

Artificial intelligence in personalized medicine



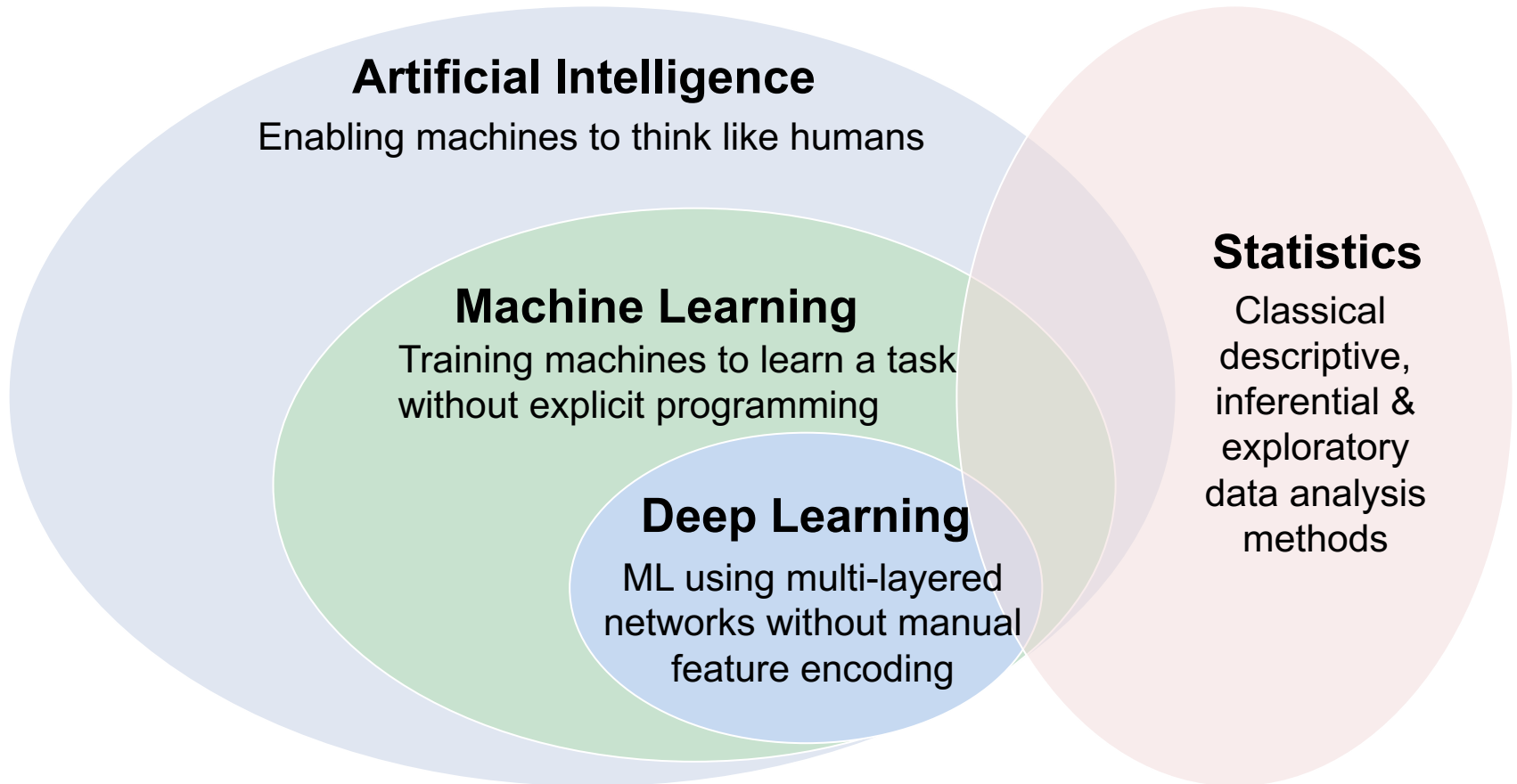
Enrico Glaab

Luxembourg Centre for Systems Biomedicine

Overview

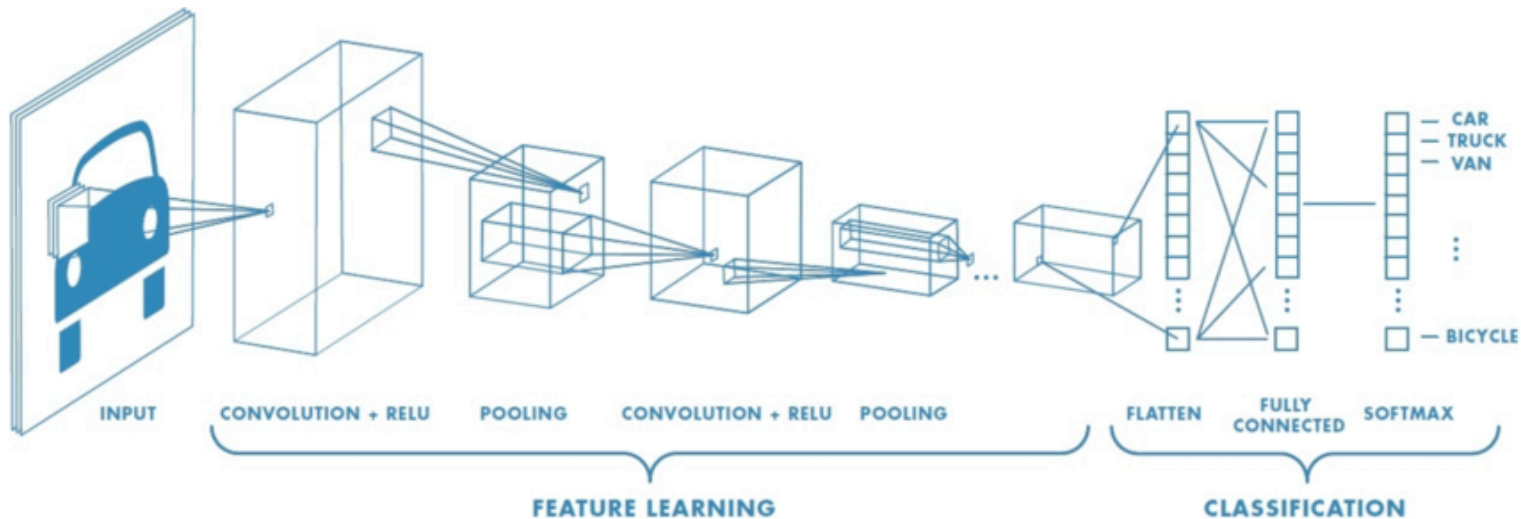
- (1) Introduction: Artificial Intelligence vs. Classical Statistics
- (2) AI success stories in recent years
- (3) AI in personalized medicine:
 - Biomarker discovery
 - Drug discovery
 - Digital health monitoring
- (4) Common pitfalls and challenges
- (5) Outlook on new AI strategies to address the challenges

AI vs. Statistics



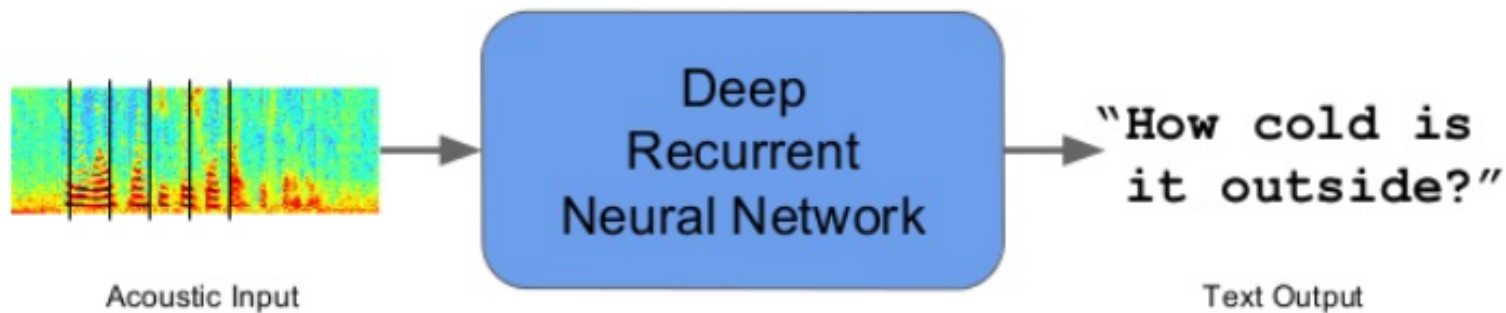
AI success stories: Image data (1)

- **Image classification:** unprecedented accuracies using deep learning (e.g. “AlexNet” approach by Krizevsky et al., 2012)
- **Novel techniques:** Convolutional Nets / Transformers, Dropout, Data Augmentation, Rectifier Nonlinearity, Local Response Normalization



AI success stories: Sequential data (2)

- **Speech recognition:** 30% less errors with new neural networks (Huang et al., ACM Communications, 2012)
- **Novel techniques:** Recurrent Neural Networks (RNNs): Long-Short-Term Memory Networks (LSTMs), Gated Recurrent Units (GRU), etc.



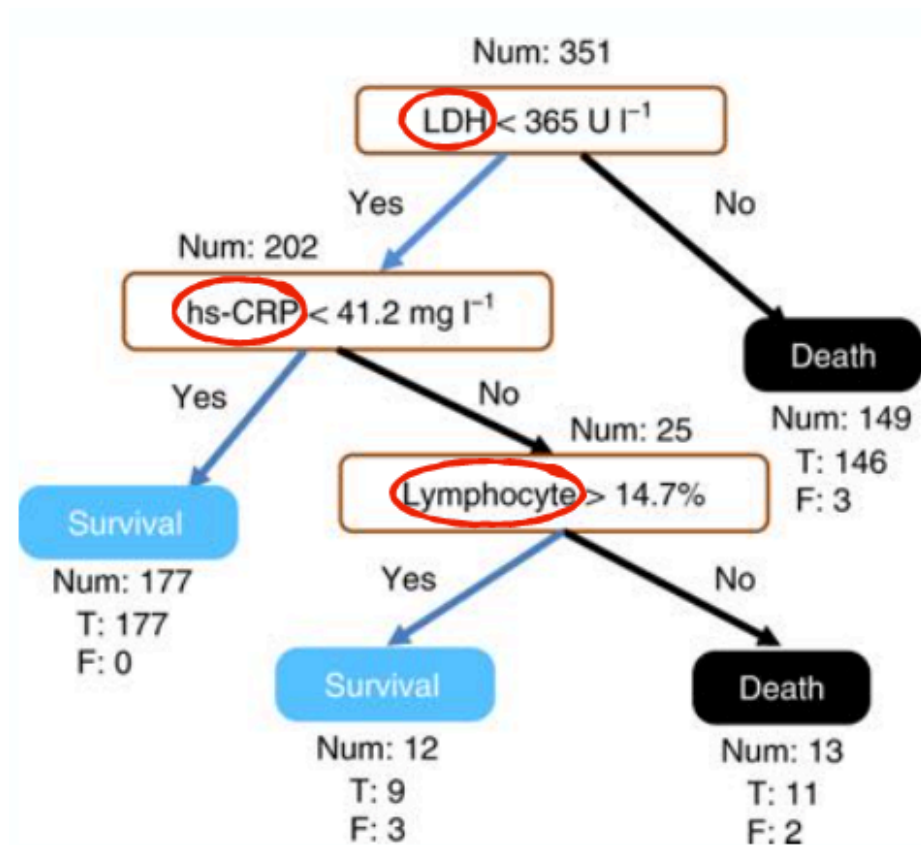
AI successes in personalized medicine - Biomarkers

Multiple omics-based AI diagnostic tools already clinically validated:

Name	Test approval (FDA-cleared and/or LDT)	Purpose	References
MammaPrint	FDA-cleared, LDT	breast cancer risk-of-recurrence assessment	Van't Veer et al., Nature, 2002
AlloMap Heart	FDA-cleared, LDT	identifying heart transplant recipients with risk of cellular rejection	Yamani et al., J Heart Lung Transplant, 2007
Prosigna Assay / PAM50	FDA-cleared, LDT	breast cancer risk of distant recurrence prediction	Nielsen et al., BMC Cancer, 2014
Oncotype DX	LDT	breast cancer risk-of-recurrence assessment	Kelley et al., Cancer, 2010
Decipher	LDT	prostate cancer metastatic risk prediction	Marrone et al., PLoS Curr., 2015

AI in biomedicine: Covid-19 hospital mortality prediction

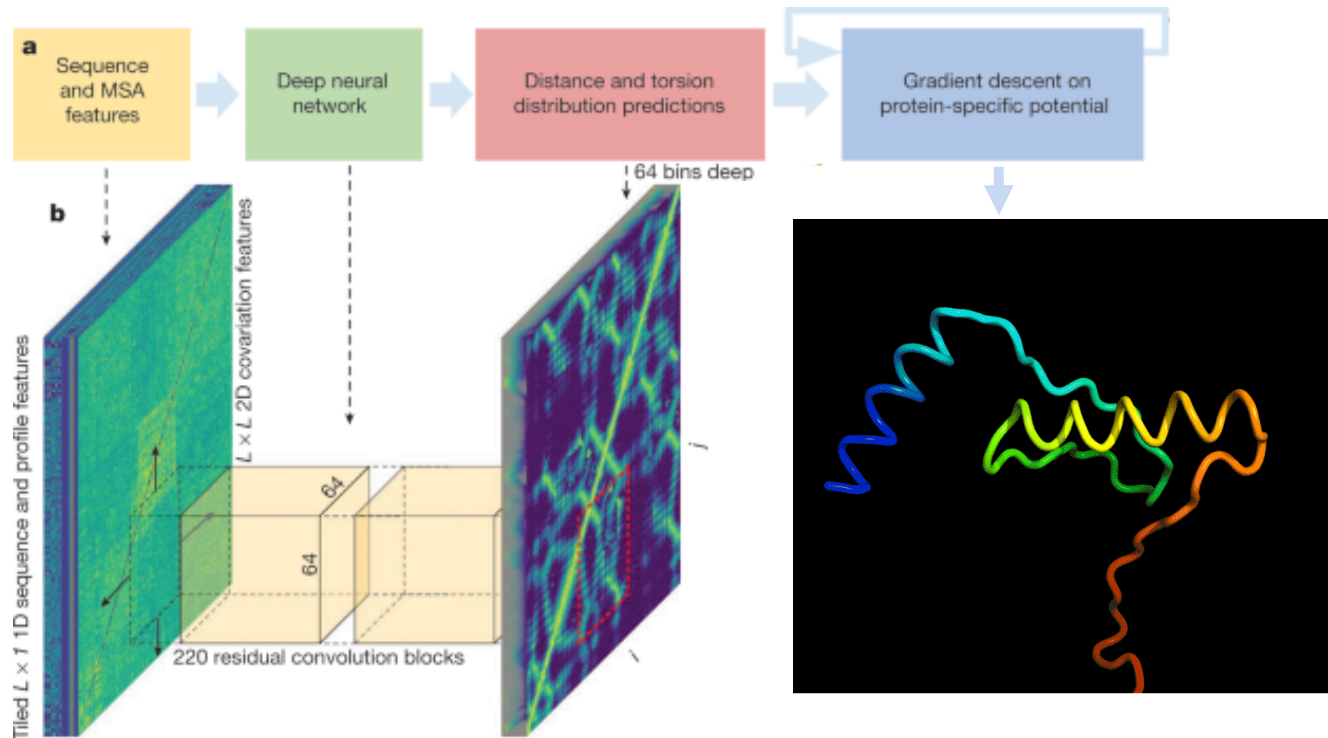
- Covid-19: alterations in common clinical blood tests when diagnosed
- Apply ML → 90% accurate predictions of mortality on test set of 110 patients (10 days in advance)



(source: Yan et al., Nat. Mach. Intell. 2, 2020)

Deep learning for biomedical research: AlphaFold 2

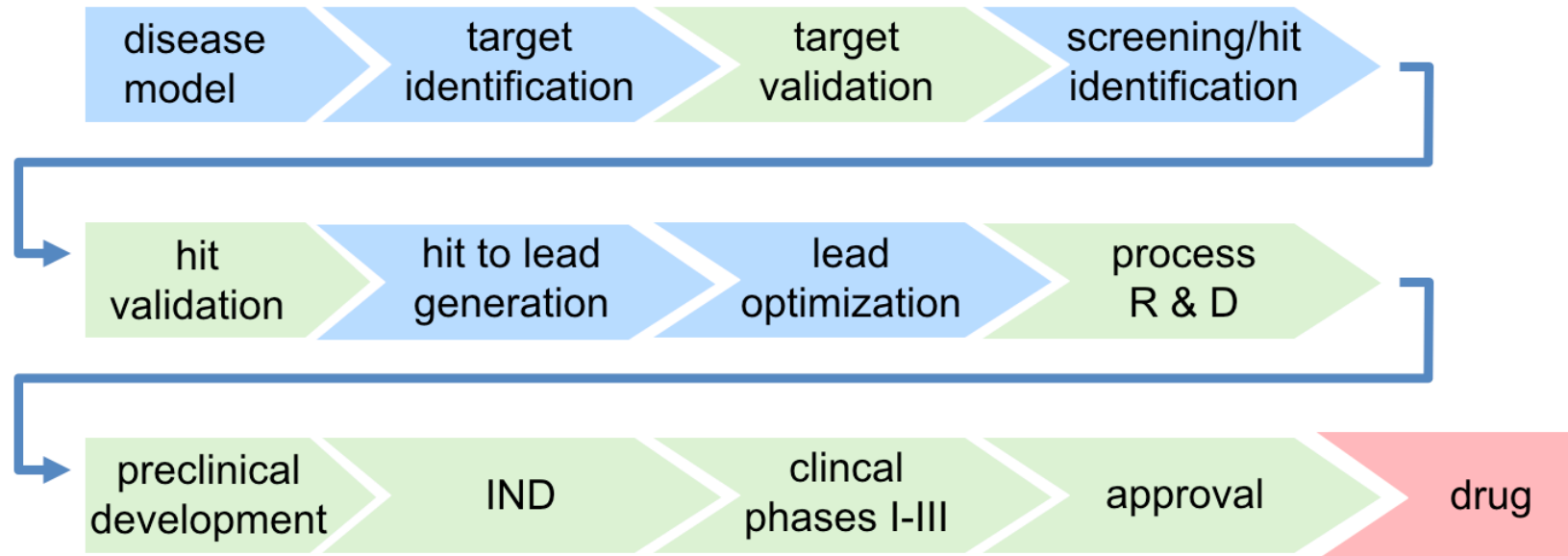
- DeepMind's AlphaFold 2 → major advance in protein structure prediction
- Scores > 90 in global distance test (GDT) in the CASP competition



(AlphaFold basic architecture; source: Senior et al., Nature 577, 2020)

AI in drug development

Common phases in drug development:

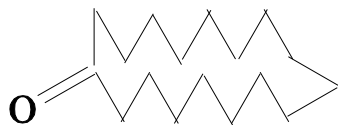
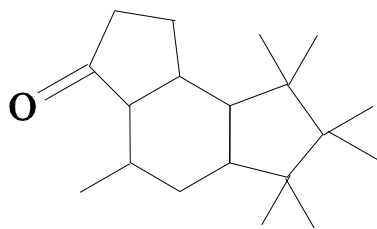
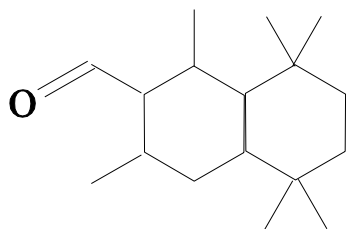


Opportunities for AI approaches highlighted in blue (➡)

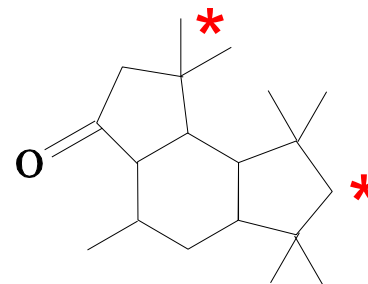
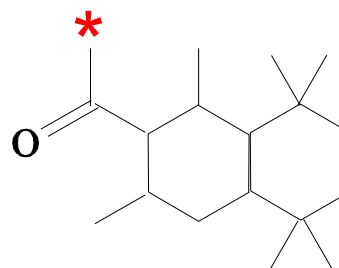
AI in drug development

- **Question:** Which drug-like compounds bind to a particular target protein?

• **Example:** **Active compounds**

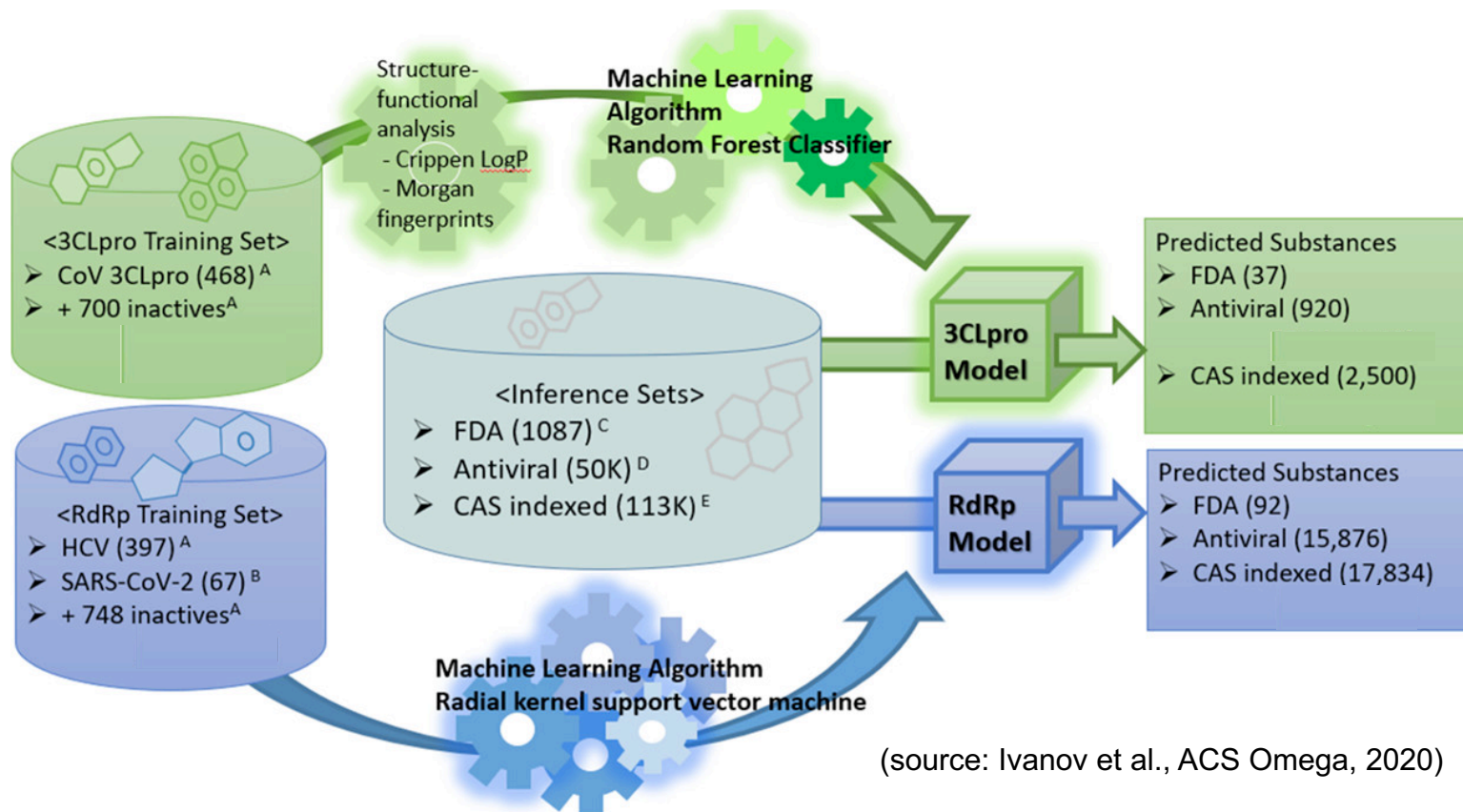


Inactive / low activity compounds



Application to SARS-CoV-2 compound screening

AI-based screening: Finding new inhibitors of viral proteins *3CLpro* and *RdRp*



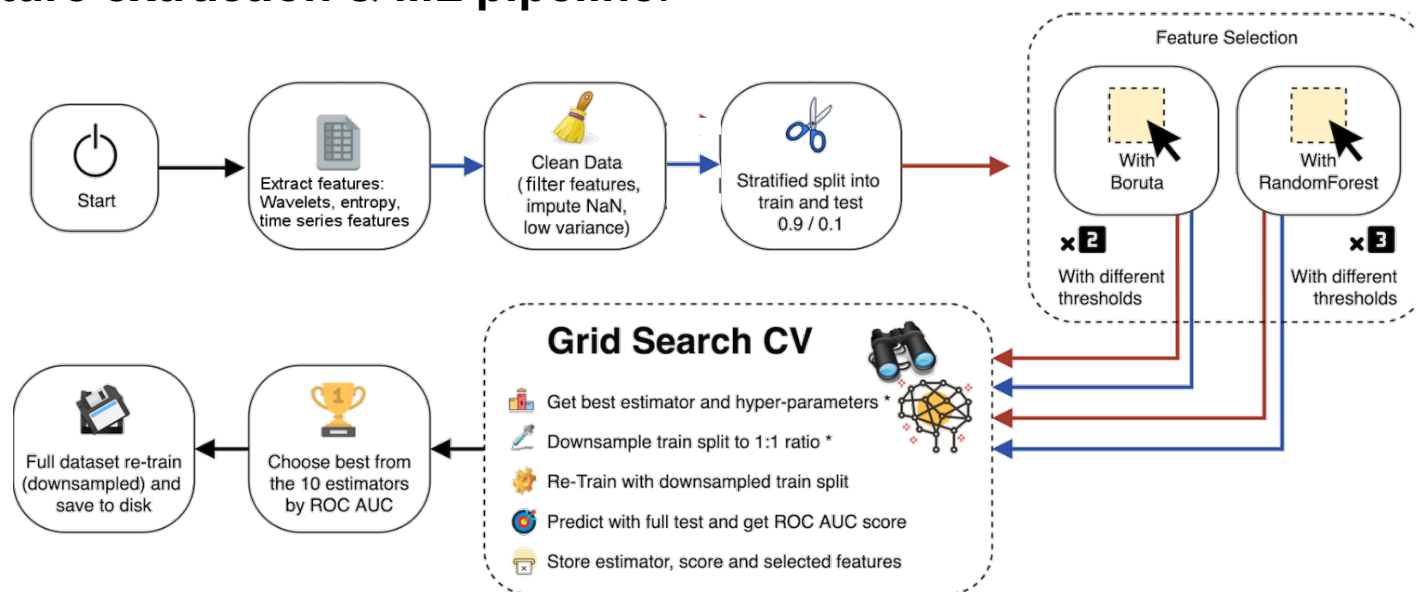
AI for personalized health monitoring / digital biomarkers

Digital biomarkers:

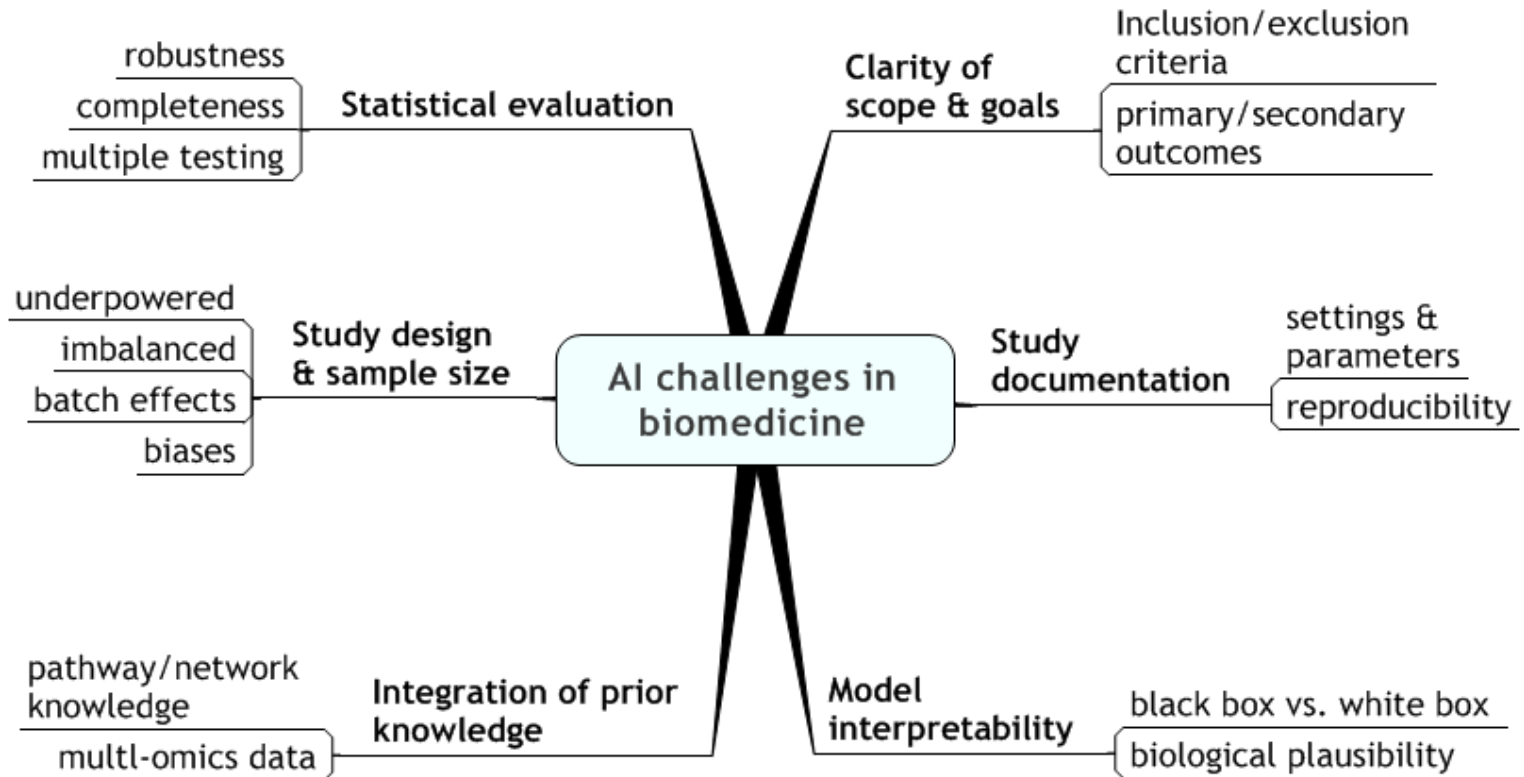
- mobile phone gyrometer & accelerometer
- gait sensors (eGalT system)



Feature extraction & ML pipeline:



Common challenges for AI in personalized medicine



Recommendations from literature

Data pre-processing, filtering & normalization:

- use **cross-validation** to check if pre-processing leads to information loss
- **compare or combine** multiple pre-processing approaches

Integration of prior knowledge & multi-omics analyses:

- **Assess cost/benefit** of multi-omics analyses using prior data, or conduct pilot analyses
- use **existing software & frameworks** for integrative biological data analysis

Ensuring model interpretability & biological plausibility:

- use dedicated methods to build **interpretable models** (e.g. rule learning methods)
- use cellular **pathway/network analysis & literature mining** to guide modeling

Outlook: New AI strategies to address the challenges

Increase statistical power

- AI-based integration of prior knowledge & multi-omics data
- Algorithmic sample matching & selection, AI for batch adjustment

Increase model robustness

- AI-based integration of models across human & animal model data, different experimental platforms and cohorts (Transfer learning)

Increase model interpretability

- Structured and graph-based machine learning
- AI-based literature mining for model interpretation

Acknowledgements

Biomedical Data Science Group



New members:



**Mirko
Ledda**



**Elisa
Gomez
de Lope**



**Loïc
Le Bescond**



Thank you for your attention!

Questions?
Comments?

References

1. E. Glaab, *Building a virtual ligand screening pipeline using free software: a survey*, Briefings in Bioinformatics (2015), 17(2), pp. 352
2. E. Glaab, *Using prior knowledge from cellular pathways and molecular networks for diagnostic specimen classification*, Briefings in Bioinformatics (2015), 17(3), 440
3. N. Vlassis, E. Glaab, *GenePEN: analysis of network activity alterations in complex diseases via the pairwise elastic net*, Statistical Applications in Genetics and Molecular Biology (2015), 14(2), 221
4. E. Glaab, J. M. Garibaldi, N. Krasnogor. *Learning pathway-based decision rules to classify microarray cancer samples*, German Conference on Bioinformatics 2010, Lecture Notes in Informatics (LNI), 173, 123-134
5. E. Glaab, J. Bacardit, J. M. Garibaldi, N. Krasnogor, *Using rule-based machine learning for candidate disease gene prioritization and sample classification of cancer gene expression data*, PLoS ONE, 7(7):e39932, 2012
6. E. Glaab, A. Baudot, N. Krasnogor, A. Valencia. *Extending pathways and processes using molecular interaction networks to analyse cancer genome data*, BMC Bioinformatics, 11(1):597, 2010
7. E. Glaab, A. Baudot, N. Krasnogor, R. Schneider, A. Valencia. *EnrichNet: network-based gene set enrichment analysis*, Bioinformatics, 28(18):i451-i457, 2012
8. Maes, M., Nowak, G., Caso, J. R., Leza, J. C., Song, C., Kubera, M., .et al. (2016). *Toward omics-based, systems biomedicine, and path and drug discovery methodologies for depression-inflammation research*. Molecular neurobiology, 53(5), 2927-2935.
9. E. Glaab, J.P. Trezzi, A. Greuel, C. Jäger, Z. Hodak, A. Drzezga, L. Timmermann, M. Tittgemeyer, N. J. Diederich, C. Eggers, *Integrative analysis of blood metabolomics and PET brain neuroimaging data for Parkinson's disease*, Neurobiology of Disease (2019), Vol. 124, No. 1, pp. 555
10. E. Glaab, R. Schneider, *Comparative pathway and network analysis of brain transcriptome changes during adult aging and in Parkinson's disease*, Neurobiology of Disease (2015), 74, 1-13
11. Z. Zhang, P. P. Jung, V. Grouès, P. May, C. Linster, E. Glaab, *Web-based QTL linkage analysis and bulk segregant analysis of yeast sequencing data*, GigaScience (2019), 8(6), 1-18
12. S. Köglberger, M. L. Cordero-Maldonado, P. Antony, J. I. Forster, P. Garcia, M. Buttini, A. Crawford, E. Glaab, *Gender-specific expression of ubiquitin-specific peptidase 9 modulates tau expression and phosphorylation: possible implications for tauopathies*, Molecular Neurobiology (2017), 54(10), pp. 7979
13. Kleiderman, S., Gutbier, S., Ugur Tufekci, K., Ortega, F., Sá, J. V., Teixeira, A. P., et al. (2016). *Conversion of Nonproliferating Astrocytes into Neurogenic Neural Stem Cells: Control by FGF2 and Interferon-γ*. Stem Cells, 34(12), 2861-2874.
14. Bolognin, S., Fossépré, M., Qing, X., Jarazo, J., Ščančar, J., Moreno, E. L., et al. (2019). *3D Cultures of Parkinson's Disease-Specific Dopaminergic Neurons for High Content Phenotyping and Drug Testing*. Advanced Science, 6(1), 1800927.
15. Jaeger, C., Glaab, E., Michelucci, A., Binz, T. M., Koeglsberger, S., Garcia, P., ... & Buttini, M. (2015). *The mouse brain metabolome: region-specific signatures and response to excitotoxic neuronal injury*. The American Journal of Pathology, 185(6), 1699-1712.
16. E. Glaab, R. Schneider, *RepExplore: Addressing technical replicate variance in proteomics and metabolomics data analysis*, Bioinformatics (2015), 31(13), pp. 2235
17. E. Glaab, R. Schneider, *PathVar: analysis of gene and protein expression variance in cellular pathways using microarray data*, Bioinformatics, 28(3):446-447, 2012
18. E. Glaab, A. Baudot, N. Krasnogor, A. Valencia. *TopoGSA: network topological gene set analysis*, Bioinformatics, 26(9):1271-1272, 2010
19. E. Glaab, J. M. Garibaldi and N. Krasnogor. *ArrayMining: a modular web-application for microarray analysis combining ensemble and consensus methods with cross-study normalization*, BMC Bioinformatics, 10:358, 2009