Crimi

We focus on three main areas:

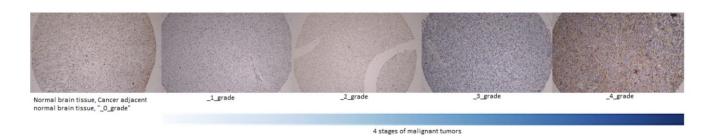
- Medical imaging (from histology/microscopy)
- Medical imaging (Neuroimaging)
- Brain Wearables (EEG, fNIRS, MEG, etc)

We are interested in studies spanning all dimensions of two disease processes (but open to others):

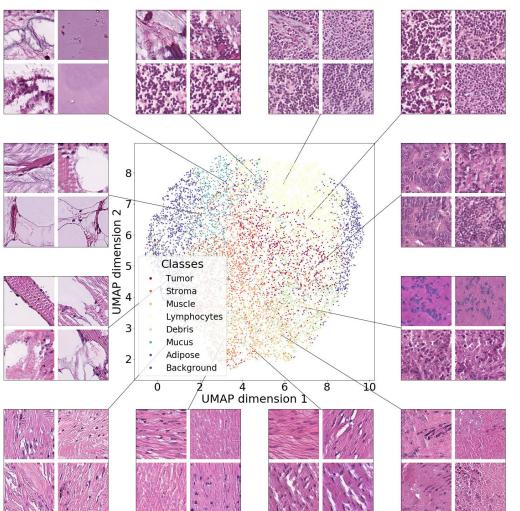
- Alzheimer/Dementia
- Brain tumors

# Brain tumor classification and image translation

Monika Pytlarz in collaboration with Nencki Institute



- A classification model is able to detect and classify the grade of a brain tumor within a biopsis
- Not just classification, but explain interaction of clusters of necrotic cells: e.g. in Grade 3 the AI algorithm found more discriminant cells clusters appearing to be more myelinating.



Pytlarz et al., SPIE 2023 Digital Imaging 2023 sano

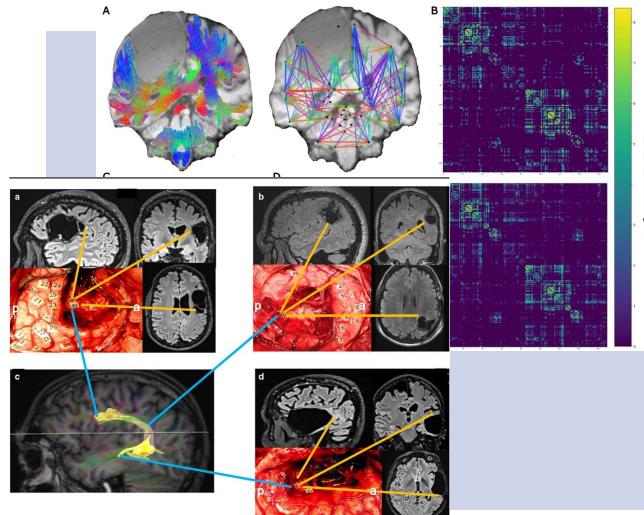
**nencki** institute



## Brain tumor surgical planning and prediction

Joan Falco-Roget, Bartlomiej Ksiazek

- A trained model is able to predict the brain connectivity of patients post-surgery and recovery
- Collaborations: University of Ghent for data, University of Messina and Padua for clinical support.
- Follow-up of the project includes the roll out in clinical practice at the University hospital of Palermo



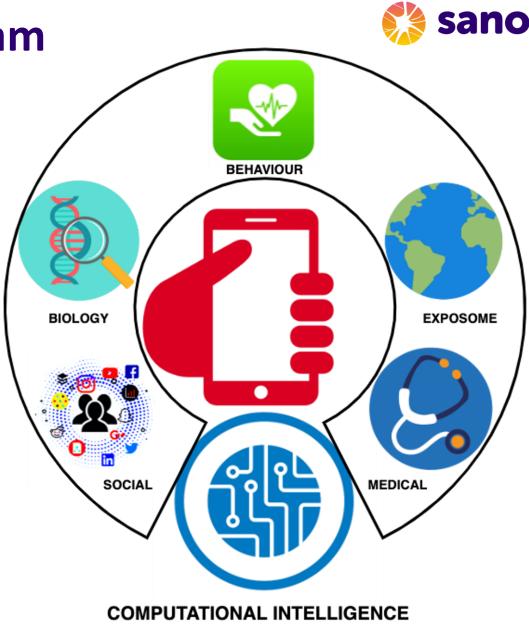
Bayesian Filtered Generation of Post-surgical Brain Connectomes on Tumor Patients" J. Roget Falco, F. Sambataro, A. Cacciola, A. Crimi MICCAI 2022, Nature Communication <u>https://link.springer.com/chapter/10.1007/978-3-031-21083-9\_8</u> <u>https://www.biorxiv.org/content/10.1101/2022.11.14.516248v2.abstract</u>

# **Personal Health Data Science Team**

### Leader: Jose Sousa

### We focus on:

- Fundamental computational approaches aimed at emulating the intricate processes of both "System 1" and "System 2" decision-making in AI systems within a concept of a digital mind
- Disease models' development to support evidence-based health care decision making

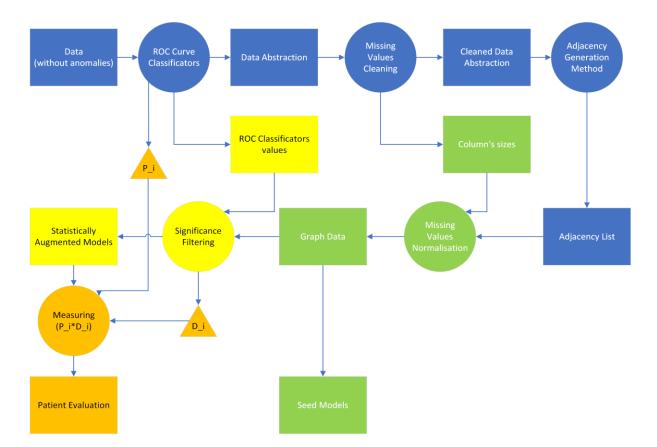


## SaNDAA small and incomplete dataset analyser



Alfredo Ibias, Varun Ravi Varma, Karol Capala, Luca Gherardini, Jose Sousa

- Personalized health often involves small datasets with missing data.
- Current Machine Learning methods struggle with such datasets due to high data volume requirements.
- SaNDA prioritizes explainability over efficiency due to dataset characteristics and domain importance.
- Evaluation against Random Forest (baseline for explainable methods) and gcForest (state-of-the-art for small datasets).
- SaNDA outperforms Random Forest with more missing data or fewer entries, but less favourable results on larger, well-curated datasets.
- Preferred over gcForest for explainability and privacy protection.
- Valuable for healthcare practitioners given data challenges in the field.



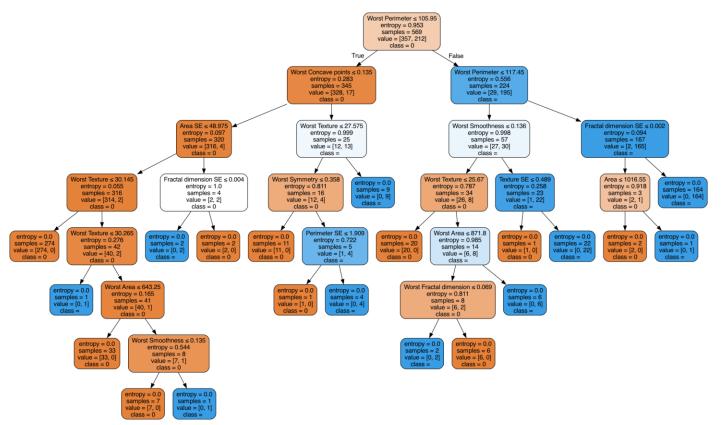
https://www.sciencedirect.com/science/article/pii/S0020025523006631, Information Sciences

### CACTUS: a Comprehensive Abstraction and Classification Tool for Uncovering Structures



Luca Gherardini, Varun Ravi Varma, Karol Capala, Roger Woods, Jose Sousa

- Availability of large data sets drives current Al developments.
- Challenges for small data sets due to practicality, cost, and opacity of deep learning models.
- CACTUS focuses on secure analytics using explainable AI.
- Enhanced support for categorical attributes while preserving their original meaning.
- Optimizes memory usage and speeds up computation through parallelization.
- Displays attribute frequency in each class and ranks them based on discriminative power.
- Assessment conducted on Wisconsin diagnostic breast cancer and Thyroid0387 data sets.



htpps://doi.org/10.48550/arXiv.2308.12031, under review: ACM Transactions on Intelligent Systems and Technology under review: IEEE Transactions on Pattern Analysis and Machine Intelligence, "Noise Reduction through Abstractions and Its Possibilities for Machine Learning"



# Clinical Data Science / Network Medicine & Al

Leader: Ahmed Abdeen Hamed

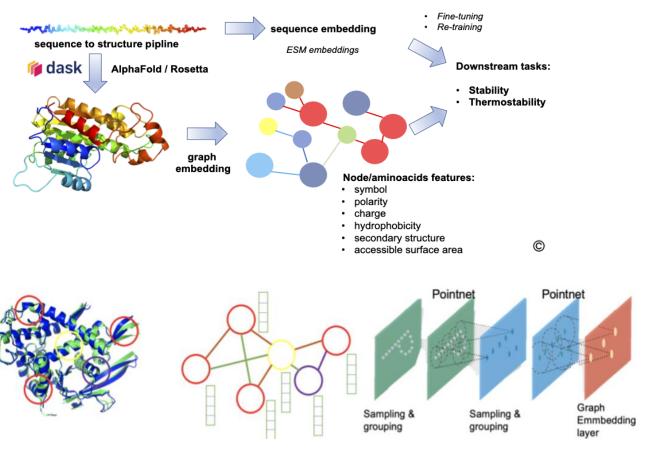
We focus on:

- Development of innovative network medicine approaches to complex disease research and management
- Development of Generative AI methods to improve clinical decision support for complex disease treatment

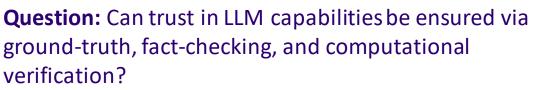


### Precision Thermostability Prediction: Fueling Drug Discovery for Healthcare's Biological Targets Adam Sulek, Jakub Jonczyk, Ahmed Abdeen Hamed

- **Question:** Can accurate prediction of protein thermostability enhance drug discovery for biological targets in healthcare?
- **Solution:** Precision thermostability prediction: fueling drug discovery for healthcare's biological targets **Features:**
- increasing reliance on thermostable enzymes in healthcare.
- challenges in protein design: substantial hurdles in designing thermostable proteins.
- cutting-edge technology use: implementation of advanced graph neural networks (GNN).
- data-driven approach: utilization of publicly available data sources for prediction.
- superior model performance: GNN model outperforms PointNet++ with higher correlation (R2~0.6).



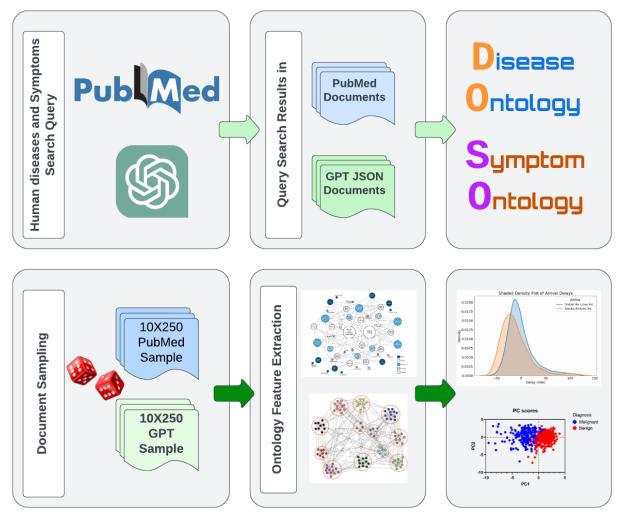
### **Establishing Trust in LLM Capabilities Ground-truth, Fact-Checking, and Computational Verification** Ahmed Abdeen Hamed, Byung Lee



**Solution:** To strengthen trust in LLM capabilities, incorporating algorithms alongside knowledge graphs and biological ontologies is key. LLMs can deliver more dependable results, especially in healthcare and biotechnology.

#### Features:

- Ground-Truth for Contextual Accuracy: Providing reliable, domain-specific information based on verified ground truth data.
- Rich BioMedical Knowledge Graphs: Enable contextrich, reproducible responses.
- Biological Ontologies: Ensure precise data interpretation.
- Algorithmic Validation: Rigorous fact-checking.
- Trust Enhancement: Greater reliability in LLM capabilities.





# **Extreme-Scale Data & Computing Team**



Leader: Maciej Malawski

**Goal:** To apply the experience in large-scale computing systems to medical applications and to push the boundaries of current technologies when required by scale of data and computing demands

### **Research topics:**

- Efficient processing of large data sets with the use of advanced computing infrastructures (HPC and Cloud)
- Development of tools for large-scale computing and data analysis
- Distributed and federated machine learning
- Performance evaluation and optimization of medical applications on emerging computing infrastructures



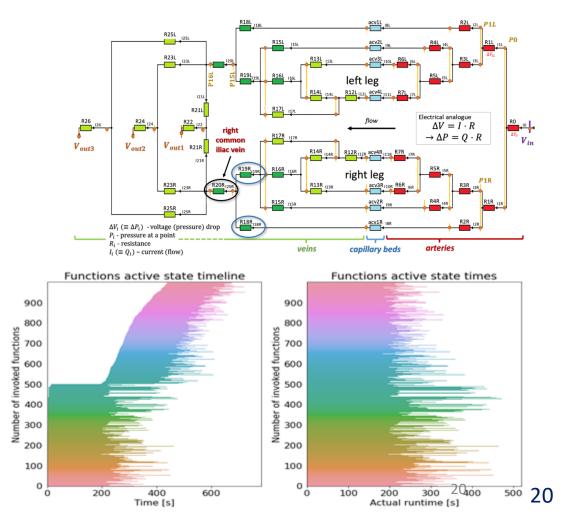
# Verification, Validation, Uncertainty Quantification of simulation models

### Magdalena Otta, Piotr Kica

- 0D, 1D, 3D models of cardiovascular systems
- Example: Venous modelling to inform treatment of patients presenting with lower limb thrombosis (PhD project with University of Sheffield)
- VVUQ, Sensitivity analysis required in the regulatory process of model certification
- Large parameter studies
  - 50 000 parameters -> tasks
- CloudVVUQ library using serverless computing
- Total time to compute locally ≈ 76.1h
- Total time to compute using Google Cloud ~ **12.5min**

https://github.com/SanoScience/CloudVVUQ

Otta, M. et al.. Sensitivity analysis of a model of lower limb haemodynamics (2022) https://doi.org/10.1007/978-3-031-08757-8\_7 Piotr Kica, Magdalena Otta, Krzysztof Czechowicz, Karol Zajac, Piotr Nowakowski, Andrew J. Narracott, Ian Halliday, Maciej Malawski: Serverless Approach to Sensitivity Analysis of Computational Models, CCGrid 2023

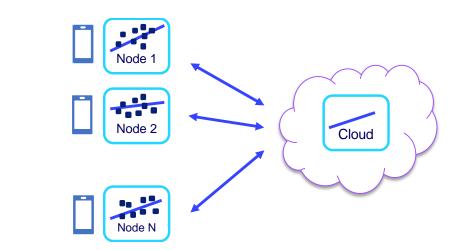


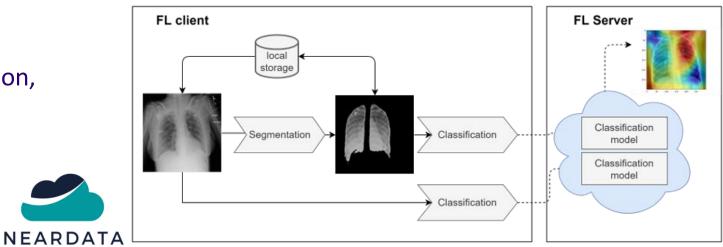
# **Federated Learning for Medical Applications**



Dominika Ciupek, Michał Daniłowski, Jan Przybyszewski

- Training of ML models without transferring data from patients / doctors / hospitals
- Data: Brain imaging, Chest X-Ray, EEG signals, genomic data
- Evaluation in real distributed environments
- Experiments on Prometheus, Ares (GPU) and Google Cloud Platform (GPU Instances)
- Large-scale Chest X-Ray studies (600,000 images) from multiple datasets (classification, segmentation)
- Collaborations: NearData EU Project
   (U. Tarragona, Barcelona Supercomputing Center, TU Dresden)





Filip Ślazyk, Przemysław Jabłecki, Maciej Malawski, Aneta Lisowska and Szymon Plotka: CXR-FL: Deep Learning-based Chest X-ray Image Analysis Using Federated Learning, ICCS, 2022

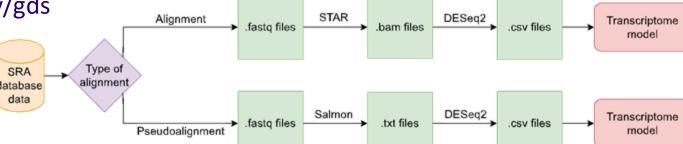
# **Transcriptomics Atlas Pipeline**



Sabina Lichołai, Piotr Kica, Jan Przybyszewski

- Big data analysis of transcriptomics databases
- Based on publicly available data: NCBI GEO https://www.ncbi.nlm.nih.gov/gds
- Differentiated at various levels: organs, tissues, cells versus diseases and conditions.
- Analysis of 15+ different tissues/organs,
   1000+ files of 10s GBs per each tissue, 1h+ on a single core per file
- Pipeline based on standard bioinformatics packages for preprocessing, alignment and reads counting (STAR, salmon, DESeq2)
- First results: Comparison of Cloud vs HPC
- Containerization for portability: Docker and Singularity/Apptainer
- Collaborations: NearData EU Project (U. Tarragona, Barcelona Supercomputing Center)

P. Kica, S. Lichołai, M. Malawski: Transcriptomics Atlas Pipeline: Cloud vs HPC, submitted to WORKS,23 Workshop at SC23 conference



# **Scientific Programming Team**



Leader: Piotr Nowakowski

- Each member of SPT is affiliated with one or more research teams, where they participate in development of artifacts, services and customized IT tools
- SPT members also work on research grant proposals, and have been quite successful in this regard (as evidenced e.g. by recent acquisition of the GEMINI research grant)

# Platform for simulations of digital twins



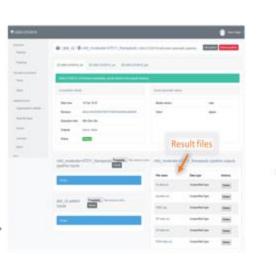
### Jan Meizner, Karol Zając, Adam Nowak, Krzysztof Gądek, Piotr Nowakowski

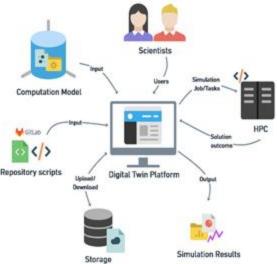
- Web-based system for management of multi-step computational pipelines on HPC systems
- Patient data-centered workflows:
  - Steps -> Pipelines -> Campaigns
  - Patients -> Cohorts
- Models implemented as software artifacts
  - Versioning: GitHub, GitLab
  - Comparison of results
  - **Reproducibility** -> Robust Science
- File management (HPC storage, Cloud storage)
- Usage in In Silico World EU Project
- Collaboration with Univ. Bologna, Univ. van Amsterdam, KU Leuven

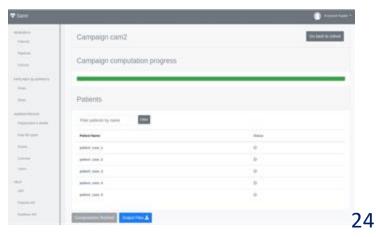


#### https://mee.cyfronet.pl/

Marek Kasztelnik, Piotr Nowakowski, Jan Meizner, Maciej Malawski, Adam Nowak, Krzysztof Gadek, Karol Zajac, Antonino Amedeo La Mattina, Marian Bubak: Digital Twin Simulation Development and Execution on HPC Infrastructures. ICCS (2) 2023: 18-32







### **HPHOB protein folding calculator**

Piotr Nowakowski, Tomasz Gubała, Krzysztof Gądek

- The Hydrophobicity Calculator (HPHOB) tool is used to simulate the folding process of proteins (or protein domains) based on the Fuzzy Oil Drop model, which has been developed at CMUJ
- We have encapsulated the core of the model (which is a standalone executable) with a GUI web application, enabling users to experiment with the model
- The system is also integrated with PDB, providing access to a broad range of protein structures.



Classification: MEMBRANE PROTEIN Organisms: Helicobacter pylori

MscS (Closed State)

Crystal Structure of Helicobacter pylori

PDB ID: 4HW9

Image and data retrieved from Protein Data Bank service of RCSB (rcsb.org). Presenting data and image of entry PDB ID 4HW9. Entry citation: Lai, J.Y., Poon, Y.S., Kaiser, J.T., Rees, D.C. Open and shut: crystal structures of the dodecylmaltoside solubilized mechanosensitive channel of small conductance from Escherichia coli and Helicobacter pylori at 4.4 angstrom and 4.1 angstrom resolutions. Protein Sci. (2013) 22 502-509



### https://hphob.sano.science

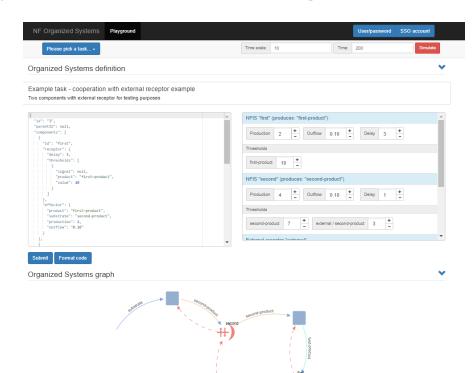


### **Systems Biology simulation tools**



Visualizing interactions between feedback loops which comprise biological systems

 We host a selection of tools developed at CMUJ to supplement their research publications and training materials



#### Information Probability (IP) Target probability - number of repetitions (elementary probability - always 0.05) Add chart Number of repetitions (k): 200 1.2 JS chart by amCharts 1.0 ability 8'0 For prob 0.2 0.003 0.006 0.009 0.012 0.015 0.018 0.033 0.036 0.039 k=200

Target probability - elementary probability (number of repetitions - always 1000)

- The Information Probability (IP) tool and the NF Organized Systems (NFS) calculator have been ported to Sano resources, and are available as training aids
- Both tools are also referenced in books published by our CMUJ collaborators

### **Sano Computational Medicine Seminars**



- A mean to enhance knowledge and build a scientific network
- Started on 22 June 2020; total 103 seminars until 26th June 2023
- The seminars are on Mondays at 14.00 CET/CEST
- Most of seminars are recorded and available at Sano YouTube also as a teaching material
- The list of Sano Seminars is available at Sano website:

http://sano.science/seminars



### Board, Foundation Council and Scientific Committee

Management Board conducts the daily operations of the Foundation

Role

Name

Prof. Maciej Malawski

 International Scientific Committee selects research team leaders, evaluates their achievements, and advises the Management Board in scientific matters

	Management Board	
<ul> <li>Foundation Council supervises Sano and</li> </ul>		

Director, President of the Management

Foundation Council supervises Sano and appoints Management Board members

Name	Affiliation
Karol Krawentek	ACC Cyfronet AGH, PL
Dr Tanja Bratan	Fraunhofer Institute ISI, DE
Dr Andrew Narracott	University of Sheffield, UK
Dr Olav Zimmermann	Forschungszentrum Jülich, DE
Kazimierz Murzyn	Klaster LifeScience Kraków, PL
President	

Name	Affiliation
Prof. Marco Viceconti, President	Università di Bologna, IT
Prof. Rod Hose	Emeritus Professor in the Department of Infection, Immunity and Cardiovascular Disease, University of Sheffield, UK
Prof. Richard Clayton	University of Sheffield, UK
Prof. Marek Behr	Aachen University, DE
Prof. Holger Gohlke	Heinrich Heine University Düsseldorf, DE
Prof. Dieter Kranzlmüller	Ludwig-Maximilian University Munich, DE
Prof. Zbigniew Nawrat	Silesian Center for Heart Diseases in Zabrze, PL
Prof. Irena Roterman-Konieczna	Jagiellonian University Medical College, PL
Prof. Jerzy Gąsowski	Jagiellonian University Medical College, PL
Prof. Knut Koschatzky	Fraunhofer Institute ISI, DE
Dr Claire Chalopin	University of Leipzig, DE
Dr Stefan Zachow	Zuse Institute Berlin, DE
Prof. Ewa Deelman	University of Southern California, USA
Prof. Peter Sloot	University of Amsterdam, NL
Prof. Jacek Kitowski	AGH University of Science and Technology, PL



### Sano in numbers (as for 31 August 2023)



### **Oversight and governance:**

- Foundation Council 5 members
- International Scientific Committee 15 members
- Management Board 2 members

#### **Research:**

- Team leaders 5
- Senior postdosc 4
- Postdocs 12

• PhD students – 19

- Scientfic programmers, technical staff 22
- Visting scientists 7
- MSc students (FNP scholarships) 13

#### Support:

- Operations 7
- Human talent management 2
- Finances 3

- Communication 3
- Business development 3
- Legal counsel 1

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Data protection – 2

### **Summary - collaboration opportunities**



# **Commercialization**

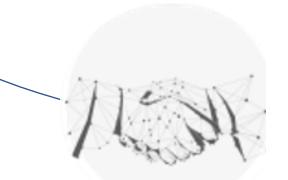
Introducing novel diagnostic methods and therapies based on computer simulations into clinical practice

### R&D

Developing new methods computing, algorithms, models and technologies for personalized medicine



sano



#### **Industrial collaboration**

Supporting enterprise development along with creation of new diagnostic and therapeutic technologies (DSS)

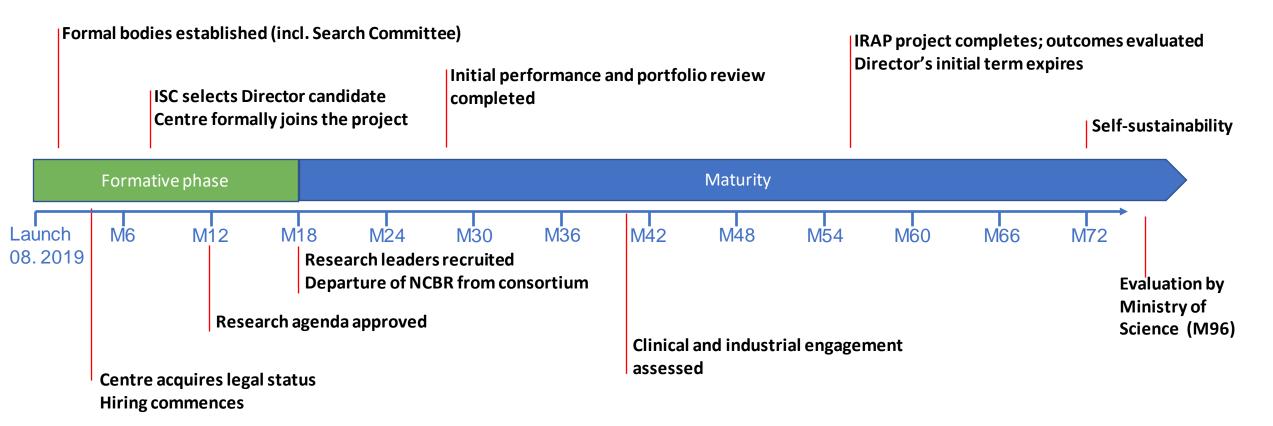
#### Education

Contribution to innovative training programs & education that meet the needs of modern personalized medicine



### Sano timeline





Sano in 2026: https://sano.science

"We prevent and heal disease through the use of computing and data"



Centre for Computational Medicine

www.sano.science

Marian Bubak Scientific Affairs Director m.bubak@sanoscience.org



This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 857533 and from the International Research Agendas Programme of the Foundation for Polish Science No MAB PLUS/2019/13.

