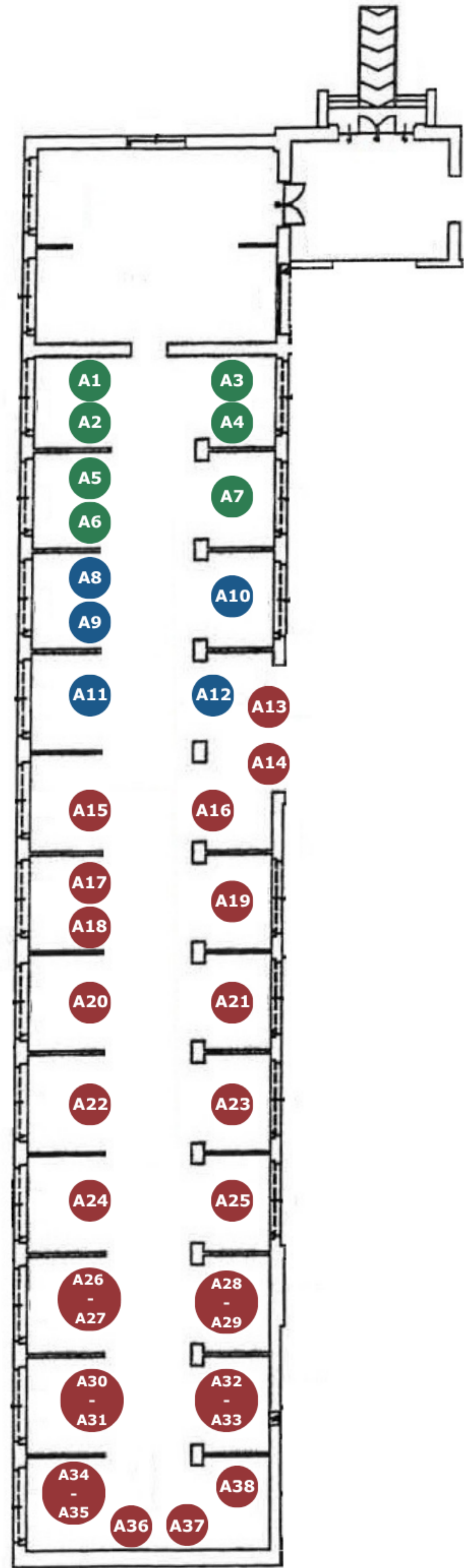




BIOSTATISTICS

- A1

ID 0040

GLM-Based Parametric Survival Modeling Under Two-Phase Sampling: A Computational Framework with Application to High-Dimensional Methylation Data
- A2

ID 5486

Functional Shapley Representations for Longitudinal Random Survival Forests using Hierarchical FPCA
- A3

ID 8845

Comparative Deep Learning and Statistical Analysis for Spatial Prediction of Lymph Node Metastasis in Gastric Cancer
- A4

ID 4182

Spatial host pathogen transcriptomics maps bacterial burden linked urothelial injury and repair in bladder infection
- A5

ID 0078

Early Warning of Extremely Rare Events from Pediatric Cardiac Intensive Care Electronic Health Records
- A6

ID 0060

QFARM - hierarchical quantitative association rule mining
- A7

ID 0024

Modified Gompertz Function in Quantitative Evaluation of Endolysin Lytic Activity in Physiological Fluids

MEDICAL INFORMATICS

- A8

ID 0085

AEGLOS V7: Hyperbolic Digital Pathology for Morphology-to-Genomics Prediction in Advanced Non-Small Cell Lung Cancer
- A9

ID 3784

A new MRI-based feature for quantifying the Diffuse Low-Grade Glioma brain infiltration and discriminating patterns of patients
- A10

ID 6293

On the adoption of Quantum Machine Learning for Privacy-Preserving and Explainable Diabetic Retinopathy Detection and Localisation
- A11

ID 0068

FFPE-Open-ST: high-resolution, unbiased spatial transcriptomics profiling of archival samples
- A12

ID 0054

Beyond the Diagnosis: Semi-Automated Risk Analysis of Inappropriate Antibiotic Prescribing in Mexico and the Potential for Real-Time Alerts

BIOINFORMATICS

- A13

ID 0072

Quantum Optimization for Protein-Protein Interaction Network Alignment
- A14

ID 0034

Quantum Annealing for De Novo Genome Assembly
- A15

ID 0087

Benchmarking LLMs for automated systems biology model replication
- A16

ID 3745

Analysis of Prompt Engineering for Drug Toxicity Prediction
- A17

ID 0059

Autoresearch Discovery of Interpretable Filter Rules for Antibody Binder Classification
- A18

ID 5995

Statistical Model Checking of Uncertain Continuous Time Markov Chain in Systems Biology
- A19

ID 5265

A ML-powered Multiscale Computational Platform Based on QSP and PBPK Modeling to Support the Development of mRNA-based Therapies
- A20

ID 0029

Computational Framework for the Design of Second-Generation Pharmacochaperones Targeting Allosteric Pockets
- A21

ID 0077

Pathway-Mediated Networks for Drug Repurposing in Breast Cancer
- A22

ID 0089

Large-scale analysis and clustering of RNA 3D structures
- A23

ID 0062

Machine learning approaches for predicting functional lncRNAs and key regulatory interactions in plant gene networks
- A24

ID 0023

Computational Prediction of Pathogenic FMR1 Variants in Fragile X Syndrome
- A25

ID 0047

VISMA: Vector Integration Site Mutation Analysis

BIOINFORMATICS (CONT.)

- A26

ID 0022

A Network Story: tumor educated platelets transcriptome and Glioblastoma
- A27

ID 0033

FLiCoN: Friendship Like differential Coexpression Network for the identification of Tumor-Educated Platelets Driver Genes in Glioma via structural Imbalance
- A28

ID 0070

Beyond Differential Expression: Network Centrality measures reveal Tissue-Specific Signatures in Tumor-Educated Platelets
- A29

ID 0066

Investigating Immunotherapy Response in Non-Small Cell Lung Cancer Using Machine Learning and Differential Networks
- A30

ID 0095

Repeats Enrichment Analysis of sequencing Datasets (READs) reveals unique repair and transcription dynamics of human satellites
- A31

ID 0079

Mutational signature in Mycobacterium tuberculosis under pretomanid and nitric oxide exposure
- A32

ID 0050

geneslator: a R package for comprehensive gene identifier mapping and annotation
- A33

ID 0044

REV-AGE and REV-AGE 2.0: From Systematic Evidence Mapping to AI-Guided Mechanistic Discovery in Aging Research
- A34

ID 0035

Toward Accessible and Reproducible Bioinformatics Workflows for Nanopore-Based Virus Surveillance
- A35

ID 0086

Learning Read-Level joint genomic and epigenomic status representations from Nanopore sequencing data using Jessica-Fetcher and NTV3-like architecture
- A36

ID 0083

Single-Molecule Tissue-of-Origin Profiling for Prenatal and Oncology cfDNA Applications
- A37

ID 0030

Integrative analysis of multi-modal single-cell data reveals chromosome alterations underlying critical disease development stages: a proof-of-principle in MDS
- A38

ID 0036

Single-cell multi-omics integration for TCR-epitope binding inference in acute myeloid leukemia