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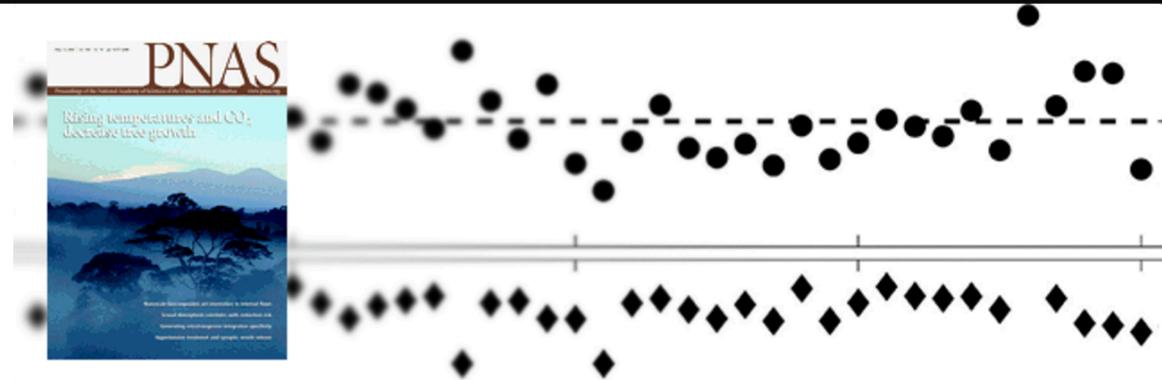


- 3 different undergraduate degrees (Med School, Mathematics, Philosophy)
- 2y PhD Course program in Mathematics.
- PhD (Medicine) 1997,
- Alfred P Sloan & Wennergren Fellow (1998-2001, Boston, USA)
- Chaired Professor, Computational Biology 2002-2009,
- Chaired Strategic Professor, Computational Medicine 2010-
- Professor Bioscience, KAUST 2016 –
- Professor Computer Science, KAUST, 2016-



If you can read the products
of the genome, can you figure
out the system if you also can
write parts of the genome?

Proceedings of National Academy of Sciences,
2003



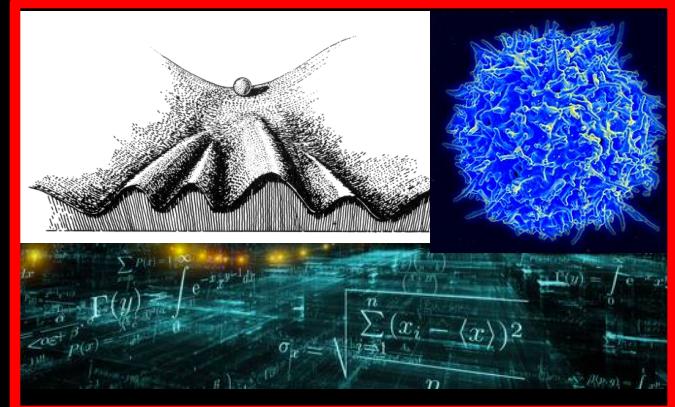
We are fundamentally intrigued by living systems. Since cells are the fundamental units of life we focus on developing and applying experimental and computational techniques for decoding the dynamics of cellular regulatory circuits. To increase the resolution of those circuits our current focus is on single cell genomics using cell culture experiments and computational techniques.

This is relevant for addressing vital questions related to the control of cellular identity, reprogramming of cells, as well as biomedical applications.

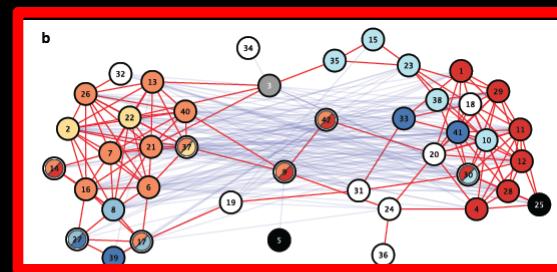
On the theory side this endeavor requires new algorithms and machine intelligence approaches for essentially extracting the fundamental equations encoding causality directly from data. Living systems have a stunning capacity to learn, represent, predict, and in extension "understand" their local world(s) over time. In our work we believe that evolved solutions in nature can provide fresh clues on how to design new powerful intelligent hybrid computational systems.

THEORY & EXPERIMENTS & COMPUTATION & DATA SCIENCE

1. EXPERIMENTALLY DERIVED EQUATIONS OF CELLULAR DYNAMICS



2. MOLECULAR UNDERSTANDING ENABLING PERSONALIZED & PRECISION MEDICINE



3. REENGINEER CELLS & DESIGN NEW ADAPTIVE SMART GENERAL PURPOSE SYSTEMS



PUBLISHED 2016

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• Quantifying loss of information in network-based dimensionality reduction techniques
H. Zenil, N. Kiani, J. Tegnér
Journal of Complex Networks, Volume 4, Issue 3, Pages 342–362, 2016
Keywords: Dimensionality reduction techniques; Graph motifs; Graph sparsification; Graph spectra; Kolmogorov complexity

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• Network based drug repositioning methodology for neurodegenerative diseases
M.-M. Shang, N. Kiani, J. Tegnér
International Web Conference on Bioinformatics and Bioengineering, IWBIBO 2016
Keywords: Biological Network analysis; Neurodegenerative disease; Drug repositioning; Flow cytometry; Statin

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• Cellular differentiation: Topology, a systematic approach to predict toxicity
S. Gómez-Cabreiro, S. V. Stoye, J. C. Tegnér
Journal of Pharmaceutical and Biomedical Analysis, Volume 77, Pages 10–15, 2016
Keywords: Cell Differentiation; Topology; Predictive models; Toxicity; Metabolism

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• TGF- β affects the differentiation of human GM-CSF+ CD4+ T cells in an activation- and sodium-dependent manner
S. Elías, A. Schmidt, V. Kannan, J. Andersson, J. Tegnér
Frontiers in Immunology, 7(603), 2016
Keywords: Autoimmune diseases; Differentiation; GM-CSF; Human CD4+ T cells; Multidimensional; Na⁺; TGF- β ; T-cell differentiation

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• In vitro differentiation of human CD4+FOXP3+ induced regulatory T cells (iTreg) from naïve CD4+ T cells using a TGF- β -containing protocol
A. Schmidt, E. Szabolcs, R. Joshi, and J. Tegnér
J. Vis. Exp. (118), 2016
Keywords: Immunology; Regulatory T cells; Treg; CD4+ T cells; Magnetic cell isolation; In vitro differentiation; Cytokines; FOXP3; TGF- β ; IL-2; Intracellular Flow cytometry; qRT-PCR

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• A perspective on bridging scales and design of models using low-dimensional manifolds and data-driven model inference
J. Tegnér, H. Zenil, N. Kiani, G. Ball, J. Gomez-Cabreiro
Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences, Volume 374, Issue 2080, Article number 20160144, 2016
Keywords: Big data; Computational biology; Living systems; Model reduction; Modelling; Systems biology

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• Human cytomegalovirus may promote tumour progression by upregulating arginase-2
X. Xu, H. Costa, G. Overbeek, S. Vasalakar, C. Pawan, K. Patro, G. Shah, S. Ananthashan, G. Tsipras, B. Davoudi, A.-A. Mohammad, H. Lam, K. Straat, J. Tegnér, J.C. Tong, K.T. Wong, C. Söderberg-Naucler, and K.-C. Yau
Oncoimmunology, 7(10):47221–47231, 2016
Keywords: Arginase; Cytomegalovirus; Glioblastoma; Treatment

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• Conditional disease development extracted from longitudinal health care cohort data using layered network construction
V. Kannan, F. Swartz, I. Abusobaesa, N. Kiani, G. Silberg, D. Gomez-Cabreiro, K. Alexanderson, and J. Tegnér
Scientific Reports, 6, Article number 26107, 2016
Keywords: Layered networks; Conditional disease; Health care data

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• Adaptive input data transformation for improved network reconstruction with information theoretic algorithms
V. Kannan, J. Tegnér
Stat. Appl. Genet. Mol., 15(1):1–20, 2016
Keywords: Algorithms; Information theoretic; Network reconstruction

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• Integrative molecular profiling during human induced regulatory T cell (iTreg) generation reveals novel regulators of Foxp3
A. Schmidt, F. Marabita, H. Johansson, J. Lethi, M. Eriksson, S. Elías, D. Gomez-Cabreiro, A. Rao, J. Tegnér
Scandinavian Journal of Immunology 83 (5), 353, 2016
Keywords: Molecular profiling; Human induced regulatory T cell (iTreg)

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• Characterization and mechanistic dissection of the differentiation of GM-CSF+ CD4+ T cells
S. Elías, A. Schmidt, V. Kannan, J. Andersson, J. Tegnér
Scandinavian Journal of Immunology 83 (5), 354–355, 2016
Keywords: GM-CSF+ CD4+ T cells

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• Topological evaluation of methods for reconstruction of genetic regulatory networks
J. Olszak, N. Kiani, H. Zenil, J. Tegnér
Proceedings - 11th International Conference on Signal-Image Technology and Internet-Based Systems, SITIS 2015, Article number 7400694, Pages 468–473, 2016
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• High-sensitivity bioinformatics framework for epigenetic profiling of discordant twins reveals specific and shared novel epigenetic variants in ACPA and ACPB genes
D. Gomez-Cabreiro, M. Almgren, L.K. Spjølmoen, A. Herwald, R. Tryggvadottir, J. Kere, A. Scheynius, N. Acevedo, L. Reinus, M.A. Taub, C. Montano, M.J. Anye, J.I. Feinberg, A.P. Feinberg, J. Tegnér, L. Klareskog, A.I. Catrina, and T.J. Ekström
Genome Medicine, Volume 8, Issue 1, Article number 124, 2016
Keywords: ACPA; Bioinformatics; DNA methylation; Epigenetics; Rheumatoid arthritis

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• From comorbidities of chronic obstructive pulmonary disease to identification of associated mechanisms
D. Gomez-Cabreiro, J. Merche, C. Vargas, I. Cano, D. Maier, A.L. Barabási, J. Tegnér, J. Roca
BMC Bioinformatics 17 (15), 441, 2016
Keywords: Associated mechanism; Chronic obstructive pulmonary disease; Disease; Mechanism; Network; Pathway

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• Experimental analysis of protocols to induce human CD4+FoxP3+ regulatory T cells by combinations of IL-2, TGF-beta, retinoic acid, cyclosporine, and bortezomib
M. Eriksson, M. Shang, J. Tegnér, M. Weyd, and J. Tegnér
PLoS One, Volume 11, Issue 2, Article number e0140474, 2016
Keywords: Animal experiment; CD4+ FoxP3+ regulatory T cell; Cell isolation; Comparative study; Controlled study

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• Machine learning for patient stratification in an integrated care scenario
M. Marabita, J. Vela, S. Pauwels, C. Bescos, I. Cano, J. Tegnér, et al.
Journal of Clinical Data Mining, 16(6): A322, pp. 1–8, 2016
Keywords: Case finding; Clinical decision making; Chronic care; Health risk assessment; Patient stratification

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• Human manipulation of human CD4+FoxP3+ regulatory T cells via binding and re-release of TGF- β
A. Schmidt, J. Zeng, N. Jia, S. Iqbal, C. Wallmark, S. Gabrilsson, R.A. Harris, and J. Tegnér
Immunology and Cell Biology 94, 747–762, 2016
Keywords: Adoptive transfer; CD4+ T lymphocyte; Cell differentiation; Controlled study; Cytokine production

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• Unraveling causal molecular networks: empirical assessment through a community-based effort
S. Hill, et al.
Nature Methods 13, 310–318, 2016
Keywords: Algorithms; Causality; Computational Biology; Computer Simulation; Gene Expression Profiling; Gene Regulatory Networks; Humans

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• Neuroswarm: a methodology to explore the constraints that function imposes on simulation parameters in large-scale networks of biological neurons
D. Gomez-Cabreiro, S. Ardid, M. Cano-Colino, J. Tegnér, A. Compte
Book chapter in *Uncertainty in Biology*, Volume 17 of the series *Studies in Mechanoobiology, Tissue Engineering and Biomaterials*, pp 427–446, 2016
Keywords: Prefrontal cortex; Workflow; Ensemble analysis; Working memory model; Neuroscience; Computational biology

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• Modeling and model simplification to facilitate biological insights and predictions
D. Eriksson, J. Tegnér
Book chapter in *Uncertainty in Biology*, Volume 17 of the series *Studies in Mechanoobiology, Tissue Engineering and Biomaterials*, pp 447–464, 2016
Keywords: Simplification; Model reduction; Data integration; Dynamical models; Ordinary differential equations; Piecewise linear; Dynamical module

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• Probabilistic computational causal discovery for systems biology
V. Lapan, S. Trantafyllou, G. Ball, J. Tegnér, I. Tsamardinos
Book chapter in *Uncertainty in Biology*, Volume 17 of the series *Studies in Mechanoobiology, Tissue Engineering and Biomaterials*, pp 53–73, 2016
Keywords: Causality; Causal graphical models; Bayesian networks; Systems biology; Biological networks

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• Human regulatory T cells rapidly rewrite the phosphoproteome of suppressed conventional T cells
R.N. Joshi, N. Brini, F. Marabita, J. Tegnér, A. Schmidt
Scandinavian Journal of Immunology 83 (5), 376–377, 2016
Keywords: Regulatory T cells; Phosphoproteome; Conventional T cells

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• Proposals for enhanced health risk assessment and stratification in an integrated care scenario
I. Duréas-Espín, E. Vela, S. Pauwels, C. Bescos, I. Cano, M. Cleries, J.C. Contel, E. de Manuel Keepon, J. García-Aymerich, D. Gomez-Cabreiro, R. García, M.M. Lah, M. Lluch-Ariet, M. Moharra, D. Montaña, J. Morà, M. Nalín, A. Pavlickova, J. Piera, S. Ponc, S. Santacruz, H. Schonenberg, S. Störk, J. Tegnér, F. Velickovic, C. Westerterp, J. Roca
BMJ Open, 6, Issue 4, 2016
Keywords: Animal experiment; Information processing; Morbidity; Population model; Prediction; Risk assessment; Scotland; Stratification; Telemedicine

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• Methods of information theory and algorithmic complexity for network biology
H. Zenil, N. Kiani, J. Tegnér
Seminars in Developmental and Cell Biology March 51: 32–43, 2016
Keywords: Algorithmic probability; Algorithmic randomness; Biological networks; Complex networks; Information theory; Kolmogorov complexity

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• Investigating the complexity of reconstructed genetic networks
N. Kiani, H. Zenil, J. Olszak, J. Tegnér
Seminars in Developmental and Cell Biology March 51: 44–52, 2016
Keywords: Network reverse engineering; Network reconstruction; Evaluation of networks; Shannon entropy; Algorithmic complexity

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• Bioinformatics mining and modeling methods for the identification of disease mechanisms in neurodegenerative disorders
M. Hofmann-Apitius, G. Ball, S. Gebel, S. Bagewadi, B. de Bon, R. Schneider, M. Page, A. Tom Kodamulli, E. Younesi, C. Ebeling, J. Tegnér, and L. Camard
International Journal of molecular science, 17(12): 29179–29206, 2016
Keywords: Bioinformatics; Data integration; Disease models; Genetics; Graphical models; Knowledge-based modeling; Mechanism-identification; Multicell; Neurodegeneration

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• Normalization of circulating microRNA expression data obtained by quantitative real-time RT-PCR
F. Marabita, P. de Candia, A. Torri, J. Tegnér, S. Abignani, R.L. Rossi
Briefings Bioinformatics, 20(4), 2016
Keywords: NormFinder; Circulating miRNA; GeNorm; Normalization; qPCR; Reference genes

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• Optimization in biology parameter estimation and the associated optimization problem
G. Cedersund, O. Samuelsson, G. Ball, J. Tegnér, D. Gomez-Cabreiro
Book chapter in *Uncertainty in Biology*, Volume 17 of the series *Studies in Mechanoobiology, Tissue Engineering and Biomaterials*, pp 177–197, 2016
Keywords: Parameter estimation; Optimization; Heuristic fitness function

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• Computational modeling under uncertainty: challenges and opportunities
D. Gomez-Cabreiro, J. Tegnér, L. Gerle
Book chapter in *Uncertainty in Biology*, Volume 17 of the series *Studies in Mechanoobiology, Tissue Engineering and Biomaterials*, pp 477–496, 2016
Keywords: Computational modeling; Uncertainty; Challenges; Opportunities

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• Systems engineering: dispersing dispersed knowledge and recommendations based on a multi-disciplinary and translational approach
J. Roca, D. Gomez-Cabreiro, J. Tegnér
Systems Biology for Medicine, Springer series "Methods in Molecular Biology" 283–303, 2016
Keywords: Clinical decision support; Integrated care; Comorbidity; Disease modeling; Knowledge management

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• Duphas-Espín, I. Vela, S. Pauwels, C. Bescos, I. Cano, M. Cleries, J.C. Contel, E. de Manuel Keepon, J. García-Aymerich, D. Gomez-Cabreiro, R. García, M.M. Lah, M. Lluch-Ariet, M. Moharra, D. Montaña, J. Morà, M. Nalín, A. Pavlickova, J. Piera, S. Ponc, S. Santacruz, H. Schonenberg, S. Störk, J. Tegnér, F. Velickovic, C. Westerterp, J. Roca
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Scandinavian Journal of Immunology 83 (5), 376–377, 2016
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I. Duréas-Espín, E. Vela, S. Pauwels, C. Bescos, I. Cano, M. Cleries, J.C. Contel, E. de Manuel Keepon, J. García-Aymerich, D. Gomez-Cabreiro, R. García, M.M. Lah, M. Lluch-Ariet, M. Moharra, D. Montaña, J. Morà, M. Nalín, A. Pavlickova, J. Piera, S. Ponc, S. Santacruz, H. Schonenberg, S. Störk, J. Tegnér, F. Velickovic, C. Westerterp, J. Roca
BMJ Open, 6, Issue 4, 2016
Keywords: Animal experiment; Information processing; Morbidity; Population model; Prediction; Risk assessment; Scotland; Stratification; Telemedicine

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J. Olszak, N. Kiani, H. Zenil, J. Tegnér
Proceedings - 11th International Conference on Signal-Image Technology and Internet-Based Systems, SITIS 2015, Article number 7400694, Pages 468–473, 2016
Keywords: Evaluating measure; Inference methods evaluation; Network reconstruction; Topological properties

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Mathematical modeling and simulation

Theory for complex systems

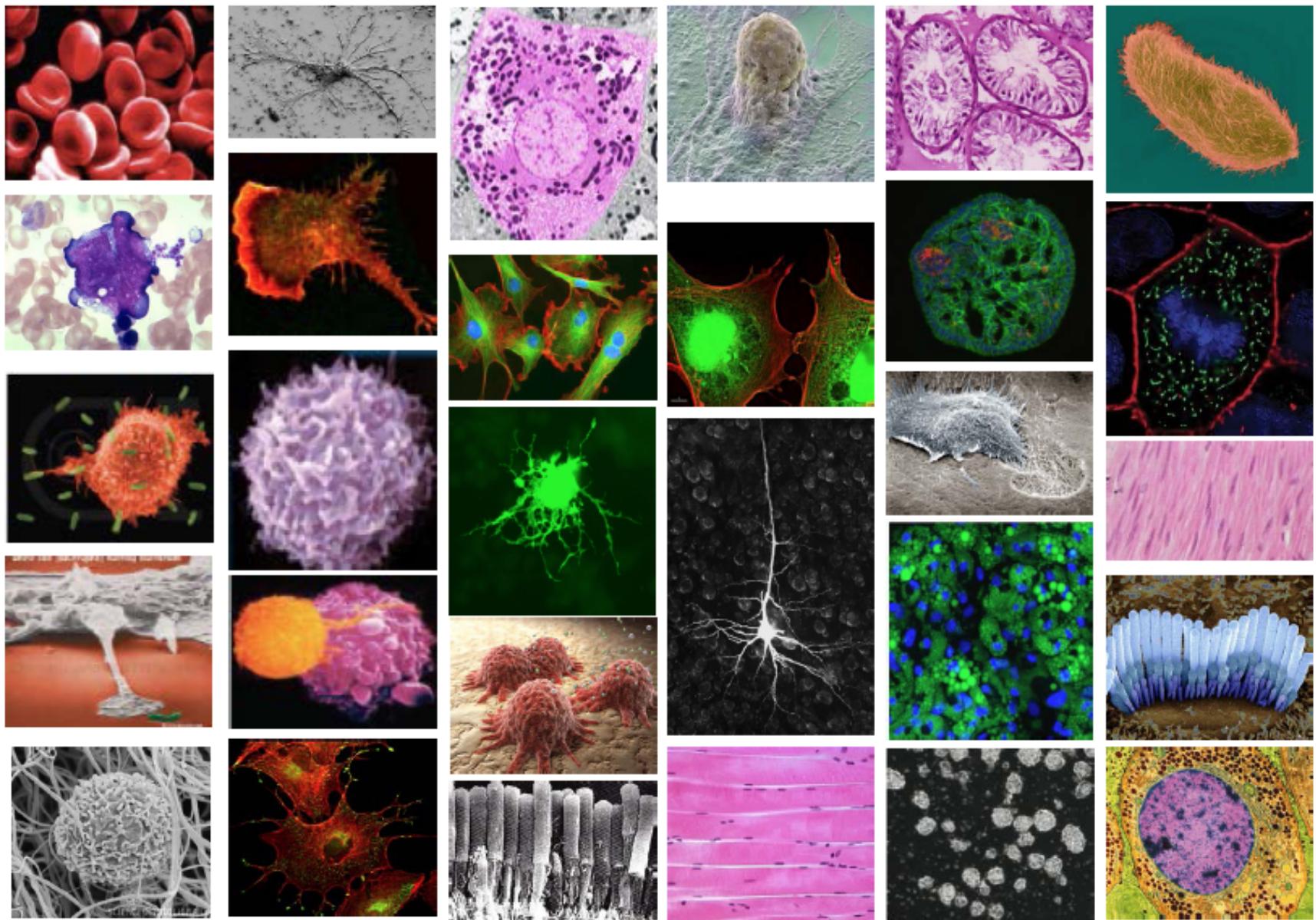
Bioinformatics algorithms and R packages

Personalized medicine & biomarkers

Cellular differentiation

Network analysis of cells, diseases, and health care data

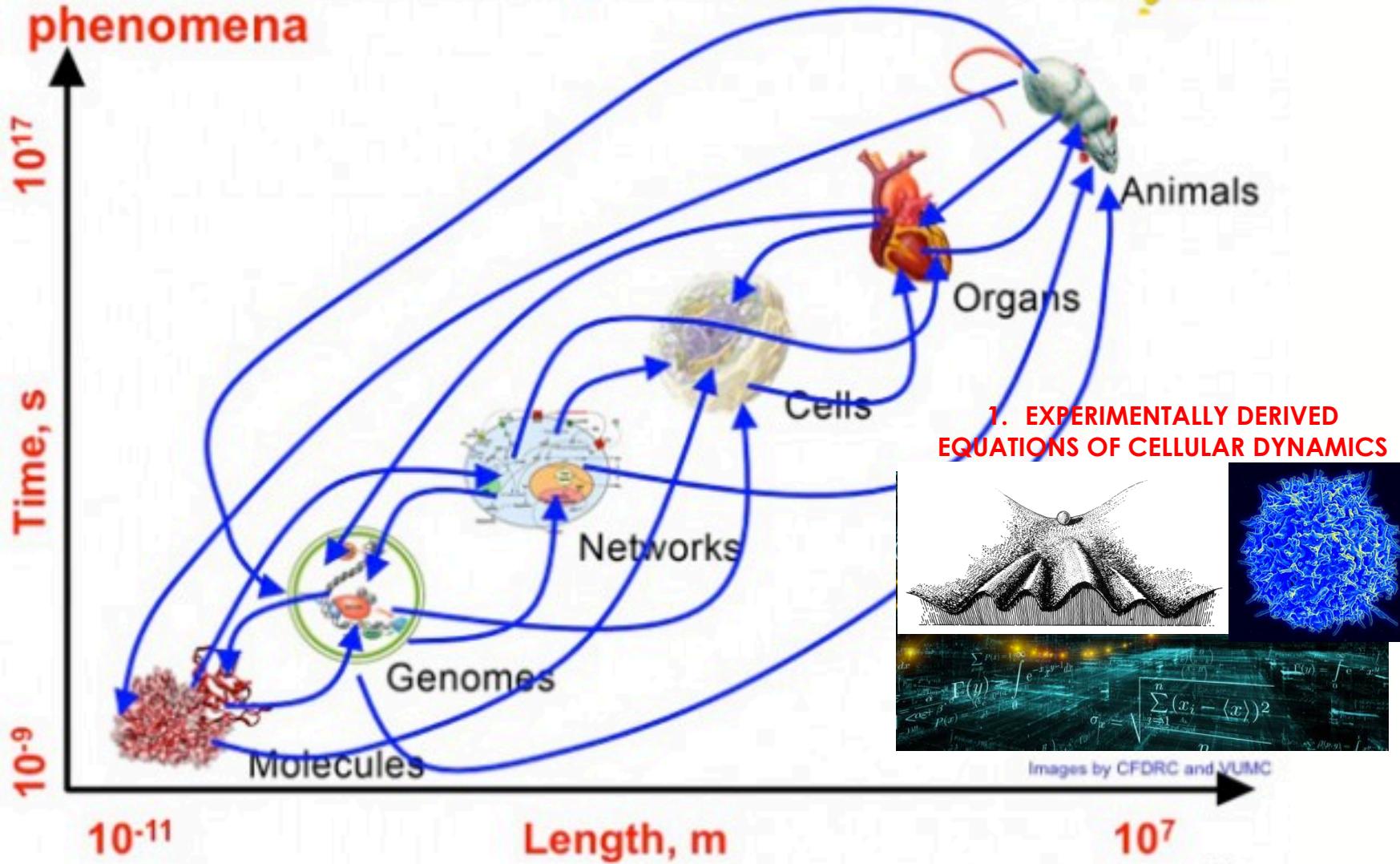
The Enigma -- Same DNA, Diversity of Cells



Cells – “Atoms” of Life

Multiscale interactions produce emergent phenomena

VI¹BRE





Professor Jesper Tegner

Living Systems Laboratory

<https://livingsystems.kaust.edu.sa/Pages/Home.aspx>

In our laboratory we mainly perform single cell genomics analysis of cells. We use cell culture experiments, and RNA expression analysis. RNAseq, ATACseq, proteomics, and PCR techniques are examples of techniques used. This analysis, generating and reading parts of living cells, is coupled with perturbations such as shRNAi, CRISPR/cas9, and live cell imaging for monitoring. To make sense of this we develop and use bioinformatics analysis, mathematical modeling, theory, construction of databases, and design of software (R-scripts, GitHub). We use cell-lines, primary cell, and clinical samples.

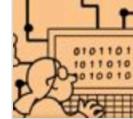
PROJECTS:

- Single cell genomics (profiling, analysis) applied to clinical samples & questions
- Melanoma (PBMC, responders/non-responders)
- Multiple sclerosis (disease vs control; CSF, RNA & TCR, PBMC)
- Alzheimer (Microglia, inflammasome mechanisms)
- Identification of single cell networks using single cell genomics (scRNAseq & scATACseq & Deep Imaging) and bioinformatics
- Human stem cells
- Development of bioinformatics tools for single cell biology

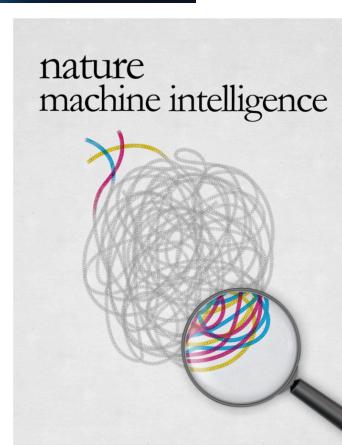
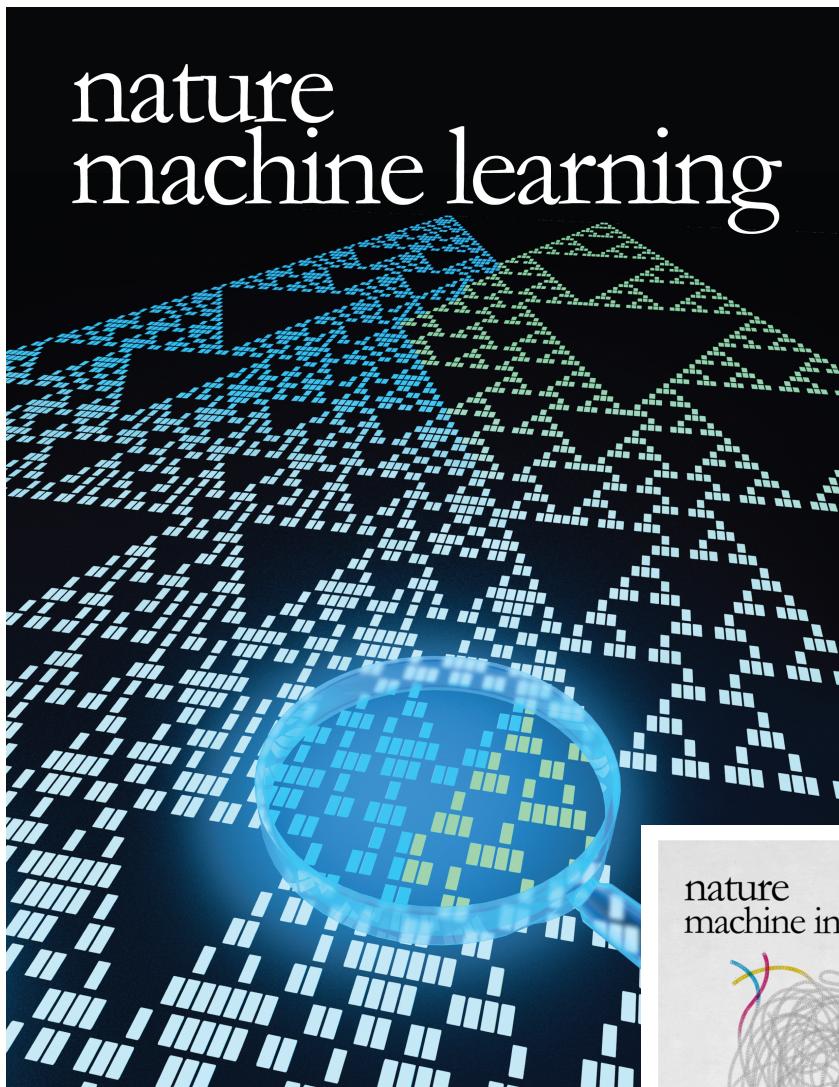
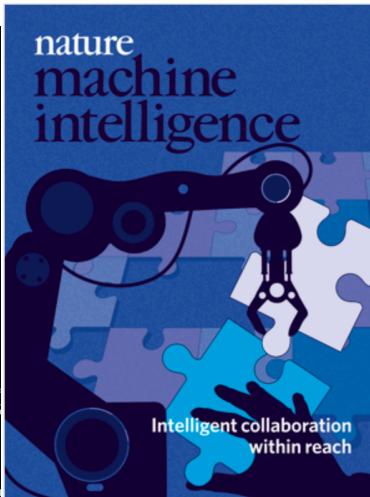
INTERESTED CANDIDATES CAN CONTACT: jesper.tegner@kaust.edu.sa

Announcement

VIDEO Remodelling machine learning: An AI that thinks like a scientist

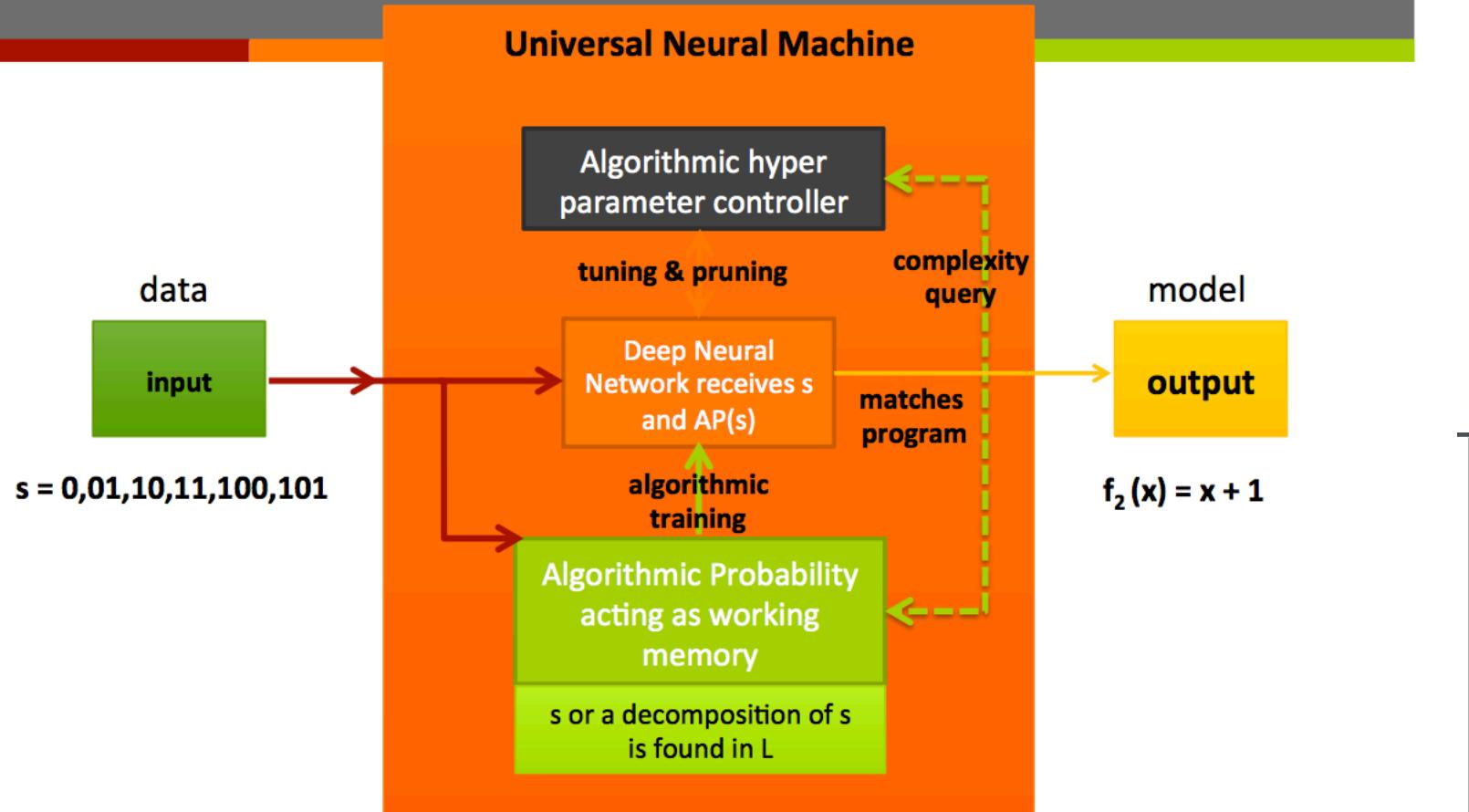


Modern machine learning is great for helping scientists sort through huge, unwieldy data sets. But it's less useful for things requiring inference or reasoning – both vital to the scientific process. One group of scientists are now trying to fix this problem with a completely new kind of machine learning. This new approach aims to find the underlying algorithmic models that interact and generate data, to help scientists uncover the dynamics of cause and effect. This could aid researchers across a huge range of scientific fields, such as cell biology and genetics, answering the kind of questions that typical machine learning is not designed for. [show less](#)



H. Zenil, N.A. Kiani, A. Zea, J. Tegnér, Causal Deconvolution by Algorithmic Generative Models
Nature Machine Intelligence, vol 1(1), pp 58-66, 2019.

Algorithmic Machine Learning

s =

H. Zenil, N.A. Kiani, A. Zea, J. Tegnér, Causal Deconvolution by Algorithmic Generative Models
Nature Machine Intelligence, vol 1(1), pp 58-66, 2019.

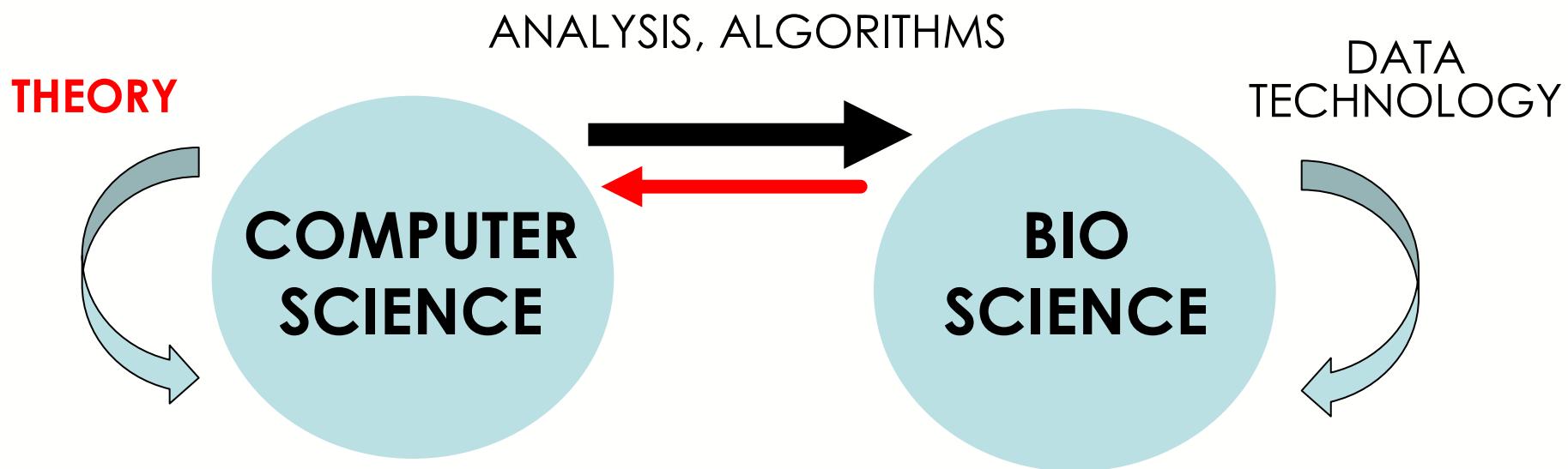
The aim is to support the development of bilingual students. Either coming from a bioscience or computer science background, thus having a firm ground in his/her area of expertise the student will develop a practical and conceptual language supporting the student with a working knowledge to be able to communicate and collaborate effectively with experts trained outside his/her domain of expertise. From the standpoint of biology, the course addresses the analysis of complex biological systems at different scales, ranging from molecules, cells, organs, to organisms. The computer scientist/data scientist will acquire a working knowledge on which techniques from machine learning, network theory, modelling, and statistics are useful and how to apply them in the analysis of biological systems also in the context of drug development and biomedicine. The biologist is provided with concepts and practical tools how to advance from data to information about significant correlated features hidden in the data and advancing to insights into biological mechanisms.

Course Description from Program Guide

The Course provides a broad and practical overview of selected techniques and concepts in rapidly developing areas such as bioinformatics, computational biology, systems biology, systems medicine, network biology, synthetic biology, data analytics, predictive modelling, machine learning, and machine intelligence. Topics are selected to be of relevance for the computer scientist, working biologist, computational scientist, and applied investigator (Biotechnology and engineering).

The aim is to support the development of bilingual students. Either coming from a bioscience or computer science background, thus having a firm ground in his/her area of expertise the student will develop a practical and conceptual language supporting the student with a working knowledge to be able to communicate and collaborate effectively with experts trained outside his/her domain of expertise. From the standpoint of biology, the course addresses the analysis of complex biological systems at different scales, ranging from molecules, cells, organs, to organisms. The computer scientist/data scientist will acquire a working knowledge on which techniques from machine learning, network theory, modelling, and statistics are useful and how to apply them in the analysis of biological systems also in the context of drug development and biomedicine. The biologist is provided with concepts and practical tools how to advance from data to information about significant correlated features hidden in the data and advancing to insights into biological mechanisms.

Birds eye view



Bioinformatics, Computational
Biology, Systems Biology, Data
Science, Biostatistics, Network
Medicine, Machine Learning,
Personalized Medicine,
Precision Medicine, Predictive
Health, Artificial Intelligence

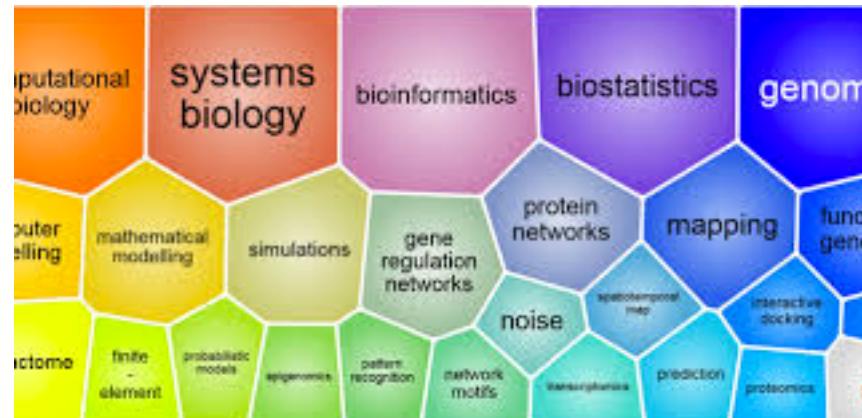
Bioinformatics

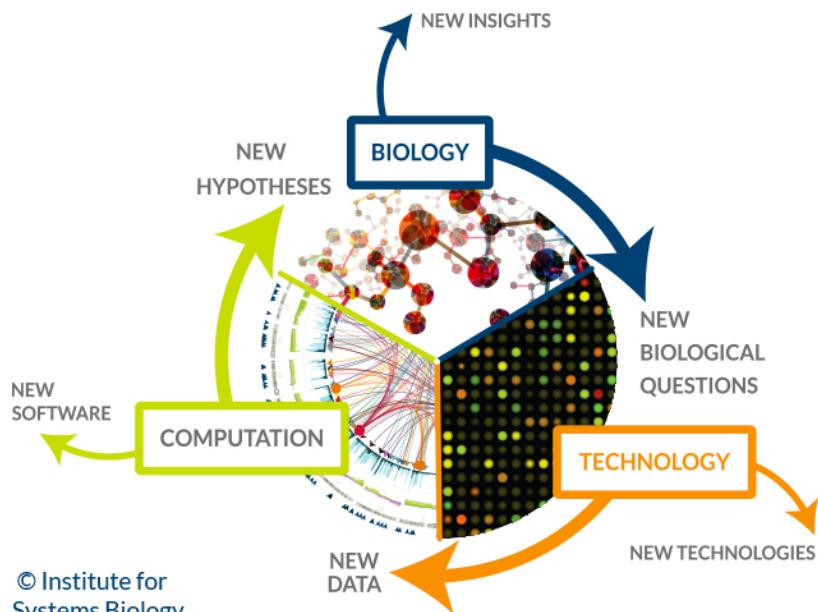
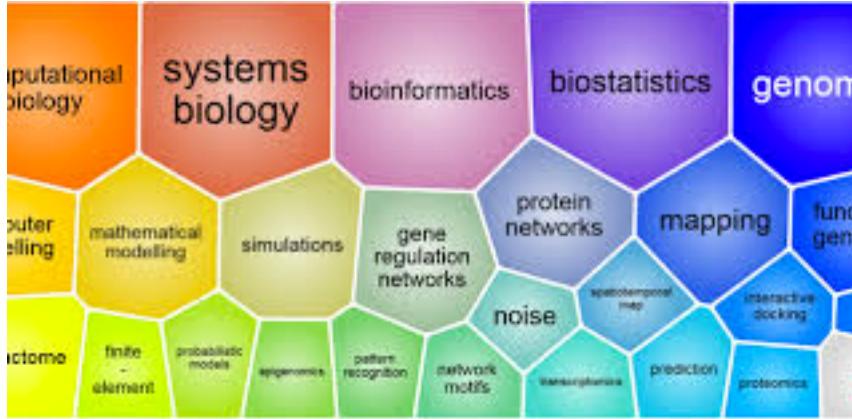


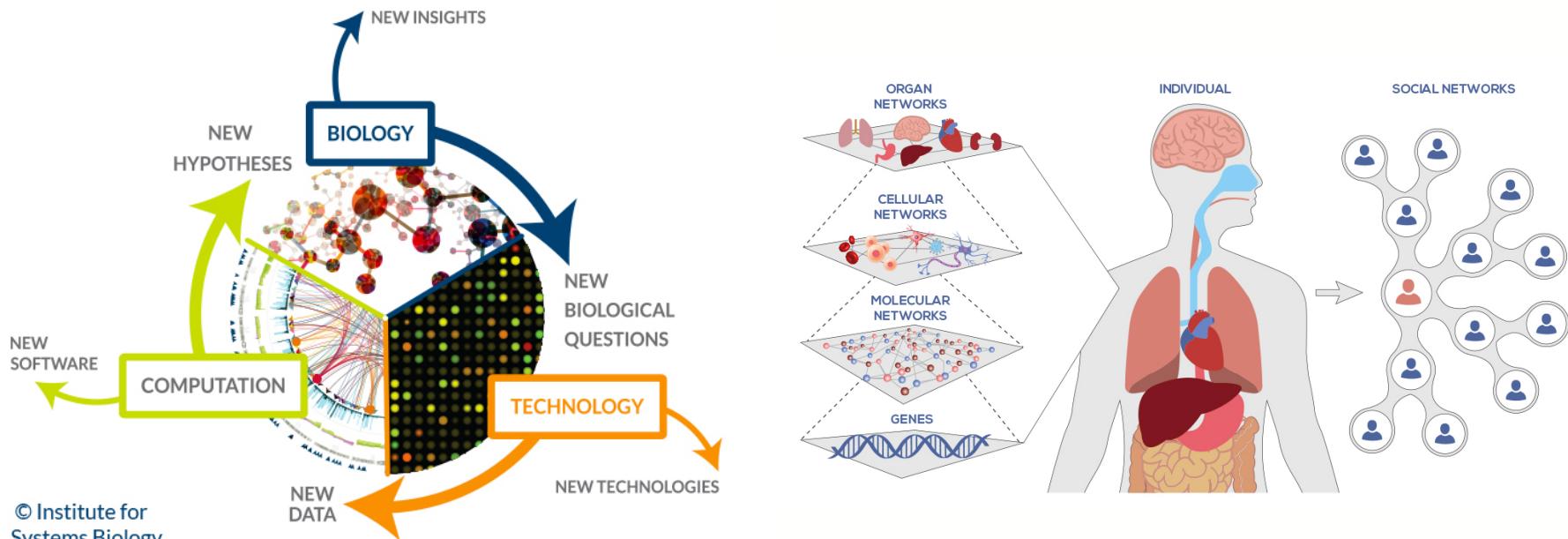
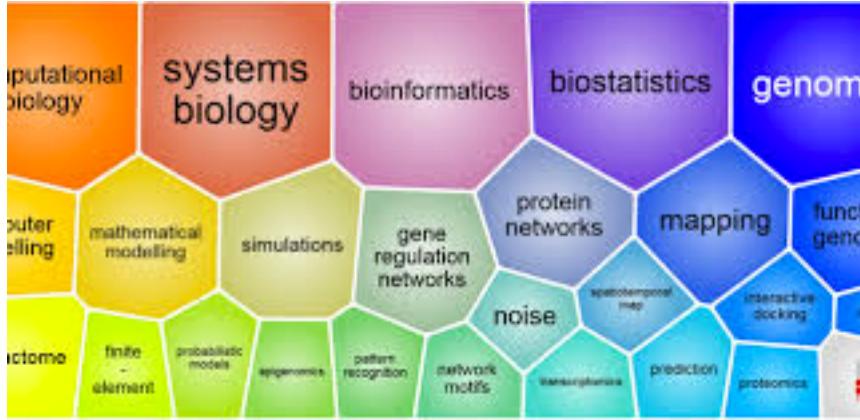
Data Science



Bioinformatics	Systems Biology	Computational Biology
Only computational	Both dry lab and wet lab	Only computational
Data Analysis of biological data	Modelling biological processes at system level: entire genome, transcriptome, or organism level.	Mechanistic understanding of part or whole of a biological process.
Provides answers by statistical inferences	Provides answer by whole cell modelling and linear optimizations.	Provides answer by modelling processes via ordinary or partial differential equations.



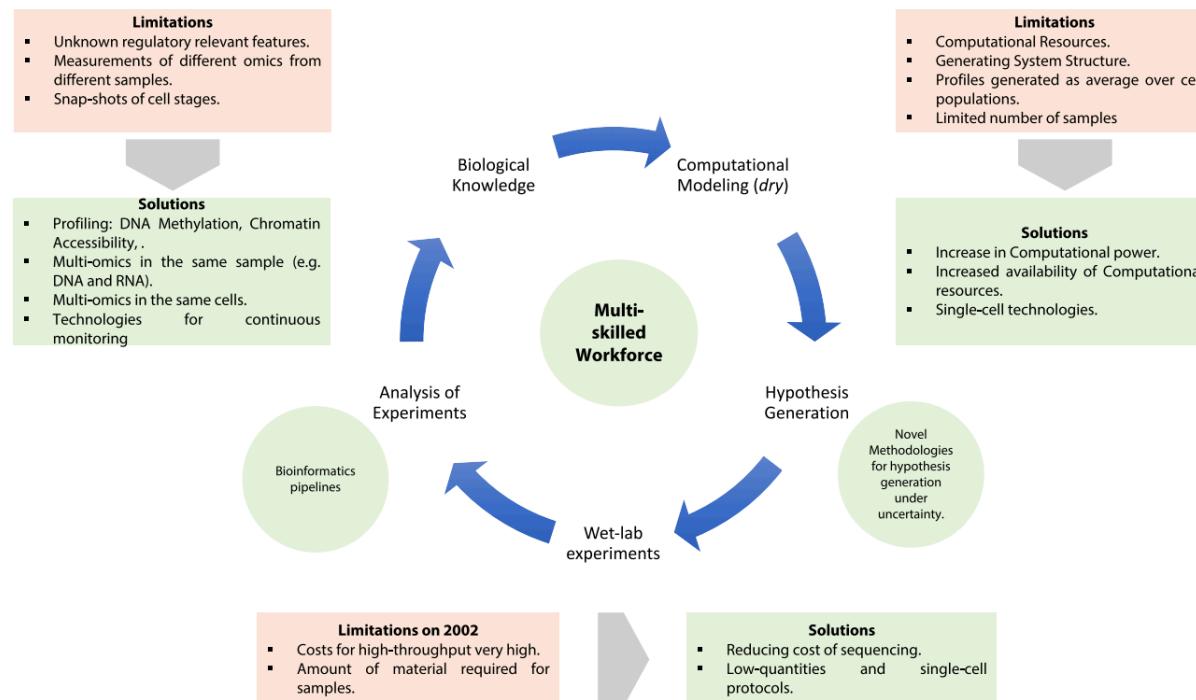




Iterative Systems Biology for Medicine – Time for advancing from network signatures to mechanistic equations

David Gomez-Cabrero^{a,b,c,d,e,f,1} and Jesper Tegnér^{a,b,c,d,g,1}

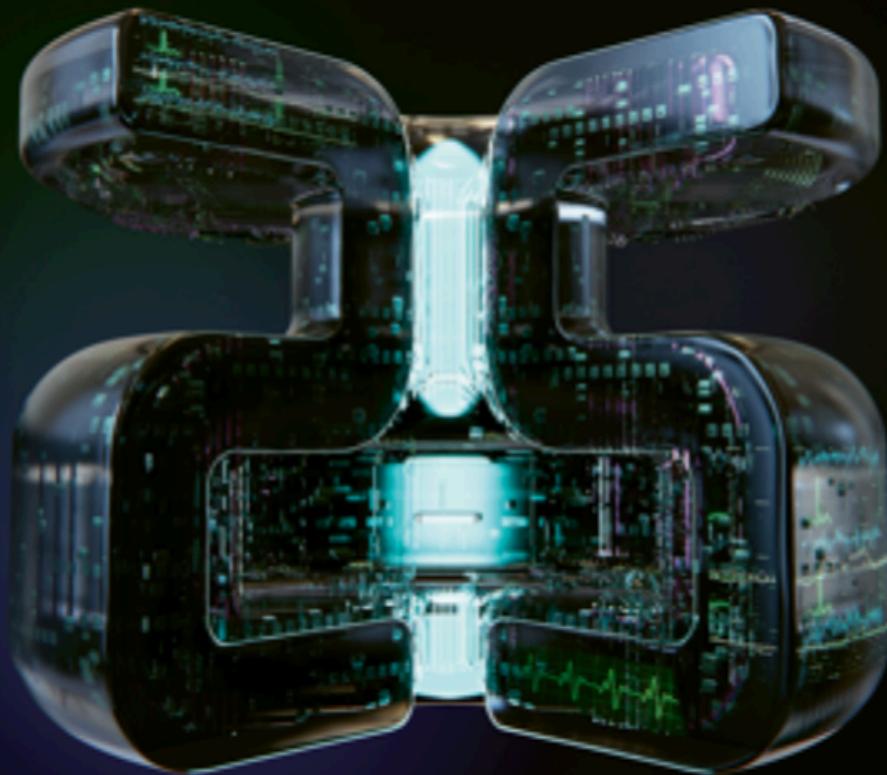
Figure 1



Reviewing hypothesis-driven research in Systems Biology. The inner circle reproduces Kitano's classical Iterative System Biology workflow. The outer boxes denote gaps and current advances and tools mitigating those gaps.

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Medicine in the Digital Age

High-performance medicine: the convergence of human and artificial intelligence

Eric J. Topol 

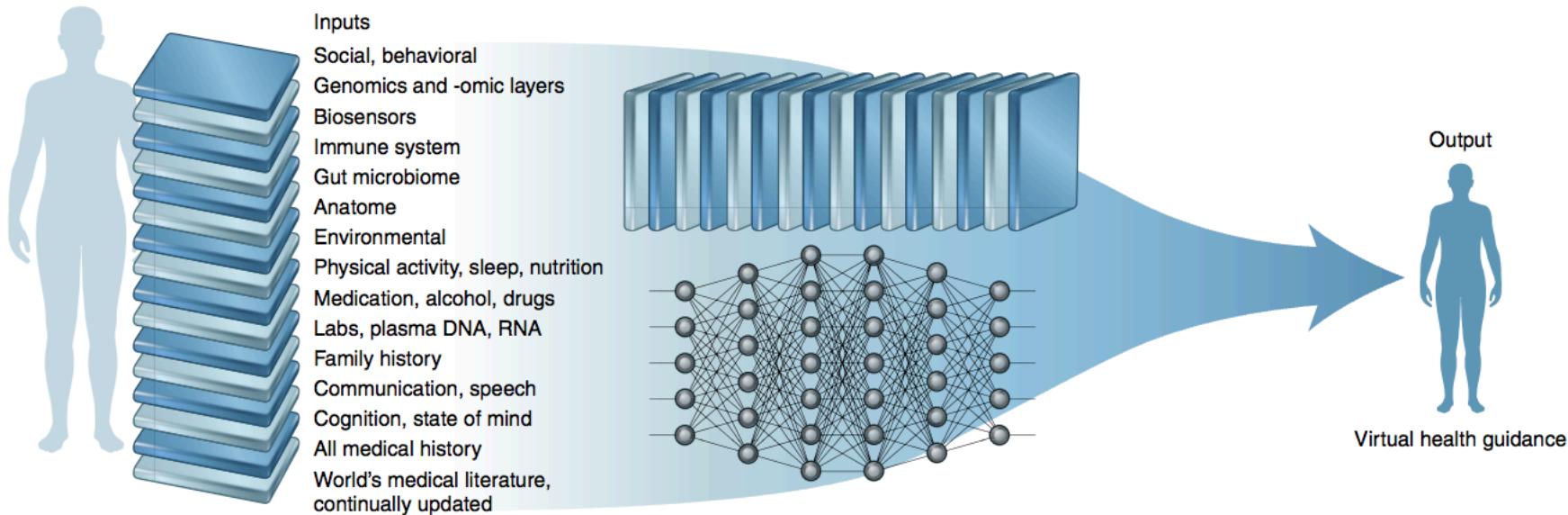
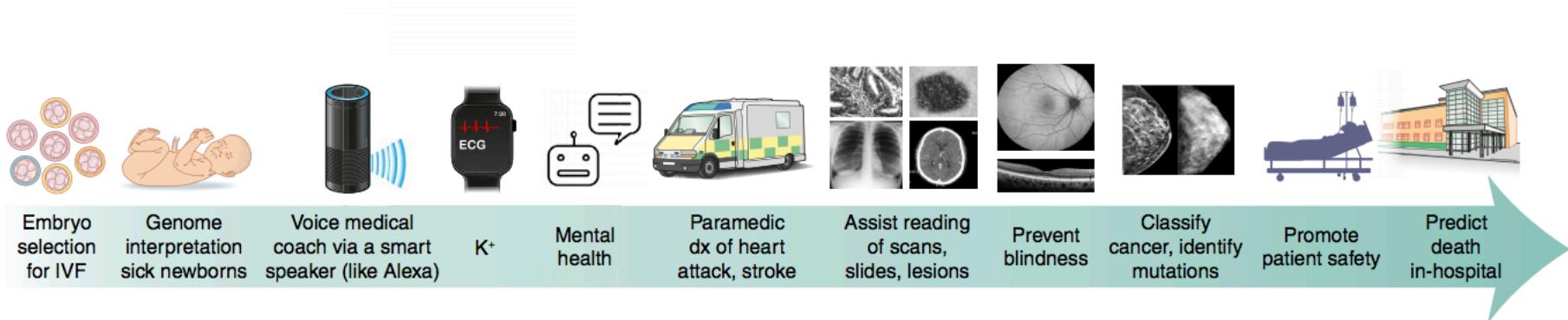


Fig. 3 | The virtual medical coach model with multi-modal data inputs and algorithms to provide individualized guidance. A virtual medical coach that uses comprehensive input from an individual that is deep learned to provide recommendations for preserving the person's health. Credit: Debbie Maizels/ Springer Nature

High-performance medicine: the convergence of human and artificial intelligence

Eric J. Topol 



Bioinformatics, Computational
Biology, Systems Biology, Data
Science, Biostatistics, Network
Medicine, Machine Learning,
Personalized Medicine,
Precision Medicine, Predictive
Health, Artificial Intelligence

Historical Overview and Conceptual Positioning. Major events in Biology, Genomics, and Computing: Turing, the Action Potential, Neumann, DNA, Cybernetics, Different modes of Computing, rise of Molecular Biology, Complex Systems, sequencing of the Human Genome, sequence based technology explosion and production of multiple data-types, Systems Biology, high-performance Computing, CRISP/CAS editing, Synthetic Biology, machine intelligence.

(1) Genomes, Transcriptomes and Epigenomes. Genome Alignment, Bioinformatics data processing and pipelines for RNA-seq, DNA methylation, microRNA, ATAC-seq, and Chip-Seq. The lectures cover the conceptual steps in data-processing as well as their respective practical implementation. This type of analysis ends with clean, normalized, and statistical relevant data. (*From Data to Information/Signals*)

(2) Bioinformatics downstream analysis. This includes differential analysis (time, samples), enrichment, pathways, clustering and PCA. Illustrated using transcriptomics and epigenomics. (*From Information to Knowledge/biological insight*).

(3) Overview of Available Databases, Resources, and Software. Alignment tools, Bioconductor, Github, IPA, STRING, cytoscape, NAR databases, tools, and software, Google Scholar. (*Practical Resources*)

(4) Transcriptional Networks. Definition, how to find them (prior knowledge, reverse-engineering), how to analyse them (network analysis), using case studies including E-Coli, Yeast, Cell lines, and primary cells. (*Beyond lists of molecular entities*)

(5) Metabolic Modelling, Analysis and Protein Bioinformatics and Analysis. Metabolite and protein networks/charts, protein sequences and 3D structure, network analysis, pathways, modelling and flux analysis. (*Interface between the inside and outside of cells*)

(6) Data Science - Concepts, Ideas, and Tools. Multiple testing, cross validation, bootstrapping, normalization, uni/multi variate statistics, networks, supervised and unsupervised learning, Dimension reduction, clustering techniques, PCA, SVM, ICA, MDS, and tSNE. (*Conceptual Resources and Challenges*)

(7) Machine Learning, Mathematical Modelling, Computing, and Artificial Intelligence – Genomics, Biomedicine, and Health Care. Motivation, models, inverse problems, forward simulation models, ODE/Boolean models, dynamical systems, and uncertainty. Machine Learning & Deep Neural Networks. (*From Associations to Causality*)

(8) Single Cell Biology. The emerging field of single cell genomics, single cell sequencing (sc-seq), scRNASeq, CyTof, scATACseq, and analytics of data. (*Towards precision biology and data-driven predictive analytics*)

Summary and Outlook. Summary of current and emerging concepts and trends. Data to Models, Data Integration, Multi-scale Biology, Biomedical and Industrial applications, Synthetic Biology, and Artificial Intelligence.

Some Example areas/systems/topics from which we will select a few during the relevant course modules to illustrate the use of integrative systems analysis, bioinformatics, and machine learning. Development Biology (Sea Urchin, Davidson), Eukaryotic Cell Cycle (Tyson/Novak), Action Potential (Hodgkin/Huxley), C-Elegance, Genomic Circuits in Stem Cells, Systems Immunology, Systems Medicine (P4 Medicine), Drug Development, Multi-scale Heart Modelling (Noble, VPH). Deep Learning for genomics and health care, AI in Medicine (*Real world examples and research programmes*)

There will be 3 topics that will be augmented with practical computer exercises. These are (a) genome alignment, (b) analysis of transcriptional (RNAseq) data, and (c) single cell genomics.



Manjula Thimma, PhD

Research Scientists

Research Interests

Dr. Manjula is bioinformatician analyzing epigenetic datasets generated by next generation sequencing technologies. Denovo genome sequencing, structural variation studies, Transcriptomic analysis, RNAi component's study and ChIP-Seq binding of Ago1 and Dicer1 are some of the project where she is involved. Majority of the projects are to understand the role retrotransposons in cell identity, reprogramming and differentiation.

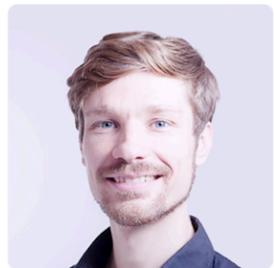
Selected Publications

Genome-wide expression analysis offers new insights into the origin and evolution of *Physcomitrella patens* stress response

Khraiwesh B., Qudeimat E., Thimma M., Chaiboonchoe A., Jijakli K., Alzahmi A., Arnoux M., Salehi-Ashtiani K.
Sci Rep. 2015 Nov 30;5:17434. doi: 10.1038/srep17434

Carotenoid metabolic profiling and transcriptome-genome mining reveal functional equivalence among blue-pigmented copepods and appendicularia

Mojib N., Amad M., Thimma M., Aldanondo N., Kumaran M., Irigoien X.
Mol Ecol. 2014 Jun;23(11):2740-56. doi: 10.1111/mec.12781



Robert Lehmann, PhD

Research Scientists

Research Interests

Dr. Lehmann is trained in bioinformatics and computational biology with a particular focus on understanding the mechanisms and impact of transcriptional control. His current research focuses data integration to gain insights into genetic responses to stress in marine organisms. Dr. Lehmann is using genomic, transcriptomic, and epigenomic approaches to understand the genetic response of marine organisms to the environmental changes caused by the global climate change.

Selected Publications

Finding Nemo's Genes: A chromosome-scale reference assembly of the genome of the orange clownfish *Amphiprion percula*

R. Lehmann, D.J. Lightfoot, C. Schunter, C.T. Michell, H. Ohyanagi, K. Mineta, S. Foret, M.L. Berumen, D.J. Miller, M. Aranda, T. Gojobori, P.L. Munday, T. Ravasi

Molecular ecology resources, 2018;00:1–16, 2018

Minimal tool set for a prokaryotic circadian clock

N. Schelling, A. Wiegard, R. Lehmann, P. Chaudhury, C. Beck, S.V. Albers, I.M. Axmann BMC Evol Biology, 2017

In practice

- Lectures
 - Hands on computer exercises – 3 topics
 - mid-term exam 21 march
 - May exam – covering second half of the course May 23d
-
- **Grades:**
 - 1/3 exercises
 - 1/3 mid term
 - 1/3 second exam
-
- Exam – mix of multiple choice, short questions, and one or few one-two paragraph questions

2 classes. (Jesper)

28/1 31/1

Historical Overview and Conceptual Positioning. Major events in Biology, Genomics, and Computing: Turing, the Action Potential, Neumann, DNA, Cybernetics, Different modes of Computing, rise of Molecular Biology, Complex Systems, sequencing of the Human Genome, sequence based technology explosion and production of multiple data-types, Systems Biology, high-performance Computing, CRISP/CAS editing, Synthetic Biology, machine intelligence.

4 + 4 classes. (Jesper first overview class, 4feb, then Manjula + Robert)

4/2

7/2

11/2

14/2

18/2

21/2

25/2

28/2

(1) Genomes, Transcriptomes and Epigenomes. Genome Alignment, Bioinformatics data processing and pipelines for RNA-seq, DNA methylation, microRNA, ATAC-seq, and Chip-Seq. The lectures cover the conceptual steps in data-processing as well as their respective practical implementation. This type of analysis ends with clean, normalized, and statistical relevant data. (*From Data to Information/Signals*)

Computer Exercises: Three topics for practical sessions - running scripts, evaluate results. The topics are (a) how to perform genome alignment, (b) how to analyse transcriptional (RNAseq) data using a pipeline of scripts and steps





KAUST Research Conference: **Artificial Intelligence in Medicine**

This event is organized by CBRC with financial support from the KAUST Office of Sponsored Research

Agenda

This agenda is not final and is subject to change.

Day 1

Monday, February 18th

Day 2

Tuesday, February 19th

Day 3

Wednesday, February 20th

2 + 2 classes. (Jesper)

4/3

7/3

11/3

14/3

(2) Bioinformatics downstream analysis. This includes differential analysis (time, samples), enrichment, pathways, clustering and PCA. Illustrated using transcriptomics and epigenomics. (*From Information to Knowledge/biological insight*).

(3) Overview of Available Databases, Resources, and Software. Alignment tools, Bioconductor, Github, IPA, STRING, cytoscape, NAR databases, tools, and software, Google Scholar. (*Practical Resources*)

MidTermExam

18/3 (study) 21/3 (mid-term-exam)

2 classes (jesper)

1/4

4/4

(4) Transcriptional Networks. Definition, how to find them (prior knowledge, reverse-engineering), how to analyse them (network analysis), using case studies including E-Coli, Yeast, Cell lines, and primary cells. (*Beyond lists of molecular entities*)

(5) Metabolic Modelling, Analysis and Protein Bioinformatics and Analysis. Metabolite and protein networks/charts, protein sequences and 3D structure, network analysis, pathways, modelling and flux analysis. (*Interface between the inside and outside of cells*)

1 class (jesper)

15/4

Some Example areas/systems/topics from which we will select a few during the relevant course modules to illustrate the use of integrative systems analysis, bioinformatics, and machine learning. Development Biology (Sea Urchin, Davidson), Eukaryotic Cell Cycle (Tyson/Novak), Action Potential (Hodgkin/Huxley), C-Elegance, Genomic Circuits in Stem Cells, Systems Immunology, Systems Medicine (P4 Medicine), Drug Development, Multi-scale Heart Modelling (Noble, VPH). Deep Learning for genomics and health care, AI in Medicine (*Real world examples and research programmes*)

2 classes (jesper)

18/4 22/4

(6) Data Science - Concepts, Ideas, and Tools. Multiple testing, cross validation, bootstrapping, normalization, uni/multi variate statistics, networks, supervised and unsupervised learning, Dimension reduction, clustering techniques, PCA, SVM, ICA, MDS, and tSNE. (*Conceptual Resources and Challenges*)

2 + 2 classes (jesper + manjula)

25/4 29/4 2/5 6/5

(8) Single Cell Biology. The emerging field of single cell genomics, single cell sequencing (sc-seq), scRNAseq, CyTof, scATACseq, and analytics of data. (*Towards precision biology and data-driven predictive analytics*)

Computer Exercises: (c) Single Cell Genomics – dropouts, normalization, and tSNE plots.

2 classes (jesper)

9/5

13/5

(7) Machine Learning, Mathematical Modelling, Computing, and Artificial Intelligence – Genomics, Biomedicine, and Health Care. Motivation, models, inverse problems, forward simulation models, ODE/Boolean models, dynamical systems, and uncertainty. Machine Learning & Deep Neural Networks. (*From Associations to Causality*)

1 classes (jesper)

16/5

Summary and Outlook. Summary of current and emerging concepts and trends. Data to Models, Data Integration, Multi-scale Biology, Biomedical and Industrial applications, Synthetic Biology, and Artificial Intelligence.

Exam

23/5

In practice

- **Hands on working knowledge**
- **Learn how to think in different ways about data and research questions**
- **Conceptual orientation of the *landscape***
- *Bioinformatics, Computational Biology, Systems Biology, Data Science, Biostatistics, Network Medicine, Machine Learning, Personalized Medicine, Precision Medicine, Predictive Health, Artificial Intelligence*

The aim is to support the development of bilingual students. Either coming from a bioscience or computer science background, thus having a firm ground in his/her area of expertise the student will develop a practical and conceptual language supporting the student with a working knowledge to be able to communicate and collaborate effectively with experts trained outside his/her domain of expertise. From the standpoint of biology, the course addresses the analysis of complex biological systems at different scales, ranging from molecules, cells, organs, to organisms. The computer scientist/data scientist will acquire a working knowledge on which techniques from machine learning, network theory, modelling, and statistics are useful and how to apply them in the analysis of biological systems also in the context of drug development and biomedicine. The biologist is provided with concepts and practical tools how to advance from data to information about significant correlated features hidden in the data and advancing to insights into