

Assoc.Prof. Dr. Andreas Holzinger

185.A83 Machine Learning for Health Informatics

2020S, VU, 2.0 h, 3.0 ECTS

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Lecture 02 - Week 13

From data to probabilistic information and knowledge

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<https://human-centered.ai/machine-learning-for-health-informatics-class-2020>

- 00 Reflection
- 01 **Data** – the underlying physics of data
- 02 Biomedical data sources – taxonomy of data
- 03 Data integration, mapping, fusion
- 04 **Information** -Theory – Entropy
- 05 **Knowledge** Representation –
Ontologies – Medical Classifications

00 Reflection



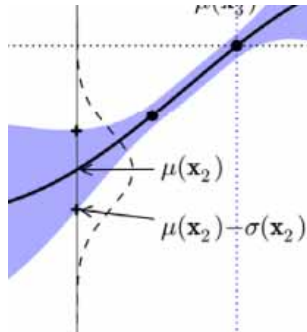
1



2

$$p(\theta|\mathcal{D}) = \frac{p(\mathcal{D}|\theta) * p(\theta)}{p(\mathcal{D})}$$

3



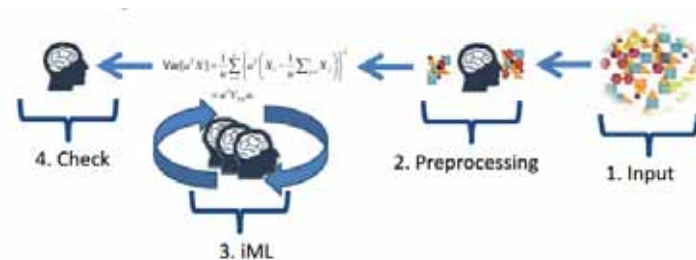
4



5



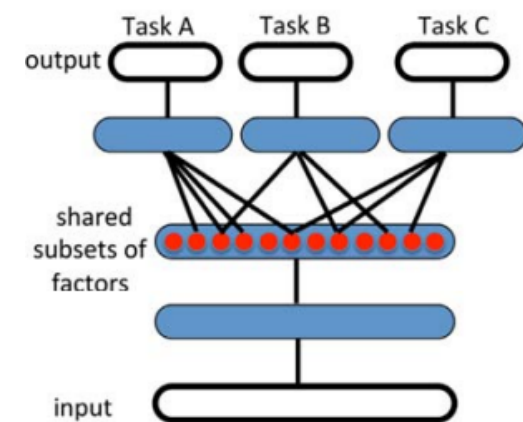
6



7



8



9



Image source: <http://www.efmc.info/medchemwatch-2014-1/lab.php>
This image is used according UrhG §42 lit. f Abs 1 as "Belegfunktion" for discussion with students

Pedro Domingos 2015. The Master Algorithm: How the Quest for the Ultimate Learning Machine Will Remake Our World, Penguin UK.



Image Source: Randall Munroe <https://xkcd.com>

This image is used according UrhG §42 lit. f Abs 1 as "Belegfunktion" for discussion with students

Leo L. Pipino, Yang W. Lee & Richard Y. Wang 2002. Data quality assessment. Communications of the ACM, 45, (4), 211-218.

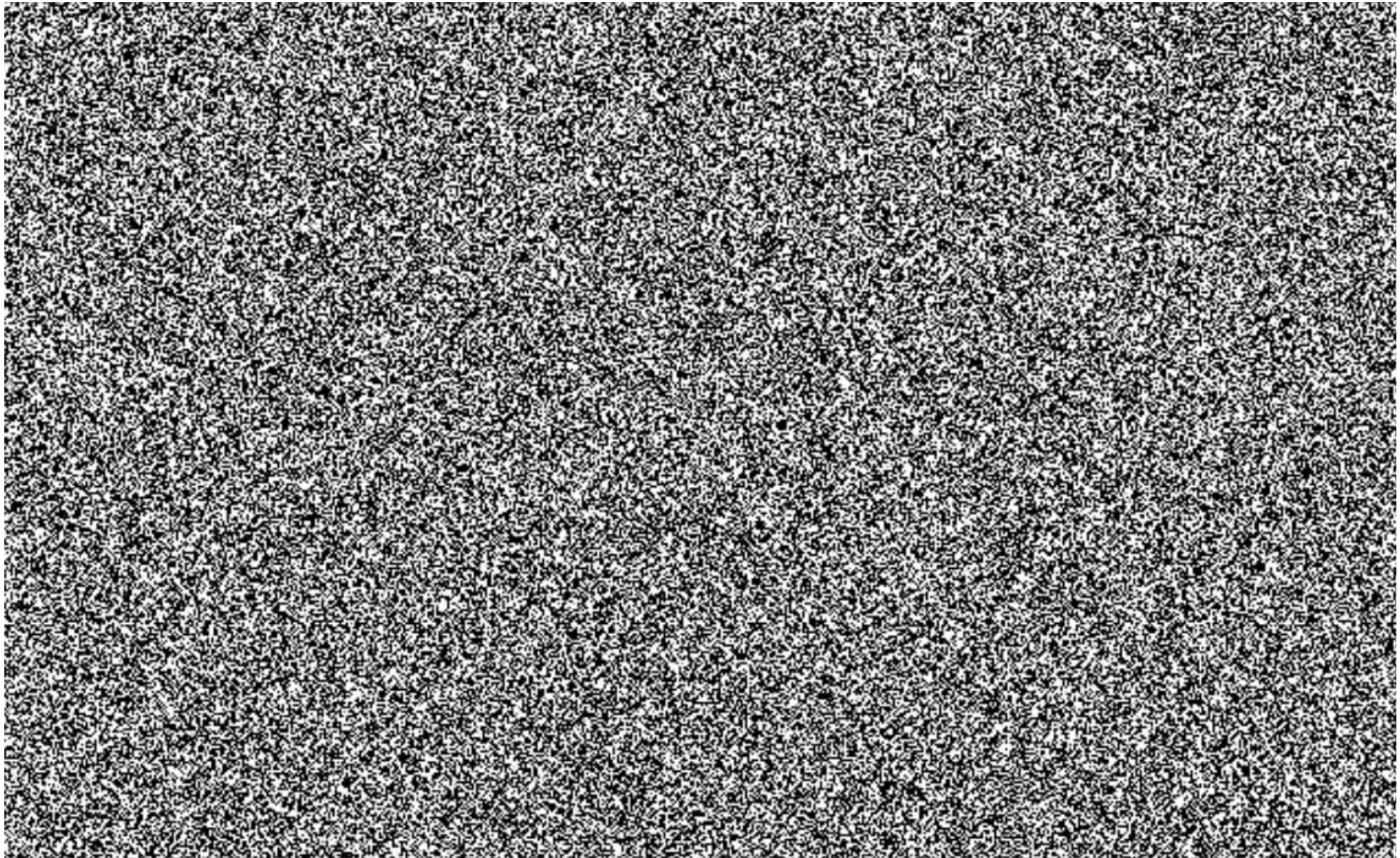
Dimensions	Definitions
Accessibility	the extent to which data is available, or easily and quickly retrievable
Appropriate Amount of Data	the extent to which the volume of data is appropriate for the task at hand
Believability	the extent to which data is regarded as true and credible
Completeness	the extent to which data is not missing and is of sufficient breadth and depth for the task at hand
Concise Representation	the extent to which data is compactly represented
Consistent Representation	the extent to which data is presented in the same format
Ease of Manipulation	the extent to which data is easy to manipulate and apply to different tasks
Free-of-Error	the extent to which data is correct and reliable
Interpretability	the extent to which data is in appropriate languages, symbols, and units, and the definitions are clear
Objectivity	the extent to which data is unbiased, unprejudiced, and impartial
Relevancy	the extent to which data is applicable and helpful for the task at hand
Reputation	the extent to which data is highly regarded in terms of its source or content
Security	the extent to which access to data is restricted appropriately to maintain its security
Timeliness	the extent to which the data is sufficiently up-to-date for the task at hand
Understandability	the extent to which data is easily comprehended
Value-Added	the extent to which data is beneficial and provides advantages from its use

- “The value of data lies in reusability”.
- What are the attributes that make data reusable?
- **Findable:** metadata -persistent identifier
- **Accessible:** retrievable by humans and machines through standards, open and free by default; authentication and authorization where necessary
- **Interoperable:** metadata use a ‘formal, accessible, shared, and broadly applicable language for knowledge representation’.
- **Reusable:** metadata provide rich and accurate information; clear usage license; detailed provenance.

Mark D. Wilkinson, Michel Dumontier, IJsbrand Jan Aalbersberg, Gabrielle Appleton, Myles Axton, Arie Baak, Niklas Blomberg, Jan-Willem Boiten, Luiz Bonino Da Silva Santos, Philip E. Bourne, Jildau Bouwman, Anthony J. Brookes, Tim Clark, Mercè Crosas, Ingrid Dillo, Olivier Dumon, Scott Edmunds, Chris T. Evelo, Richard Finkers, Alejandra Gonzalez-Beltran, Alasdair J. G. Gray, Paul Groth, Carole Goble, Jeffrey S. Grethe, Jaap Heringa, Peter A. C. 'T Hoen, Rob Hooft, Tobias Kuhn, Ruben Kok, Joost Kok, Scott J. Lusher, Maryann E. Martone, Albert Mons, Abel L. Packer, Bengt Persson, Philippe Rocca-Serra, Marco Roos, Rene Van Schaik, Susanna-Assunta Sansone, Erik Schultes, Thierry Sengstag, Ted Slater, George Strawn, Morris A. Swertz, Mark Thompson, Johan Van Der Lei, Erik Van Mulligen, Jan Velterop, Andra Waagmeester, Peter Wittenburg, Katherine Wolstencroft, Jun Zhao & Barend Mons 2016. The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 3, 160018, doi:10.1038/sdata.2016.18.

<https://www.go-fair.org/fair-principles>

01 The underlying physics of data

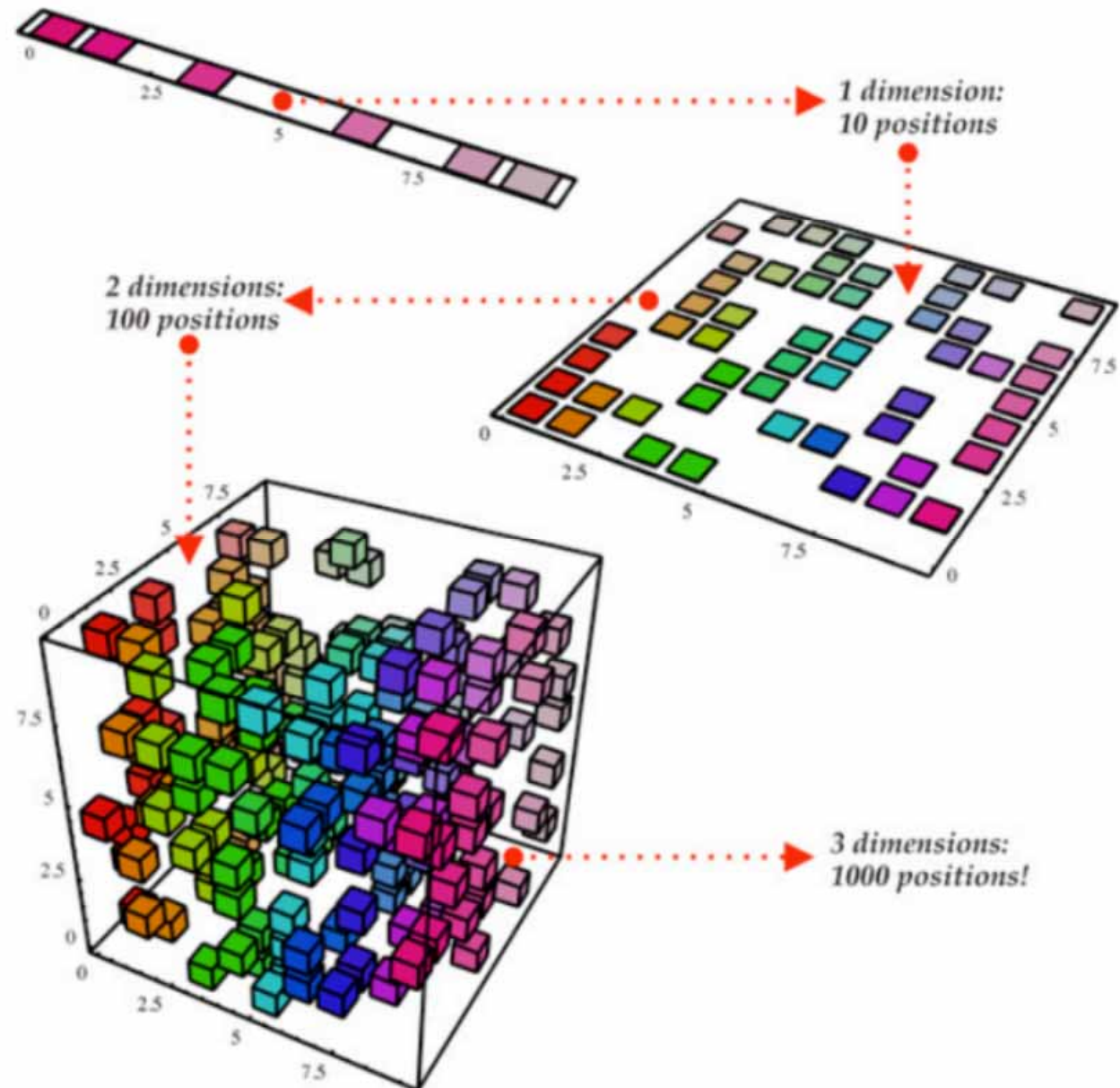


- Heterogeneous, distributed, inconsistent data sources (need for **data integration** & fusion) [1]
- **Complex data** (high-dimensionality – challenge of dimensionality reduction and visualization) [2]
- Noisy, uncertain, missing, dirty, and imprecise, imbalanced data (challenge of **pre-processing**)
- The discrepancy between data-information-knowledge (**various definitions**)
- **Big data** sets in high-dimensions (manual handling of the data is often impossible) [3]

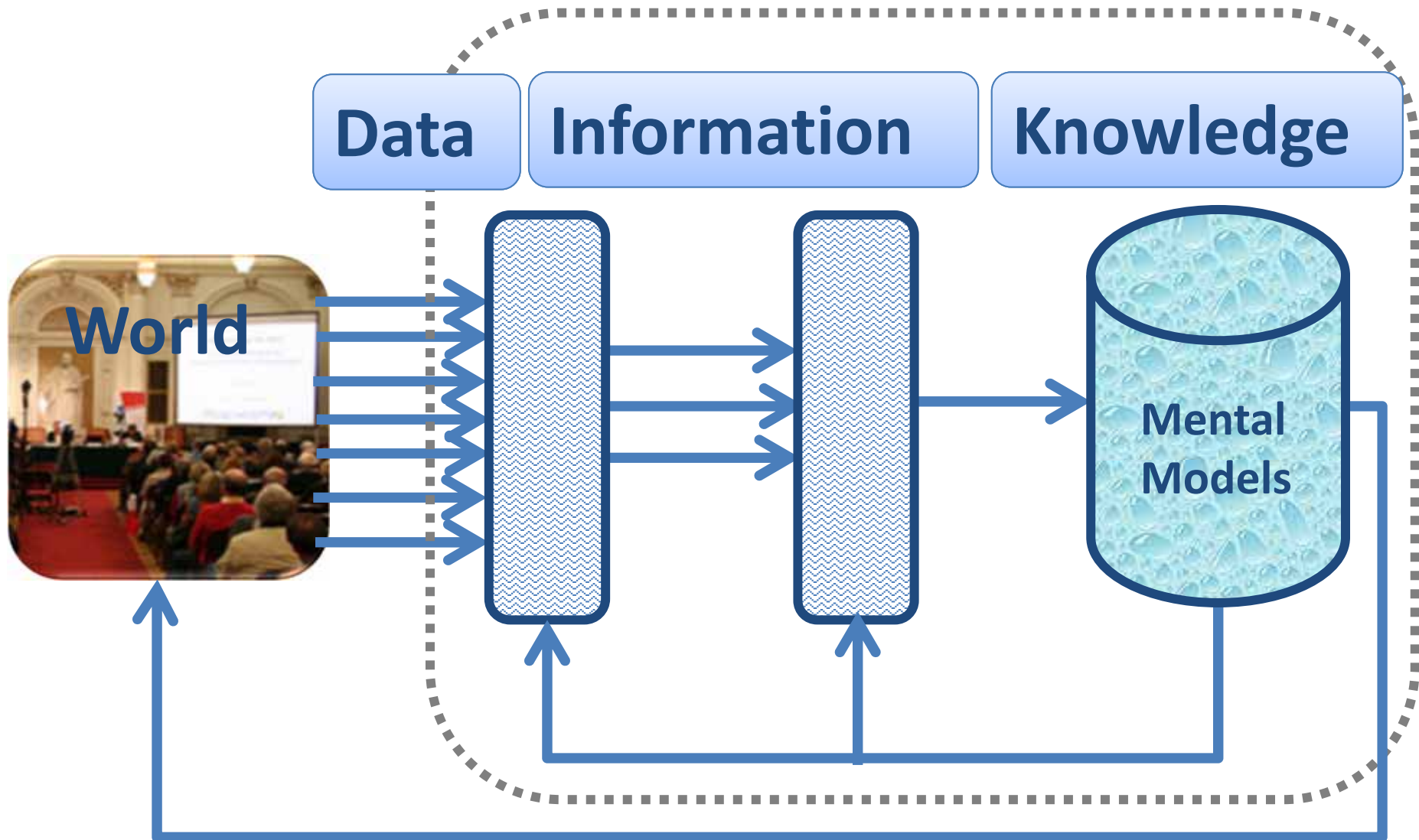
1. Holzinger A, Dehmer M, & Jurisica I (2014) Knowledge Discovery and interactive Data Mining in Bioinformatics - State-of-the-Art, future challenges and research directions. BMC Bioinformatics 15(S6):11.
2. Hund, M., Sturm, W., Schreck, T., Ullrich, T., Keim, D., Majnaric, L. & Holzinger, A. 2015. Analysis of Patient Groups and Immunization Results Based on Subspace Clustering. In: LNAI 9250, 358-368.
3. Holzinger, A., Stocker, C. & Dehmer, M. 2014. Big Complex Biomedical Data: Towards a Taxonomy of Data. in CCIS 455. Springer 3-18.

- Data in traditional Statistics
- Low-dimensional data ($< \mathbb{R}^{100}$)
- Problem: Much noise in the data
- Not much structure in the data but it can be represented by a simple model
- Data in Machine Learning
- High-dimensional data ($>> \mathbb{R}^{100}$)
- Problem: not noise , but complexity
- Much structure, but the structure can **not** be represented by a simple model

Yann LeCun, Yoshua Bengio & Geoffrey Hinton 2015. Deep learning. Nature, 521, (7553), 436-444, doi:10.1038/nature14539



Samy Bengio & Yoshua Bengio
2000. Taking on the curse of
dimensionality in joint
distributions using neural
networks. IEEE Transactions on
Neural Networks, 11, (3), 550-
557, doi:10.1109/72.846725.

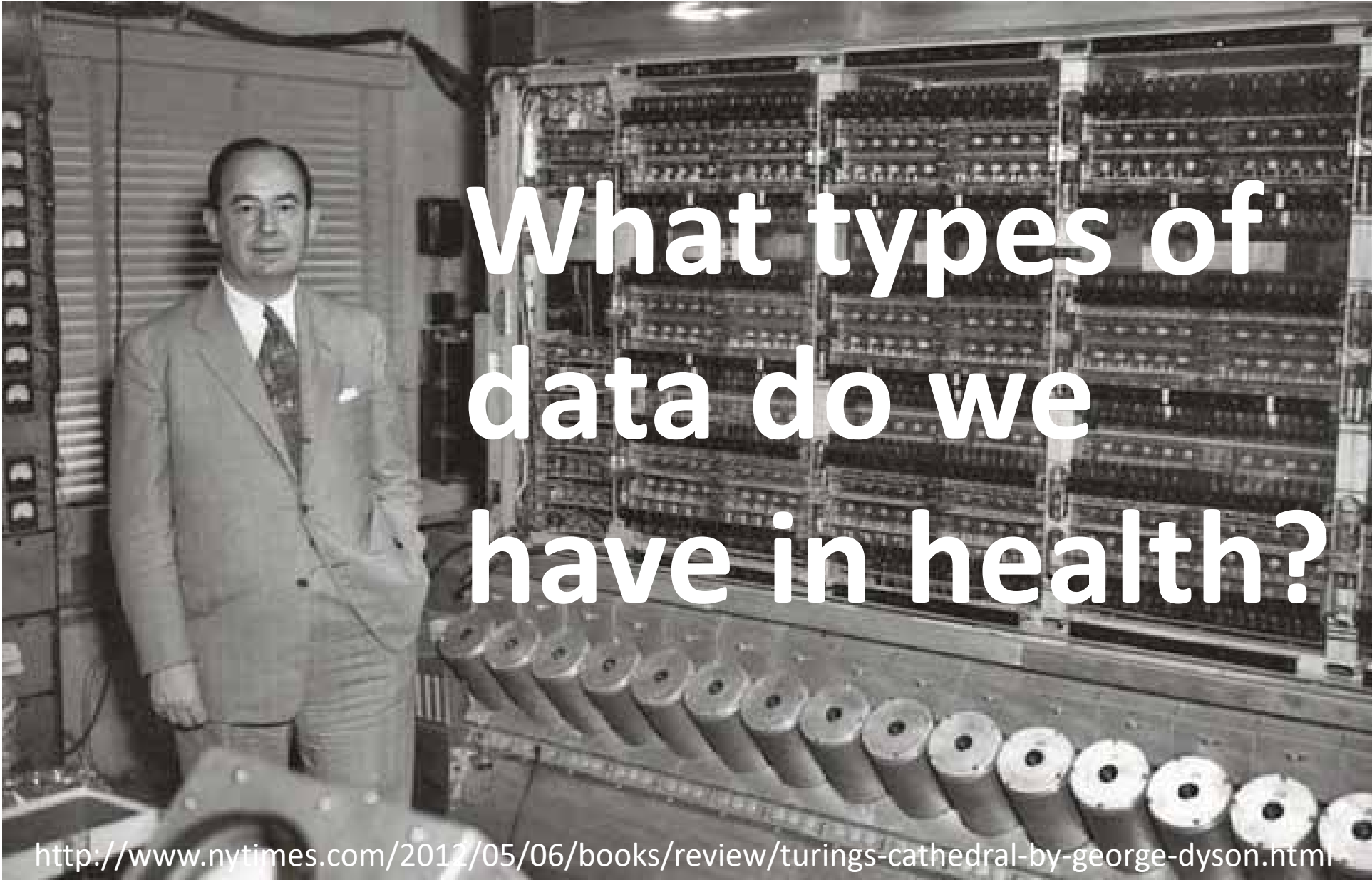


Knowledge := a set of expectations



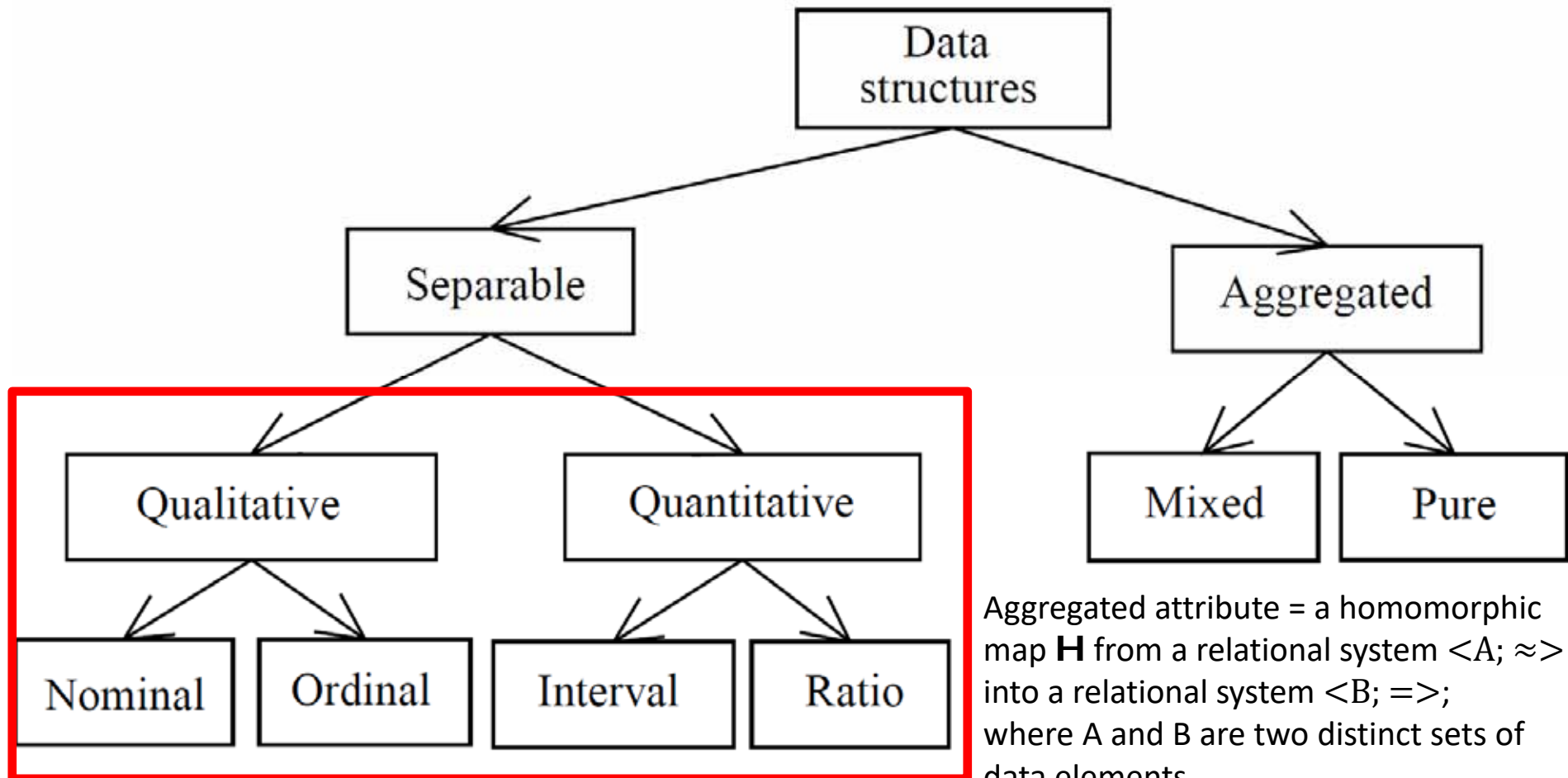
Biomedical informatics (BMI) is the interdisciplinary field that studies and pursues the effective use of biomedical data, information, and knowledge for scientific problem solving, and decision making, motivated by efforts to improve human health

Edward H. Shortliffe 2011. Biomedical Informatics: Defining the Science and its Role in Health Professional Education. In: Holzinger, Andreas & Simon, Klaus-Martin (eds.) Information Quality in e-Health. Lecture Notes in Computer Science LNCS 7058. Heidelberg, New York: Springer, pp. 711-714.



What types of data do we have in health?

<http://www.nytimes.com/2012/05/06/books/review/turings-cathedral-by-george-dyson.html>



Aggregated attribute = a homomorphic map \mathbf{H} from a relational system $\langle A; \approx \rangle$ into a relational system $\langle B; = \rangle$; where A and B are two distinct sets of data elements.

This is in contrast with other attributes since the set B is the set of data elements instead of atomic values.

Dastani, M. (2002) The Role of Visual Perception in Data Visualization. *Journal of Visual Languages and Computing*, 13, 601-622.

SCIENCE

Vol. 103, No. 2684

Friday, June 7, 1946

On the Theory of Scales of Measurement

S. S. Stevens

Director, Psycho-Acoustic Laboratory, Harvard University

Scale	Basic Empirical Operations	Mathematical Group Structure	Permissible Statistics (invariantive)
NOMINAL	Determination of equality	<i>Permutation group</i> $x' = f(x)$ $f(x)$ means any one-to-one substitution	Number of cases Mode Contingency correlation
ORDINAL	Determination of greater or less	<i>Isotonic group</i> $x' = f(x)$ $f(x)$ means any monotonic increasing function	Median Percentiles
INTERVAL	Determination of equality of intervals or differences	<i>General linear group</i> $x' = ax + b$	Mean Standard deviation Rank-order correlation Product-moment correlation
RATIO	Determination of equality of ratios	<i>Similarity group</i> $x' = ax$	Coefficient of variation

Stanley S. Stevens 1946. On the theory of scales of measurement. Science, 103, (2684), 677-680.

Scale	Empirical Operation	Mathem. Group Structure	Transf. in \mathbb{R}	Basic Statistics	Mathematical Operations
NOMINAL	Determination of equality	Permutation $x' = f(x)$ $x \dots 1\text{-to-1}$	$x \mapsto f(x)$	Mode, contingency correlation	$=, \neq$
ORDINAL	Determination of more/less	Isotonic $x' = f(x)$ $x \dots \text{mono-tonic incr.}$	$x \mapsto f(x)$	Median, Percentiles	$=, \neq, >, <$
INTERVAL	Determination of equality of intervals or differences	General linear $x' = ax + b$	$x \mapsto rx + s$	Mean, Std.Dev. Rank-Order Corr., Prod.-Moment Corr.	$=, \neq, >, <, -, +$
RATIO	Determination of equality or ratios	Similarity $x' = ax$	$x \mapsto rx$	Coefficient of variation	$=, \neq, >, <, -, +, *, \div$

- **Physical level** -> bit = binary digit = **basic** indissoluble unit (= Shannon, Sh), \neq Bit (!) in Quantum Systems -> qubit
- **Logical Level** -> integers, booleans, characters, floating-point numbers, alphanumeric strings, ...
- **Conceptual (Abstract) Level** -> data-structures, e.g. lists, arrays, trees, graphs, ...
- **Technical Level** -> Application data, e.g. text, graphics, images, audio, video, multimedia, ...
- **“Hospital Level”** -> Narrative (textual) data, numerical measurements (physiological data, lab results, vital signs, ...), recorded signals (ECG, EEG, ...), Images (x-ray, MR, CT, PET, ...) ; -omics

- **Clinical workplace data sources**

- Medical documents: text (non-standardized (“free-text”), semi-structured, standard terminologies (ICD, SNOMED-CT)
- Measurements: lab, time series, ECG, EEG, EOG, ...
- Surveys, Clinical study data, trial data

- **Image data sources**

- Radiology: MRI (256x256, 200 slices, 16 bit per pixel, uncompressed, ~26 MB); CT (512x512, 60 slices, 16 bit per pixel, uncompressed ~32MB; MR, US;
- Digital Microscopy : WSI (15mm slide, 20x magn., 24 bits per pixel, uncompressed, 2,5 GB, WSI 10 GB; confocal laser scanning, etc.

- **-omics data sources**

- Sanger sequencing, NGS whole genome sequencing (3 billion reads, read length of 36) ~ 200 GB; NGS exome sequencing (“only” 110,000,000 reads, read length of 75) ~7GB; Microarray, mass-spectrometry, gas chromatography, ...

Andreas Holzinger, Christof Stocker & Matthias Dehmer 2014. Big Complex Biomedical Data: Towards a Taxonomy of Data. In: Communications in Computer and Information Science CCIS 455. Berlin Heidelberg: Springer pp. 3-18, doi:10.1007/978-3-662-44791-8_1.

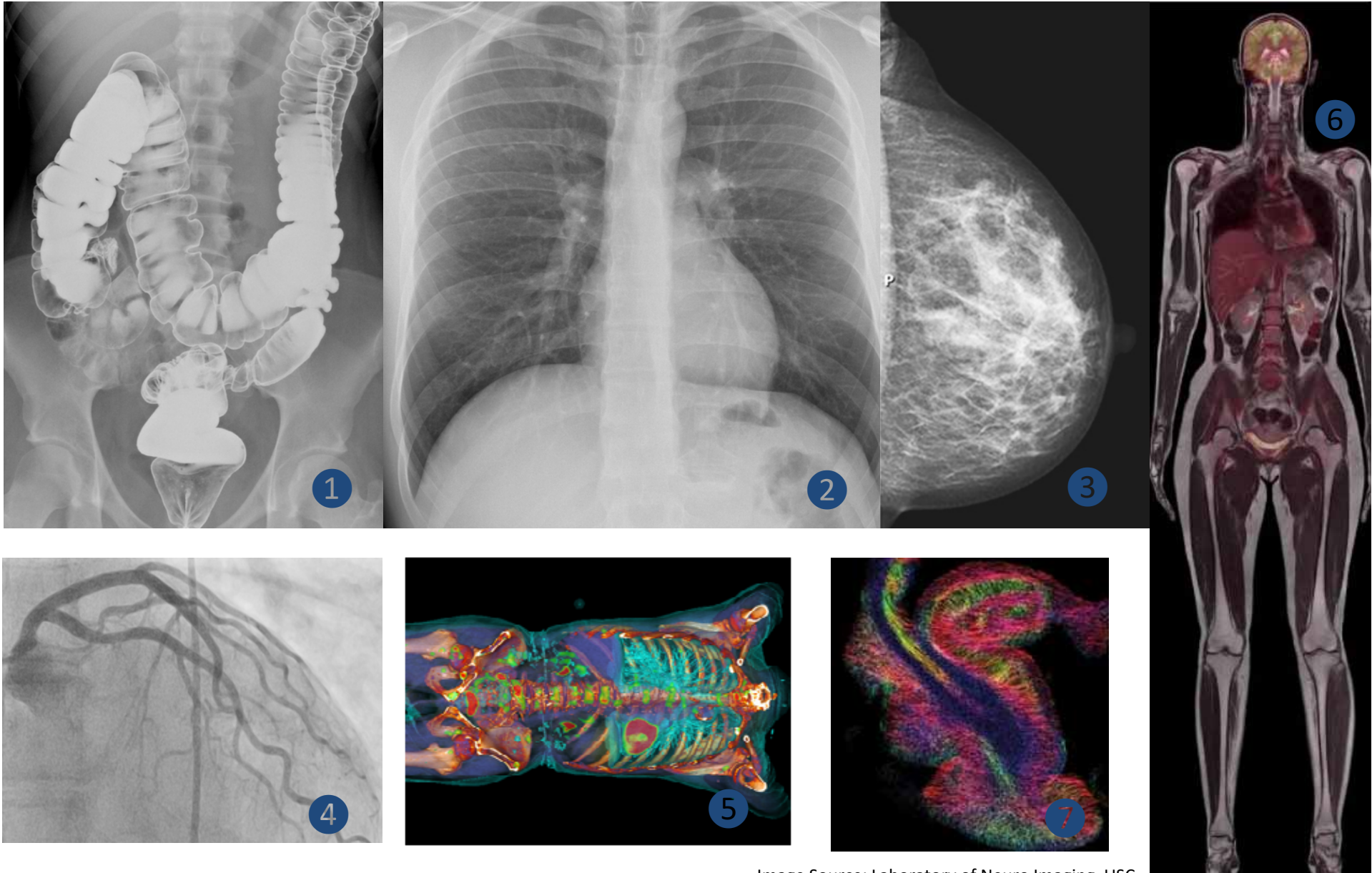
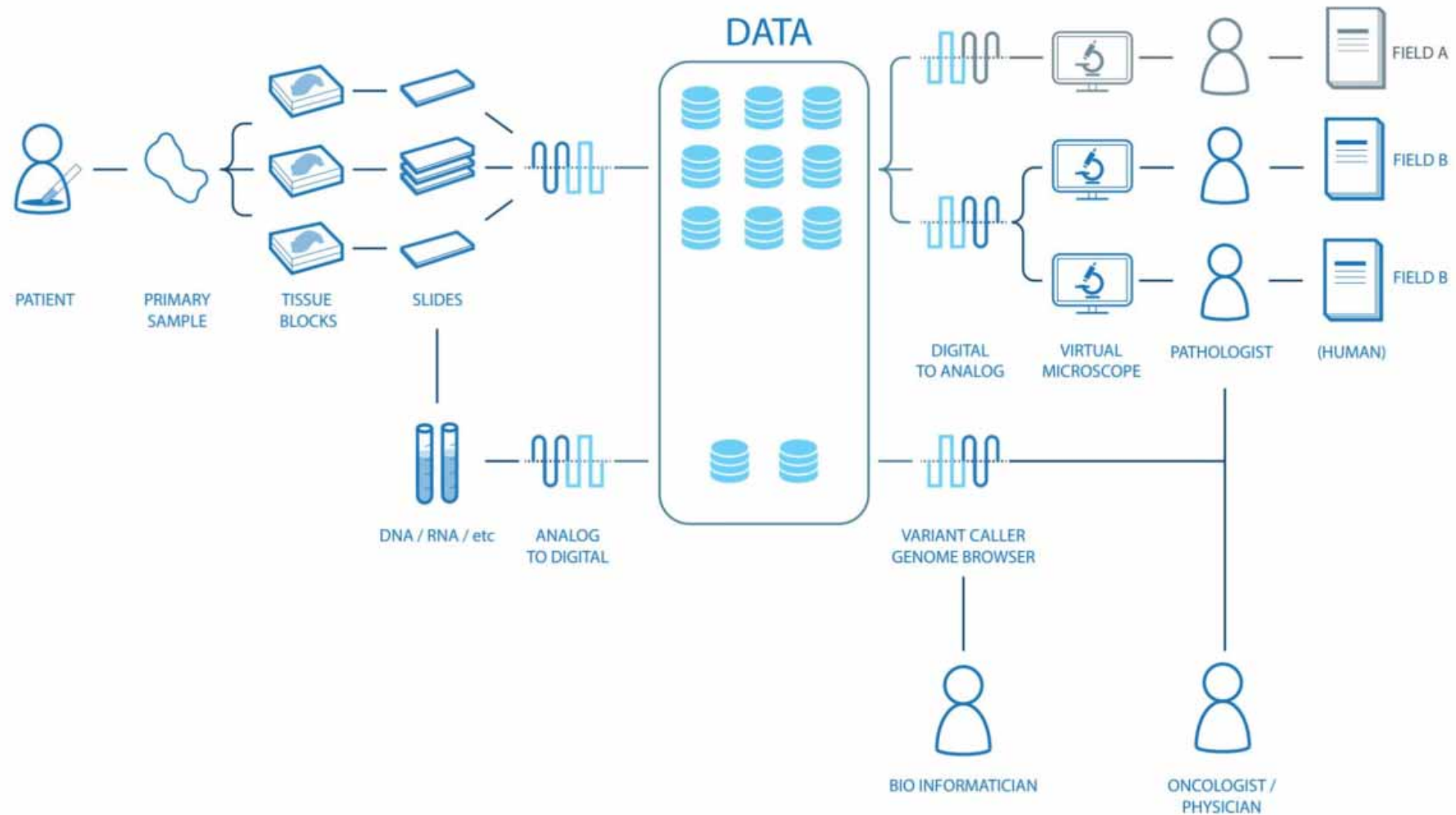
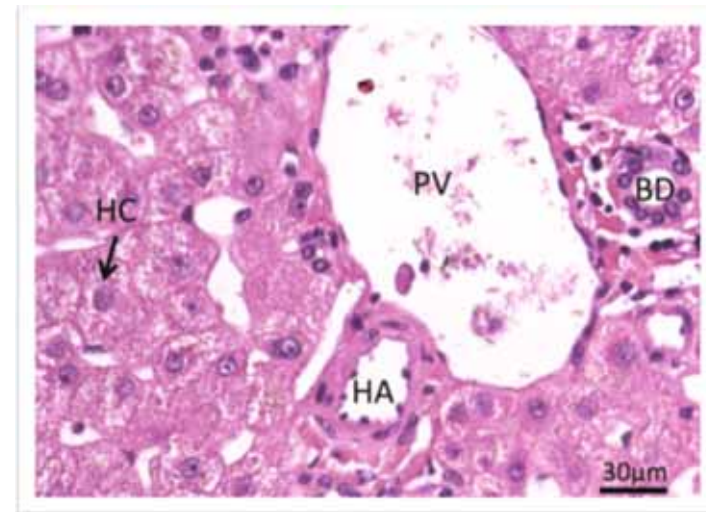
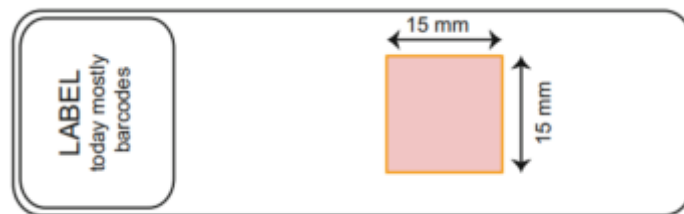
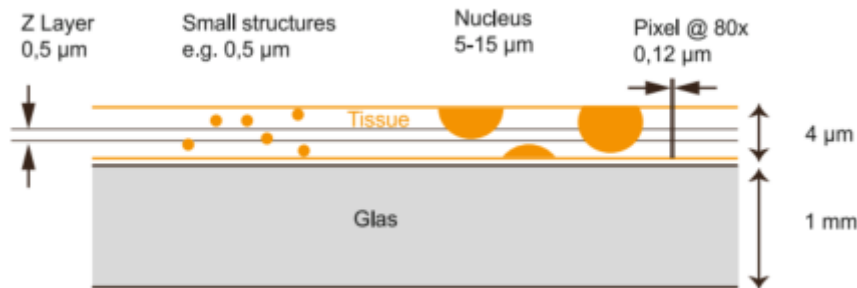
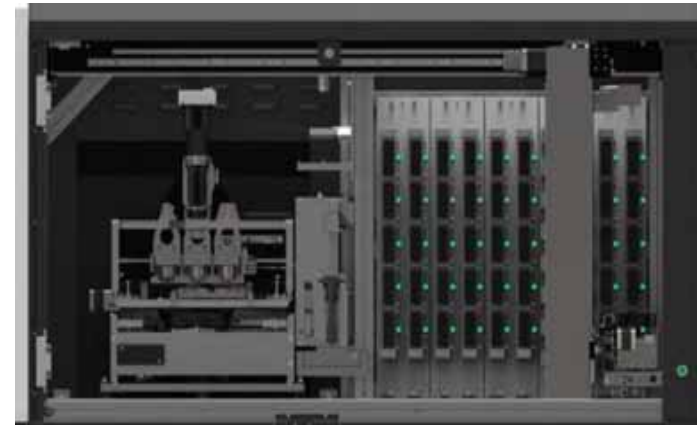


Image Source: Laboratory of Neuro Imaging, USC

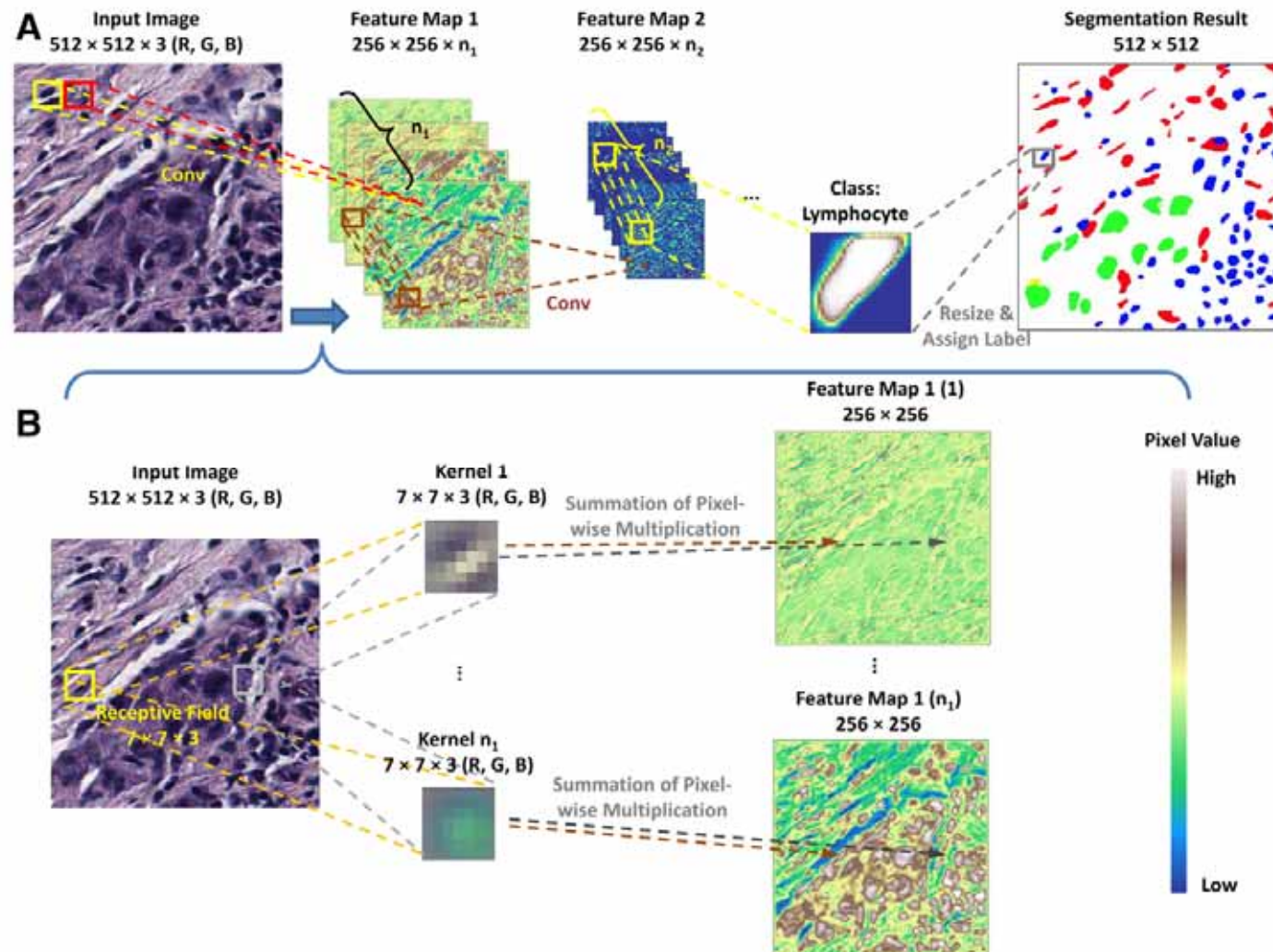


Andreas Holzinger, Bernd Malle, Peter Kieseberg, Peter M. Roth, Heimo Müller, Robert Reihs & Kurt Zatloukal 2017. Towards the Augmented Pathologist: Challenges of Explainable-AI in Digital Pathology. arXiv:1712.06657.

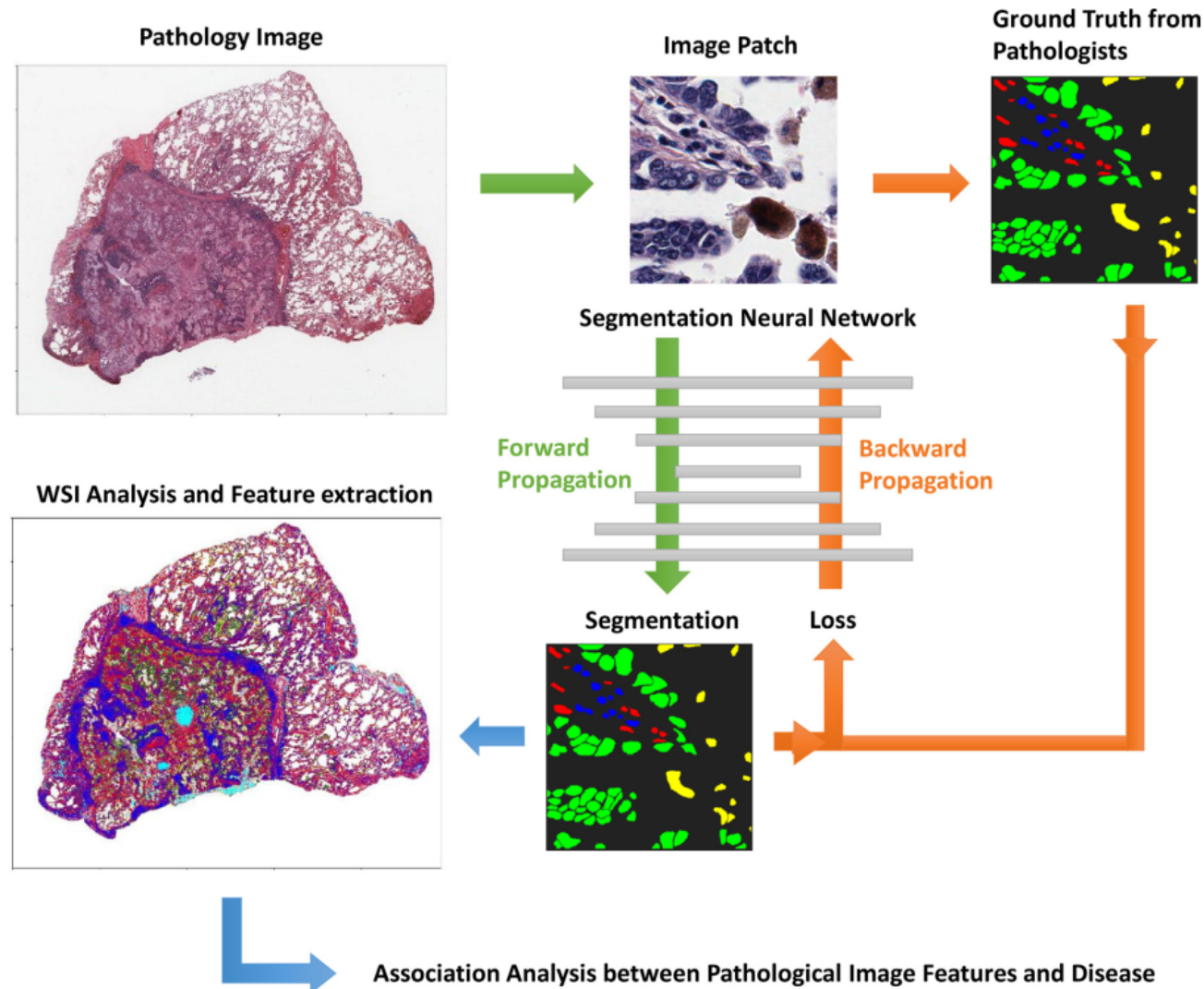


(Image Sources: Pathology Graz)

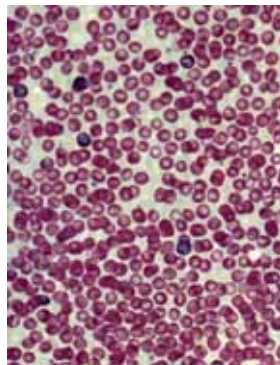
Andreas Holzinger, Bernd Malle, Peter Kieseberg, Peter M. Roth, Heimo Müller, Robert Reihs & Kurt Zatloukal 2017. Machine Learning and Knowledge Extraction in Digital Pathology needs an integrative approach. Towards Integrative Machine Learning and Knowledge Extraction, Springer Lecture Notes in Artificial Intelligence Volume LNAI 10344. Cham: Springer, pp. 13-50, doi:10.1007/978-3-319-69775-8_2.



Shidan Wang, Donghan M Yang, Ruichen Rong, Xiaowei Zhan & Guanghua Xiao 2019. Pathology image analysis using segmentation deep learning algorithms. The American journal of pathology, 189, (9), 1686-1698, doi:10.1016/j.ajpath.2019.05.007

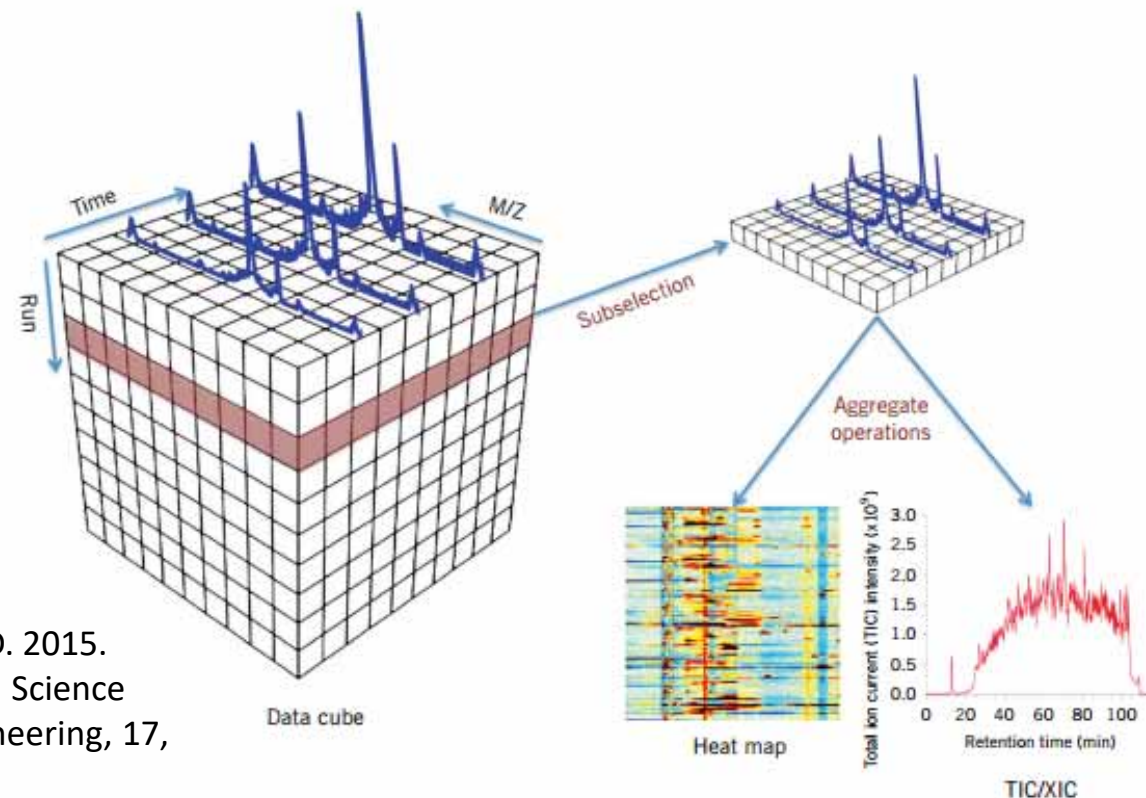


Shidan Wang, Donghan M Yang, Ruichen Rong, Xiaowei Zhan & Guanghua Xiao 2019. Pathology image analysis using segmentation deep learning algorithms. The American journal of pathology, 189, (9), 1686-1698, doi:10.1016/j.ajpath.2019.05.007



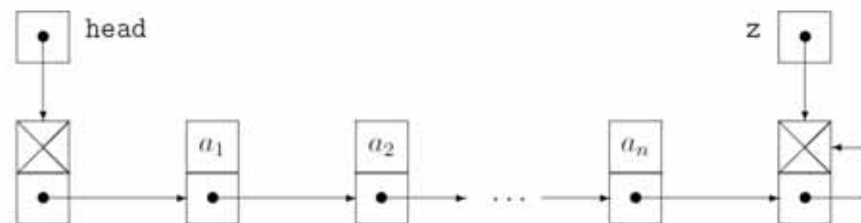
Amino acids (symbols)	Fatty acids (symbols)	Fatty acids (symbols)
Alanine (Ala)	Free carnitine (C0)	Hexadecenyl-carnitine (C16:1)
Arginine (Arg)	Acetyl-carnitine (C2)	Octadecenyl-carnitine (C18:1)
Argininosuccinate (Argsuc)	Propionyl-carnitine (C3)	Decenyl-carnitine (C10:2)
Citrulline (Cit)	Butyryl-carnitine (C4)	Tetradecadienyl-carnitine (C14:2)
Glutamate (Glu)	Isovaleryl-carnitine (C5)	Octadecadienyl-carnitine (C18:2)
Glycine (Gly)	Hexanoyl-carnitine (C6)	Hydroxy-isovaleryl-carnitine (C5-OH)
Methionine (Met)	Octanoyl-carnitine (C8)	Hydroxytetradecadienyl-carnitine (C14-OH)
Ornithine (Orn)	Decanoyl-carnitine (C10)	Hydroxypalmitoyl-carnitine (C16-OH)
Phenylalanine (Phe)	Dodecanoyl-carnitine (C12)	Hydroxypalmitoleyl-carnitine (C16:1-OH)
Pyroglutamate (Pyrglt)	Myristoyl-carnitine (C14)	Hydroxyoleyl-carnitine (C18:1-OH)
Serine (Ser)	Hexadecanoyl-carnitine (C16)	Dicarboxyl-butyl-carnitine (C4-DC)
Tyrosine (Tyr)	Octadecanoyl-carnitine (C18)	Glutaryl-carnitine (C5-DC)
Valine (Val)	Tiglyl-carnitine (C5:1)	Methylglutaryl-carnitine (C6-DC)
Leucine + Isoleucine (Xle)	Decenyl-carnitine (C10:1)	Methylmalonyl-carnitine (C12-DC)
	Myristoleyl-carnitine (C14:1)	

Fourteen amino acids and 29 fatty acids are analyzed from a single blood spot using MS/MS. The concentrations are given in $\mu\text{mol/L}$.

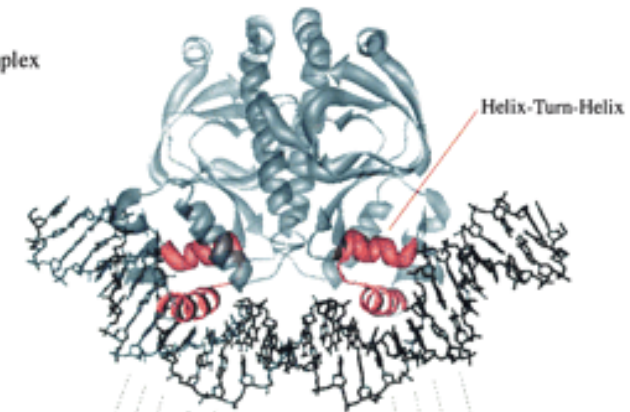


Yao, Y., Bowen, B. P., Baron, D. & Poznanski, D. 2015. SciDB for High-Performance Array-Structured Science Data at NERSC. Computing in Science & Engineering, 17, (3), 44-52, doi:10.1109/MCSE.2015.43.

<pre>TYPE link = REF node ; node = RECORD key : ItemType; next : link; END;</pre>	<div>key</div> <div>next</div> <div>•</div>	<pre>class link { ItemType key; link next; }</pre>
VAR p, q : link ;	<div>p</div> <div>•</div> <div>q</div> <div>•</div>	link p,q;
p := NEW(link);	<div>p</div> <div>•</div> <div>•</div>	p=new link();
p^.key:=x;	<div>p</div> <div>•</div> <div>x</div> <div>•</div>	p.key=x;
q := NEW(link) ;	<div>p</div> <div>•</div> <div>x</div> <div>•</div> <div>q</div> <div>•</div> <div>•</div>	q=new link();



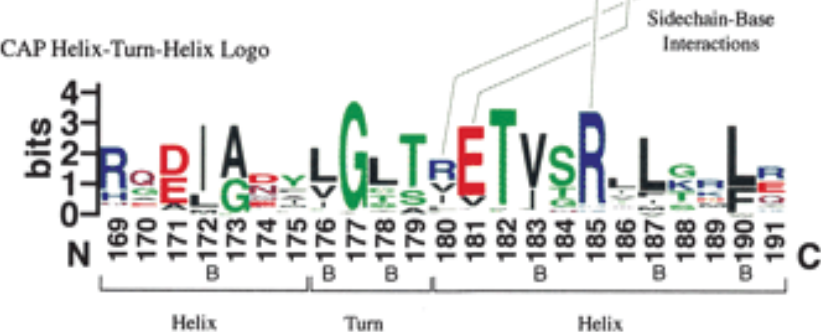
A CAP-DNA Complex



B CAP recognition site DNA Logo

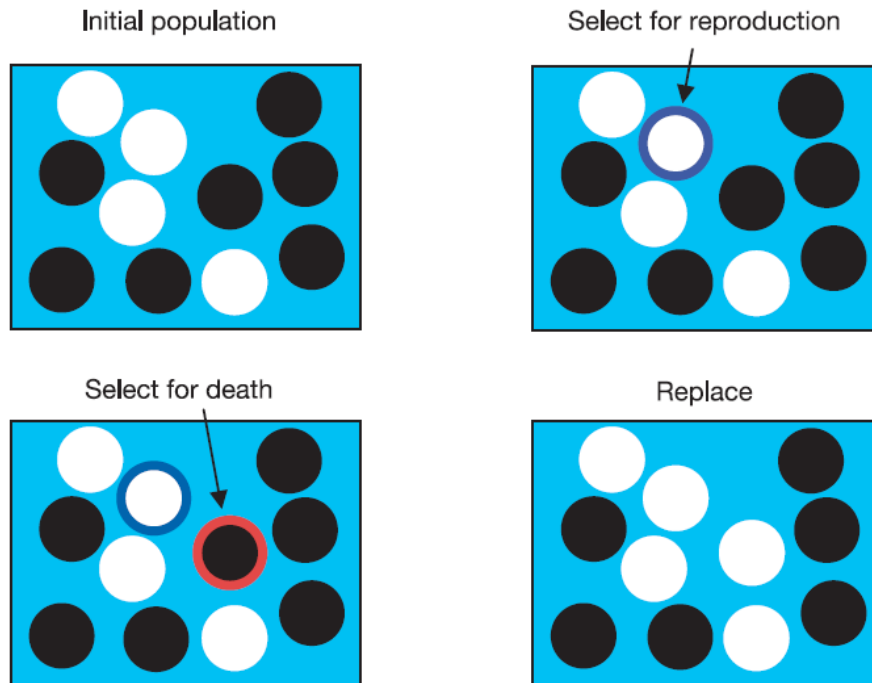


C CAP Helix-Turn-Helix Logo

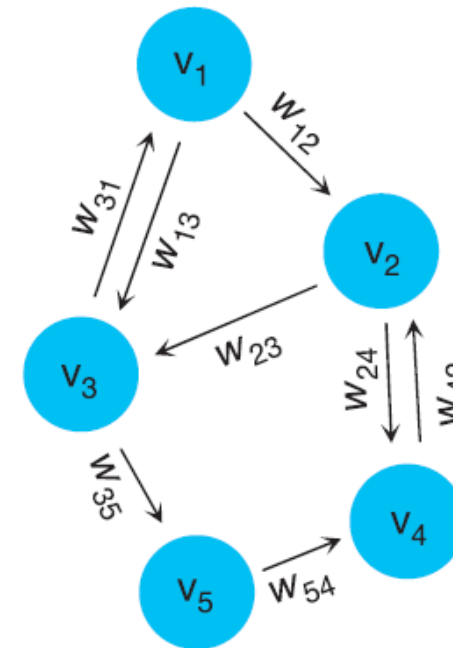


Crooks, G. E., Hon, G., Chandonia, J. M. & Brenner, S. E. (2004) WebLogo: A sequence logo generator. *Genome Research*, 14, 6, 1188-1190.

Evolutionary dynamics act on populations.
Neither genes, nor cells, nor individuals evolve;
only populations evolve.

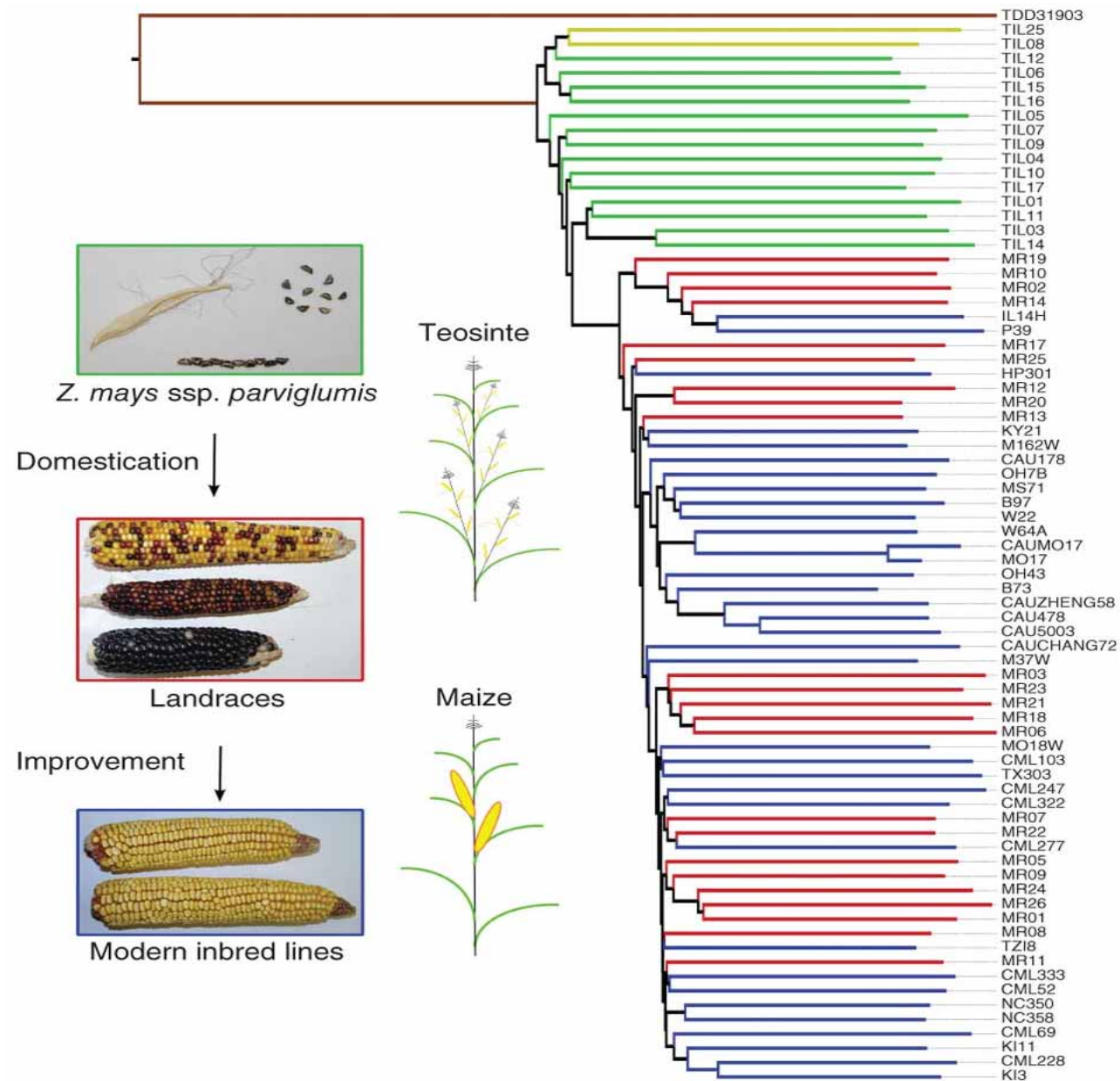


Lieberman, E., Hauert, C. & Nowak, M. A.
(2005) Evolutionary dynamics on graphs.
Nature, 433, 7023, 312-316.



$$W = \begin{bmatrix} 0 & w_{12} & w_{13} & 0 & 0 \\ 0 & 0 & w_{23} & w_{24} & 0 \\ w_{31} & 0 & 0 & 0 & w_{35} \\ 0 & w_{42} & 0 & 0 & 0 \\ 0 & 0 & 0 & w_{54} & 0 \end{bmatrix}$$

Hufford et. al.
2012. Comparative
population
genomics of maize
domestication and
improvement.
Nature Genetics,
44, (7), 808-811.



02 Biomedical data sources: Taxonomy of data

Andreas Holzinger, Matthias Dehmer & Igor Jurisica 2014. Knowledge Discovery and interactive Data Mining in Bioinformatics - State-of-the-Art, future challenges and research directions. Springer/Nature BMC Bioinformatics, 15, (S6), I1, doi:10.1186/1471-2105-15-S6-I1.

10^{-12}

Ecosystem



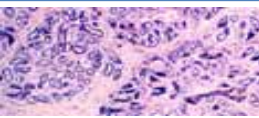
Collective



Individual



Tissue



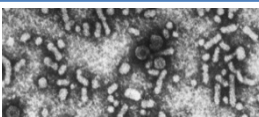
Cell



Bacteria



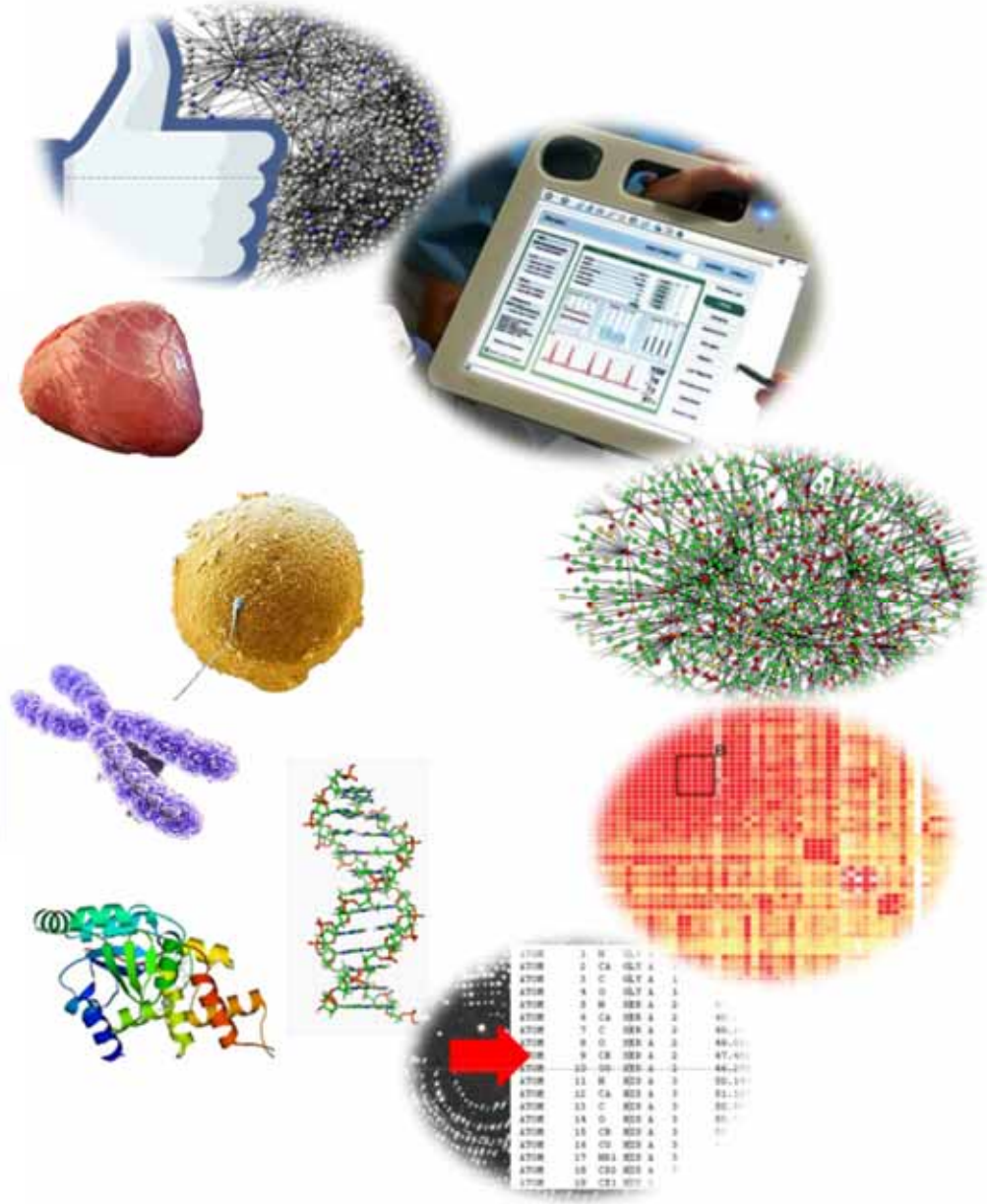
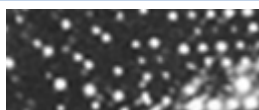
Virus

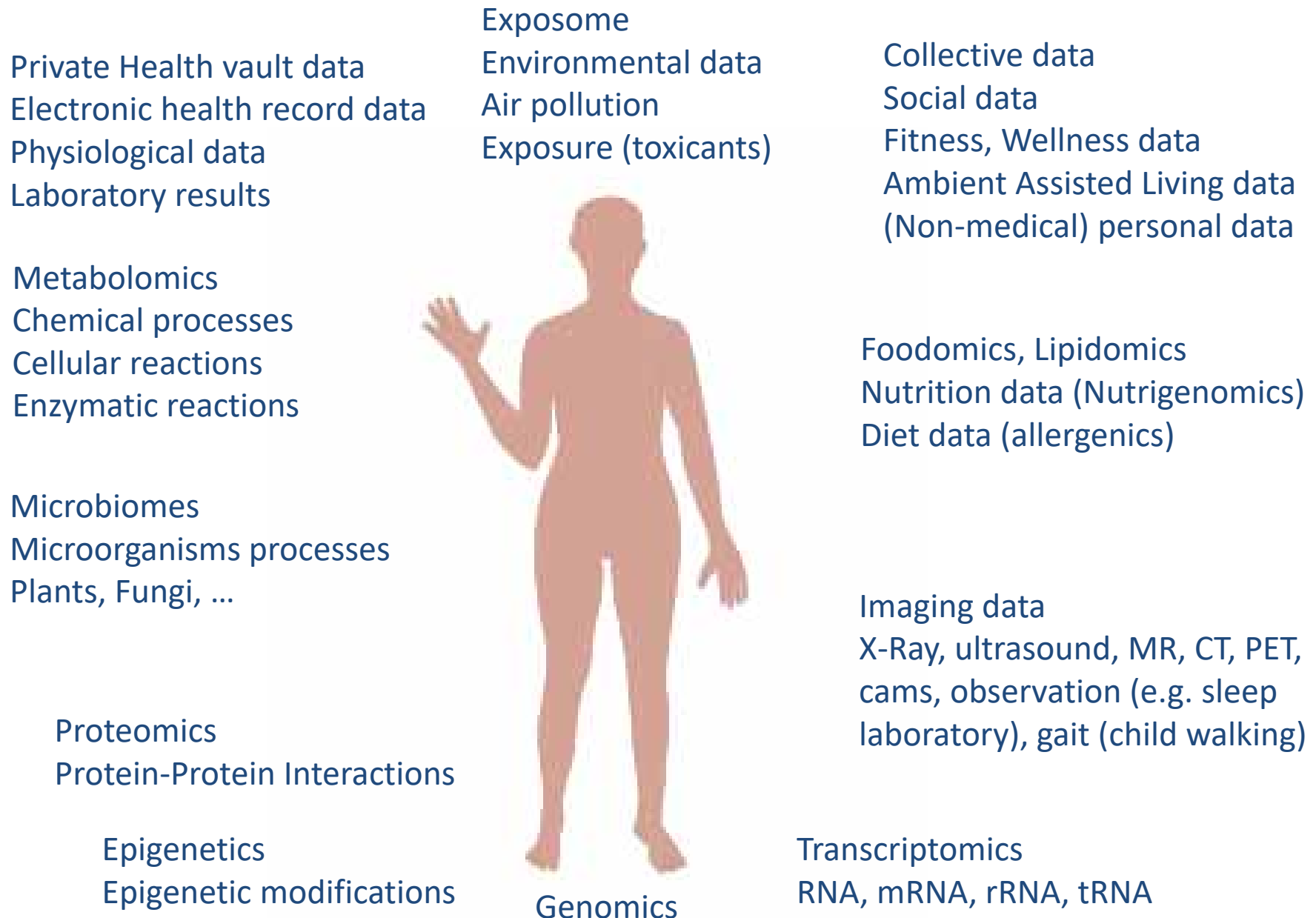


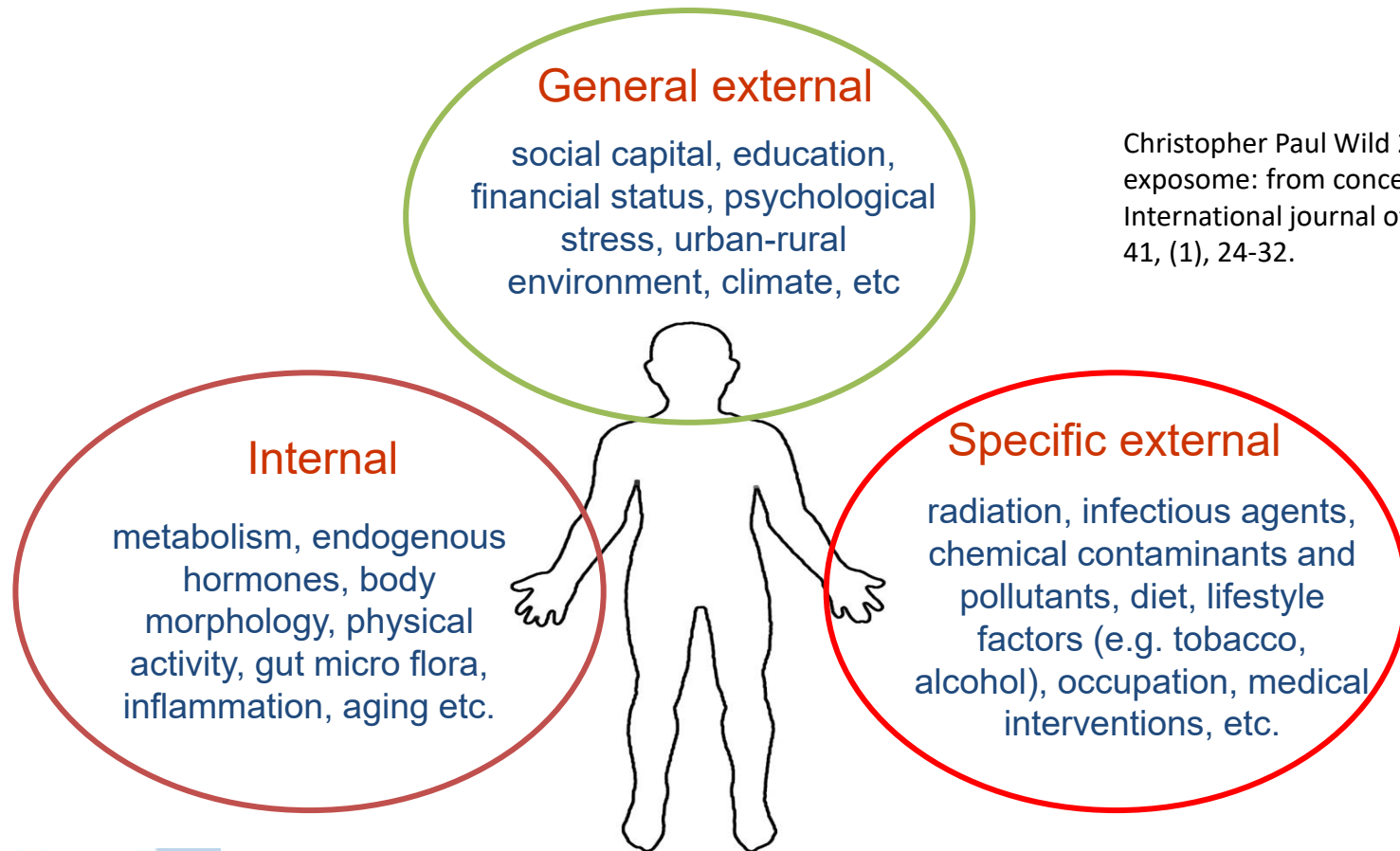
Molecule



Atom



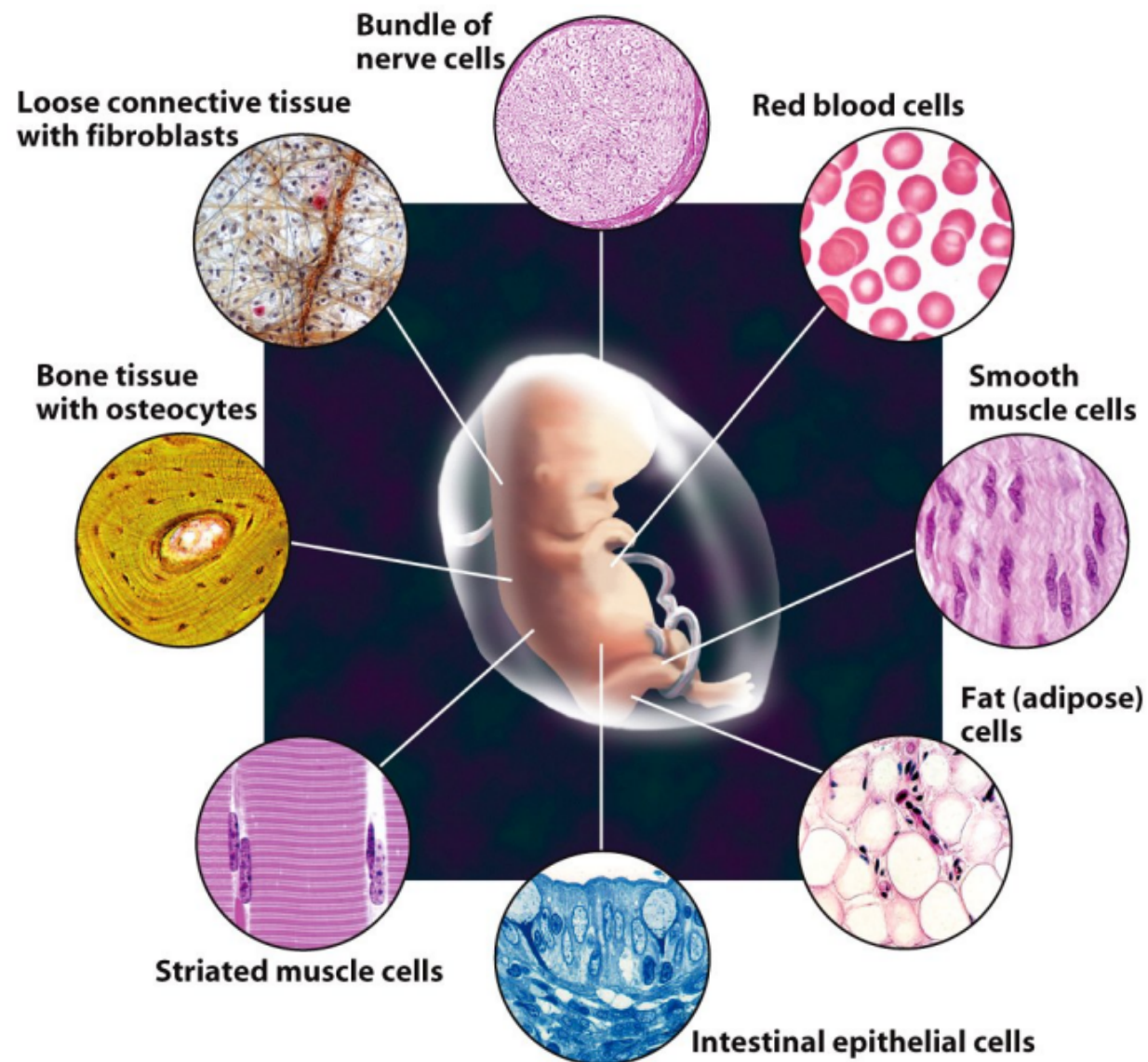




Christopher Paul Wild 2012. The exposome: from concept to utility. International journal of epidemiology, 41, (1), 24-32.



<https://human-centered.ai/project/eu-project-heap-human-exposome-assessment-platform>



Karp, G. 2010. Cell and Molecular Biology: Concepts and Experiments, Gainesville, John Wiley.

to reproduce ...

to grow ...

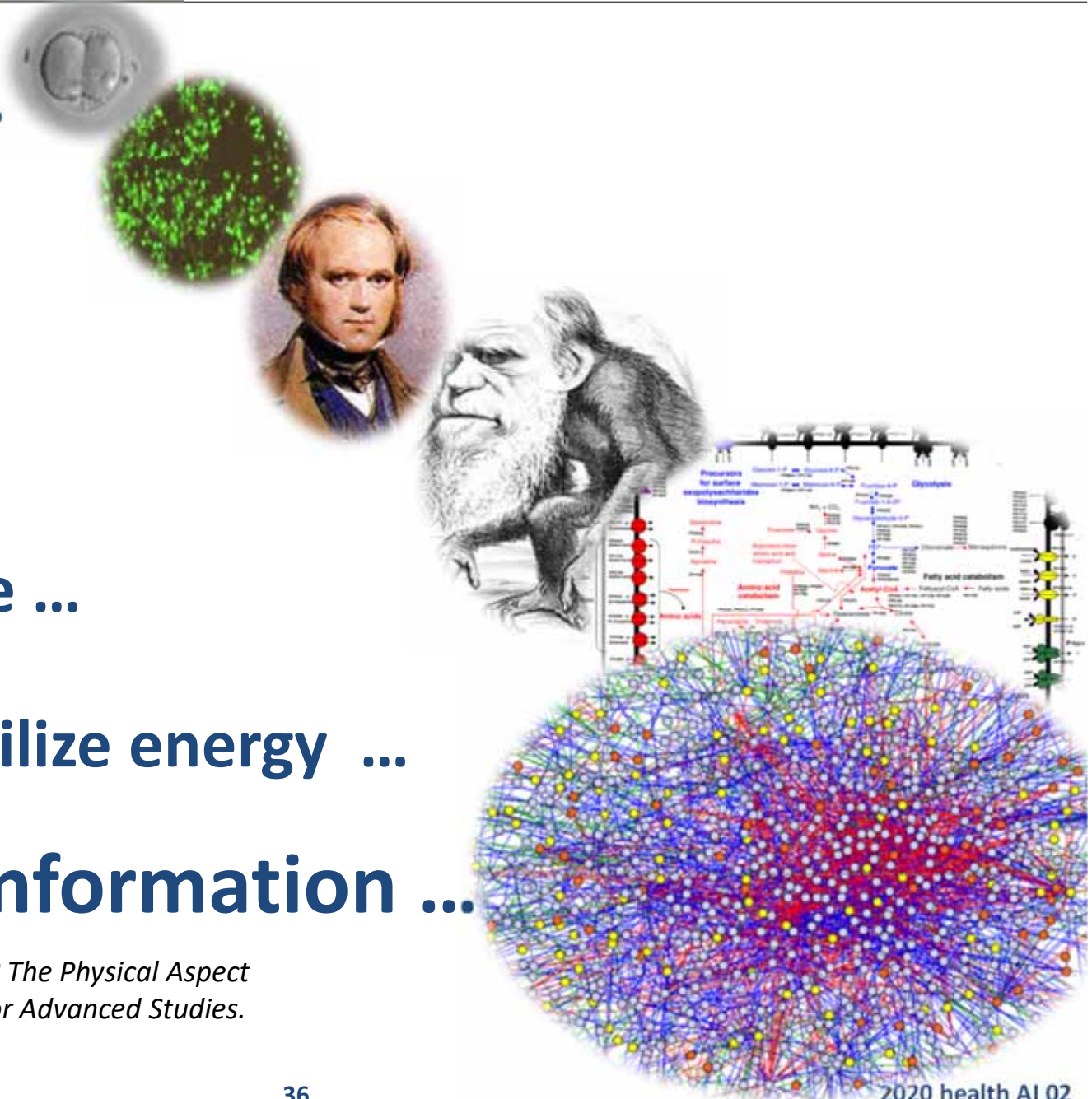
to evolve ...

to self-replicate ...

to generate/utilize energy ...

to process information ...

Schrödinger, E. (1944) *What Is Life? The Physical Aspect of the Living Cell*. Dublin Institute for Advanced Studies.





- Billions of biological data sets are openly available, here only some examples:
- General Repositories:
 - GenBank, EMBL, HMCA, ...
- Specialized by data types:
 - UniProt/SwissProt, MMMP, KEGG, PDB, ...
- Specialized by organism:
 - WormBase, FlyBase, NeuroMorpho, ...
- <https://human-centered.ai/open-data-sets>

- **Genomics** (sequence annotation)
- **Transcriptomics** (microarray)
- **Proteomics** (Proteome Databases)
- **Metabolomics** (enzyme annotation)
- **Fluxomics** (isotopic tracing, metabolic pathways)
- **Phenomics** (biomarkers)
- **Epigenomics** (epigenetic modifications)
- **Microbiomics** (microorganisms)
- **Lipidomics** (pathways of cellular lipids)



Genomics	Transcriptomics	Proteomics	Metabolomics	Protein-DNA interactions	Protein-protein interactions	Fluxomics	Phenomics
Genomics (sequence annotation)	<ul style="list-style-type: none"> • ORF validation • Regulatory element identification⁷⁴ 	<ul style="list-style-type: none"> • SNP effect on protein activity or abundance 	<ul style="list-style-type: none"> • Enzyme annotation 	<ul style="list-style-type: none"> • Binding-site identification⁷⁵ 	<ul style="list-style-type: none"> • Functional annotation⁷⁹ 	<ul style="list-style-type: none"> • Functional annotation 	<ul style="list-style-type: none"> • Functional annotation^{71,103} • Biomarkers¹²⁵
	Transcriptomics (microarray, SAGE)	<ul style="list-style-type: none"> • Protein: transcript correlation²⁰ 	<ul style="list-style-type: none"> • Enzyme annotation¹⁰⁹ 	<ul style="list-style-type: none"> • Gene-regulatory networks⁷⁶ 	<ul style="list-style-type: none"> • Functional annotation⁸⁹ • Protein complex identification⁶² 		<ul style="list-style-type: none"> • Functional annotation¹⁰²
		Proteomics (abundance, post-translational modification)	<ul style="list-style-type: none"> • Enzyme annotation⁸⁹ 	<ul style="list-style-type: none"> • Regulatory complex identification 	<ul style="list-style-type: none"> • Differential complex formation 	<ul style="list-style-type: none"> • Enzyme capacity 	<ul style="list-style-type: none"> • Functional annotation
			Metabolomics (metabolite abundance)	<ul style="list-style-type: none"> • Metabolic-transcriptional response 		<ul style="list-style-type: none"> • Metabolic pathway bottlenecks 	<ul style="list-style-type: none"> • Metabolic flexibility • Metabolic engineering¹⁰⁹
				Protein-DNA interactions (ChIP-chip)	<ul style="list-style-type: none"> • Signalling cascades^{89,102} 		<ul style="list-style-type: none"> • Dynamic network responses⁸⁴
					Protein-protein interactions (yeast 2H, coAP-MS)		<ul style="list-style-type: none"> • Pathway identification activity⁸⁹
						Fluxomics (isotopic tracing)	<ul style="list-style-type: none"> • Metabolic engineering
							Phenomics (phenotype arrays, RNAi screens, synthetic lethals)



Joyce, A. R. & Palsson, B. Ø. 2006. The model organism as a system: integrating 'omics' data sets. *Nature Reviews Molecular Cell Biology*, 7, 198-210.

- 0-D data = a data point existing isolated from other data, e.g. integers, letters, Booleans, etc.
- 1-D data = consist of a string of 0-D data, e.g. Sequences representing nucleotide bases and amino acids, SMILES etc.
- 2-D data = having spatial component, such as images, NMR-spectra etc.
- 2.5-D data = can be stored as a 2-D matrix, but can represent biological entities in three or more dimensions, e.g. PDB records
- 3-D data = having 3-D spatial component, e.g. image voxels, e-density maps, etc.
- H-D Data = data having arbitrarily high dimensions

SMILES (Simplified Molecular Input Line Entry Specification)

... is a compact machine and human-readable chemical nomenclature:

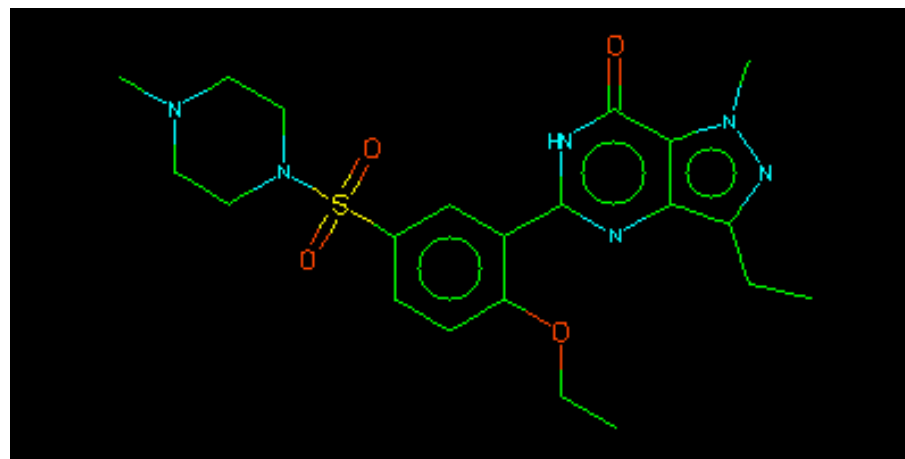
e.g. Viagra:

```
CCc1nn(C)c2c(=O)[nH]c(nc12)c3cc(ccc3OCC)S(=O)(=O)N4CC  
N(C)CC4
```

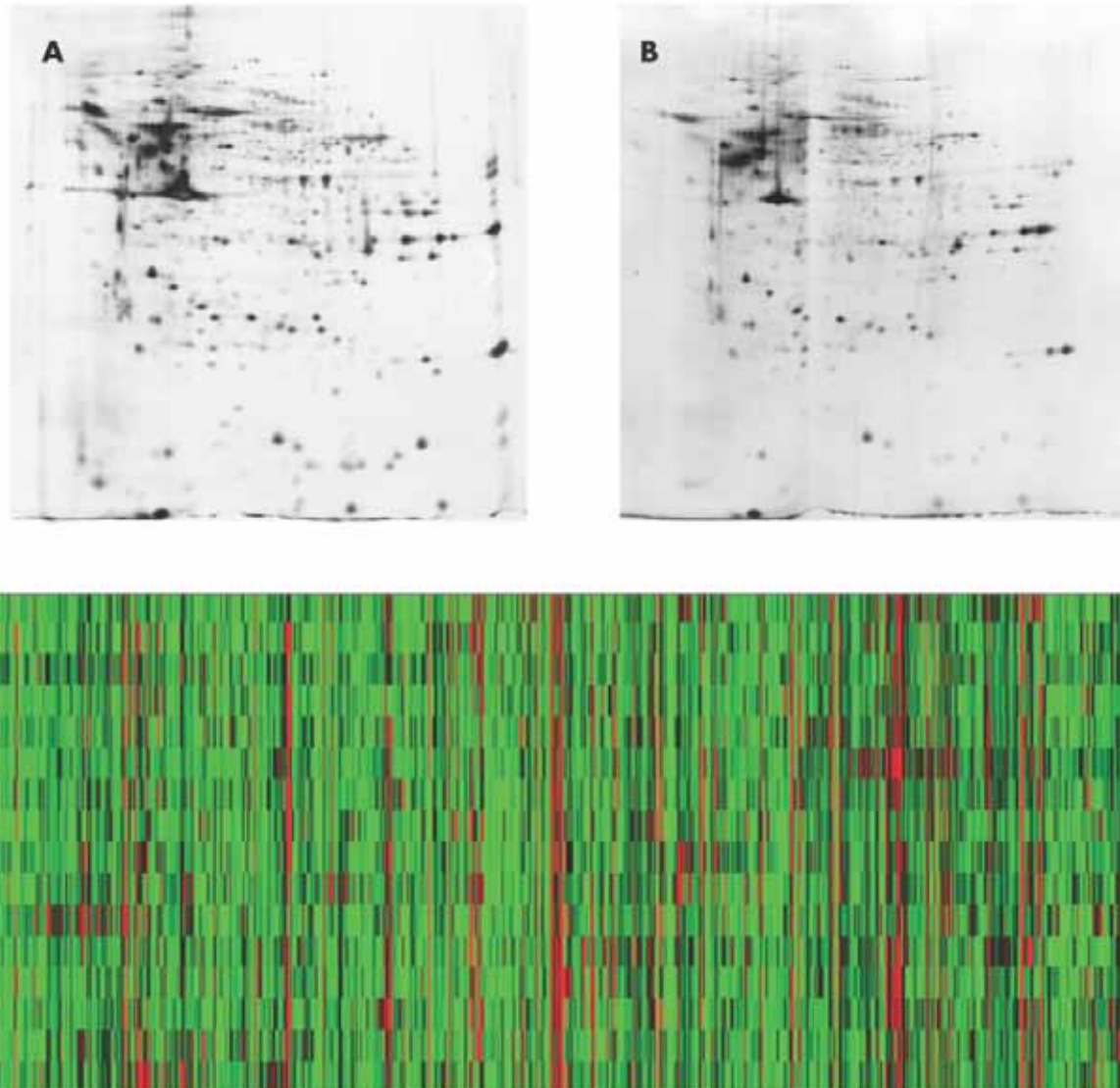
...is Canonicalizable

...is Comprehensive

...is Well Documented



http://www.daylight.com/dayhtml_tutorials/languages/smiles/index.html



Kastrinaki et al. (2008) Functional, molecular & proteomic characterisation of bone marrow mesenchymal stem cells in rheumatoid arthritis. *Annals of Rheumatic Diseases*, 67, 6, 741-749.

RCSB PDB PROTEIN DATA BANK

As of Tuesday Aug 30, 2011 at 5 PM PDT there are 75594 Structures | PDB Statistics

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X-ray | NMR
Validation Server
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New Structure Papers
Sequence Search
Chemical Components
Unreleased Entries
Browse Database
Histograms

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Widgets

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Structural View of Biology
Understanding PDB Data
Molecule of the Month
Educational Resources

Help Hide

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S. aureus Dihydrofolate Reductase complexed with novel 7-aryl-2,4-diaminoquinazolines

DOI:10.2210/pdb3sqy/pdb

3SQY

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Primary Citation

Structure-based design of new DHFR-based antibacterial agents: 7-aryl-2,4-diaminoquinazolines

Li, X., Hilgers, M., Cunningham, M., Chen, Z., Trzoss, M., Zhang, J., Koh, K., Nelson, K., Kwan, B., Stidham, M., Brown-Driver, V., Shaw, K.J., Finn, R.S.

Journal: (2011) Bioorg.Med.Chem.Lett.

PubMed: 21831637
DOI: 10.1016/j.bmcl.2011.07.059
Search Related Articles in PubMed

PubMed Abstract:

Dihydrofolate reductase (DHFR) inhibitors such as trimethoprim (TMP) have long played a significant role in the treatment of bacterial infections. Not surprisingly, after decades of use there is now bacterial resistance to TMP and therefore a need for new inhibitors. [Read More & Search PubMed Abstracts]

Molecular Description

Classification: Oxidoreductase/oxidoreductase Inhibitor
Structure Weight: 20357.01

Molecule: Dihydrofolate reductase
Polymer: 1 Type: polypeptide(L)
Chains: X
EC#: 1.5.1.3

Source

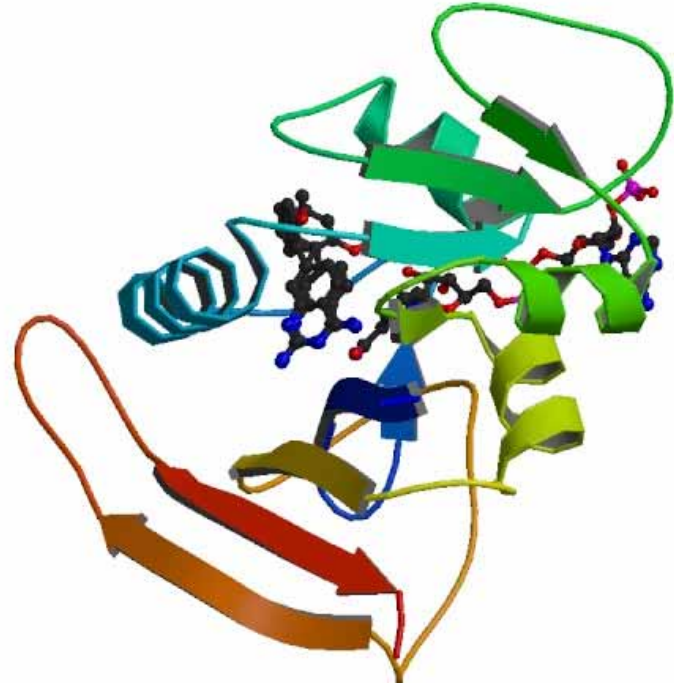
Polymer: 1
Scientific Name: Staphylococcus aureus Taxonomy Express

Related PDB Entries

Id	Details
3SR5	
3SRQ	
3SRR	
3SRS	
3SRU	

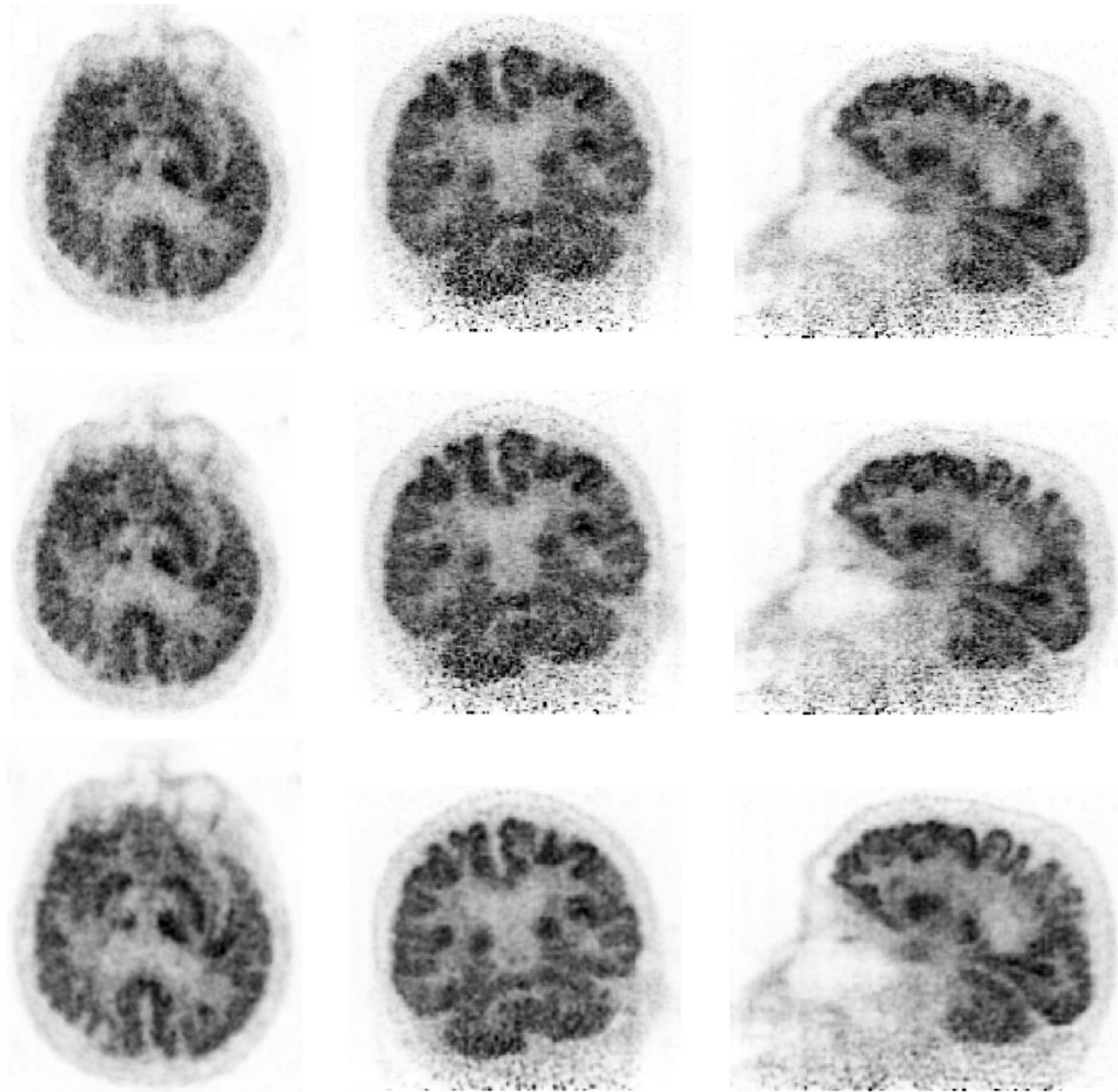
Deposition: 2011-07-06
Release: 2011-08-31

Experimental Details Hide
Method: X-RAY DIFFRACTION
Exp. Data:

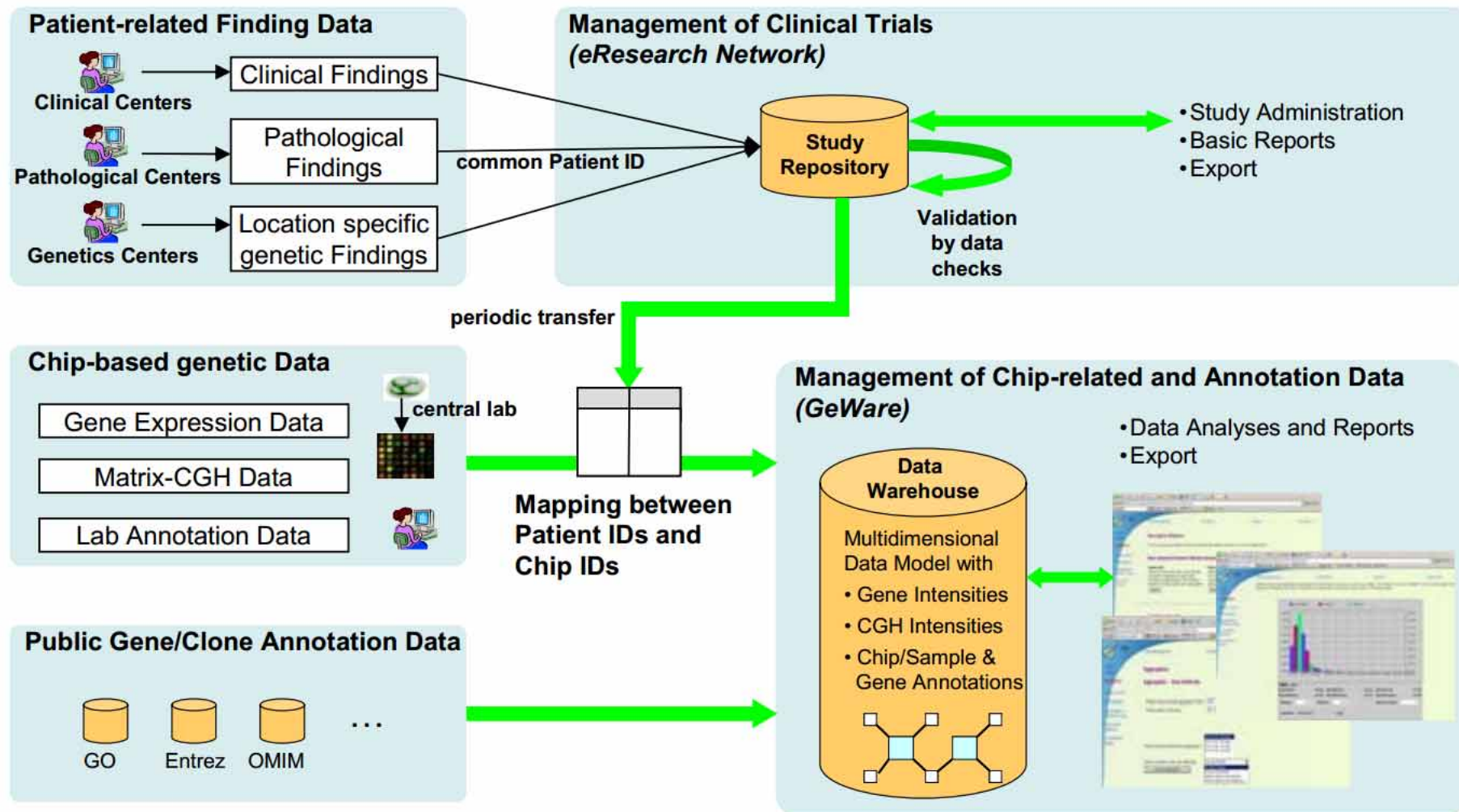


<http://www.pdb.org>

Scheins, J. J., Herzog, H. & Shah, N. J. (2011)
Fully-3D PET Image
Reconstruction Using
Scanner-Independent,
Adaptive Projection
Data and Highly
Rotation-Symmetric
Voxel Assemblies.
*Medical Imaging, IEEE
Transactions on*, 30, 3,
879-892.



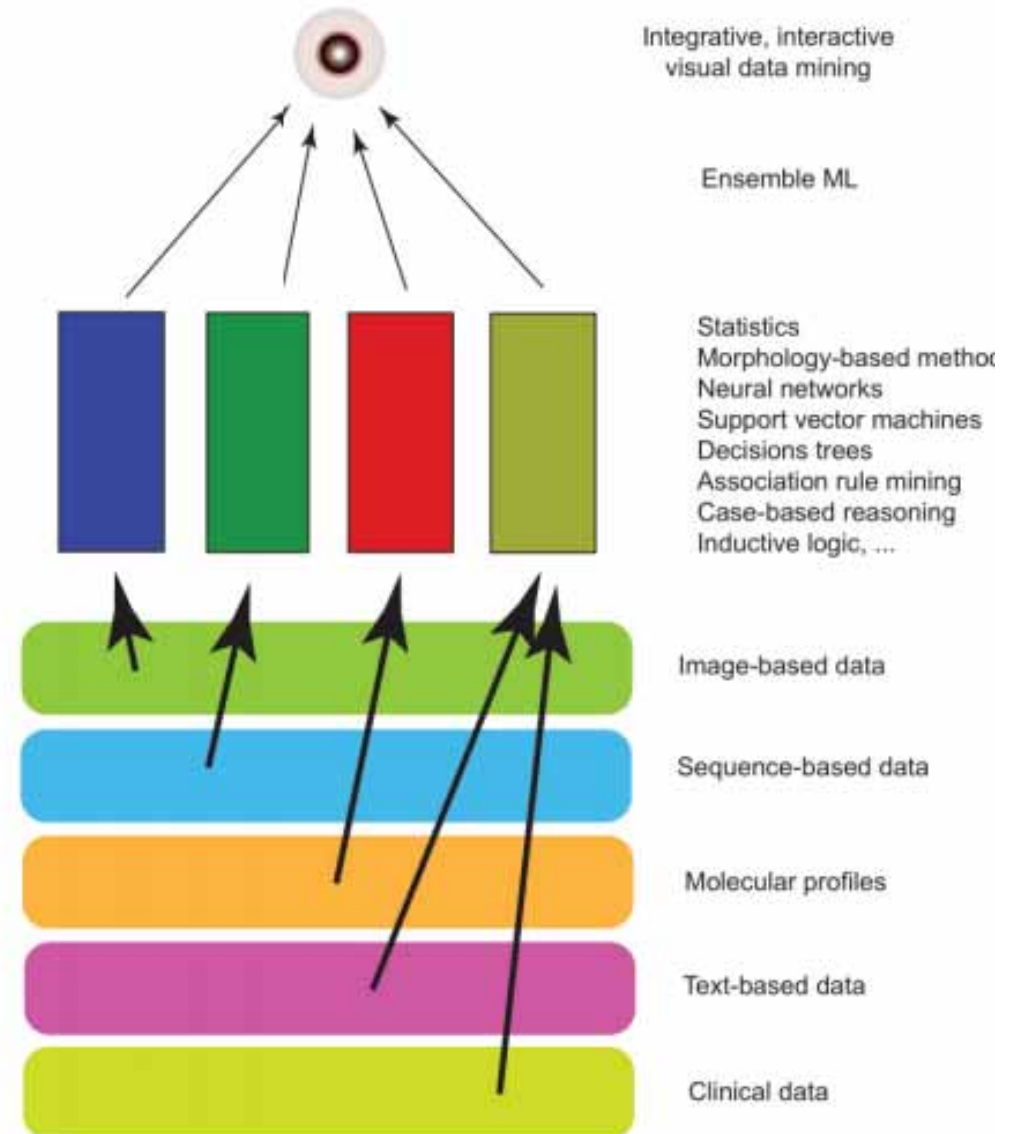
03 Data Integration, mapping, fusion



Kirsten, T., Lange, J. & Rahm, E. 2006. An integrated platform for analyzing molecular-biological data within clinical studies. Current Trends in Database Technology–EDBT 2006. Heidelberg: Springer, pp. 399-410, doi:10.1007/11896548_31.

Goal: Unified View for decision support ("what is relevant?")

Holzinger, A. & Jurisica, I. 2014. Knowledge Discovery and Data Mining in Biomedical Informatics: The future is in Integrative, Interactive Machine Learning Solutions In: Lecture Notes in Computer Science LNCS 8401. Heidelberg, Berlin: Springer, pp. 1-18, doi:10.1007/978-3-662-43968-5_1.



DOI:10.1145/2678280

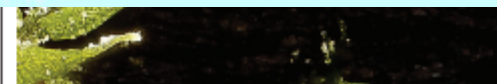
**Exploring the similarities and differences
between distributed computations in
biological and computational systems.**

BY SAKET NAVLAKHA AND ZIV BAR-JOSEPH

Distributed Information Processing



How to combine these different data types together to obtain a unified view of the activity in the cell is one of the major challenges of systems biology

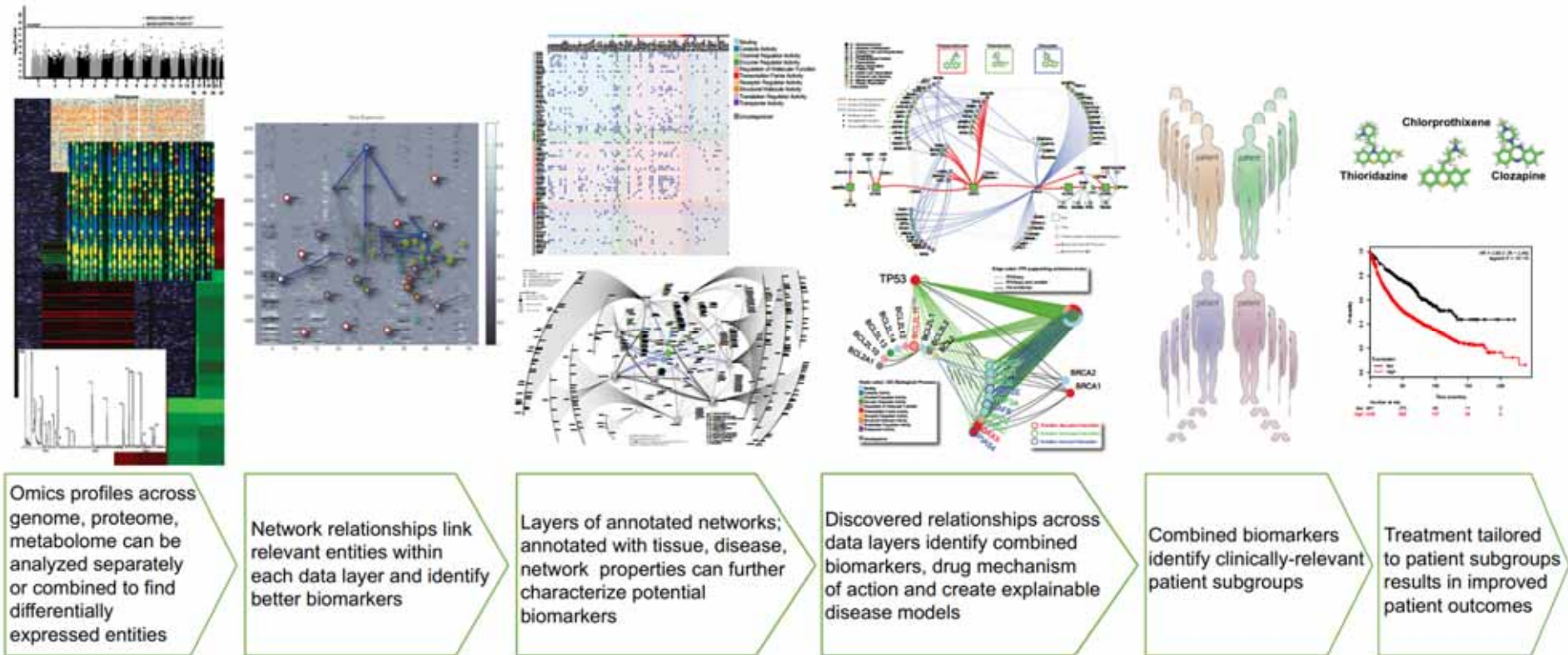


Navlakha, S. & Bar-Joseph, Z. 2014. Distributed information processing in biological and computational systems. *Commun. ACM*, 58, (1), 94-102, doi:10.1145/2678280.



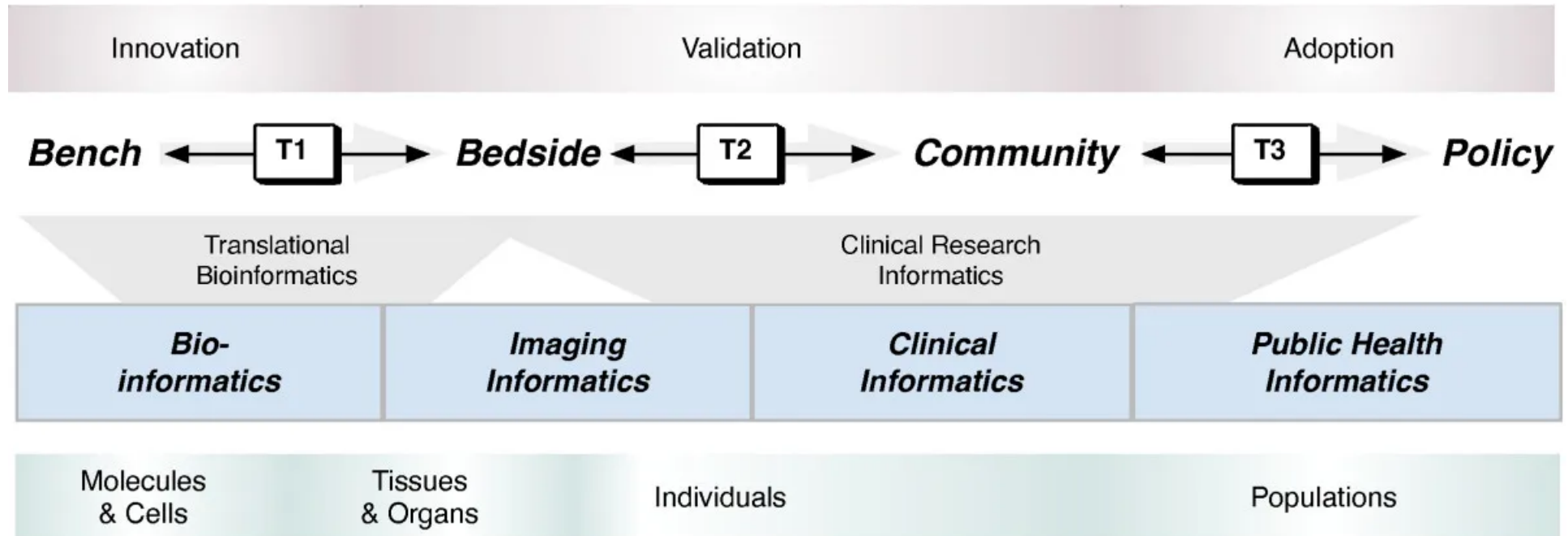
Our central hypothesis: Information may bridge this gap

Holzinger, A. & Simonic, K.-M. (eds.) 2011. *Information Quality in e-Health. Lecture Notes in Computer Science LNCS 7058, Heidelberg, Berlin, New York: Springer.*



Andreas Holzinger, Benjamin Haibe-Kains & Igor Jurisica 2019. Why imaging data alone is not enough: AI-based integration of imaging, omics, and clinical data. European Journal of Nuclear Medicine and Molecular Imaging, 46, (13), 2722-2730, doi:10.1007/s00259-019-04382-9.

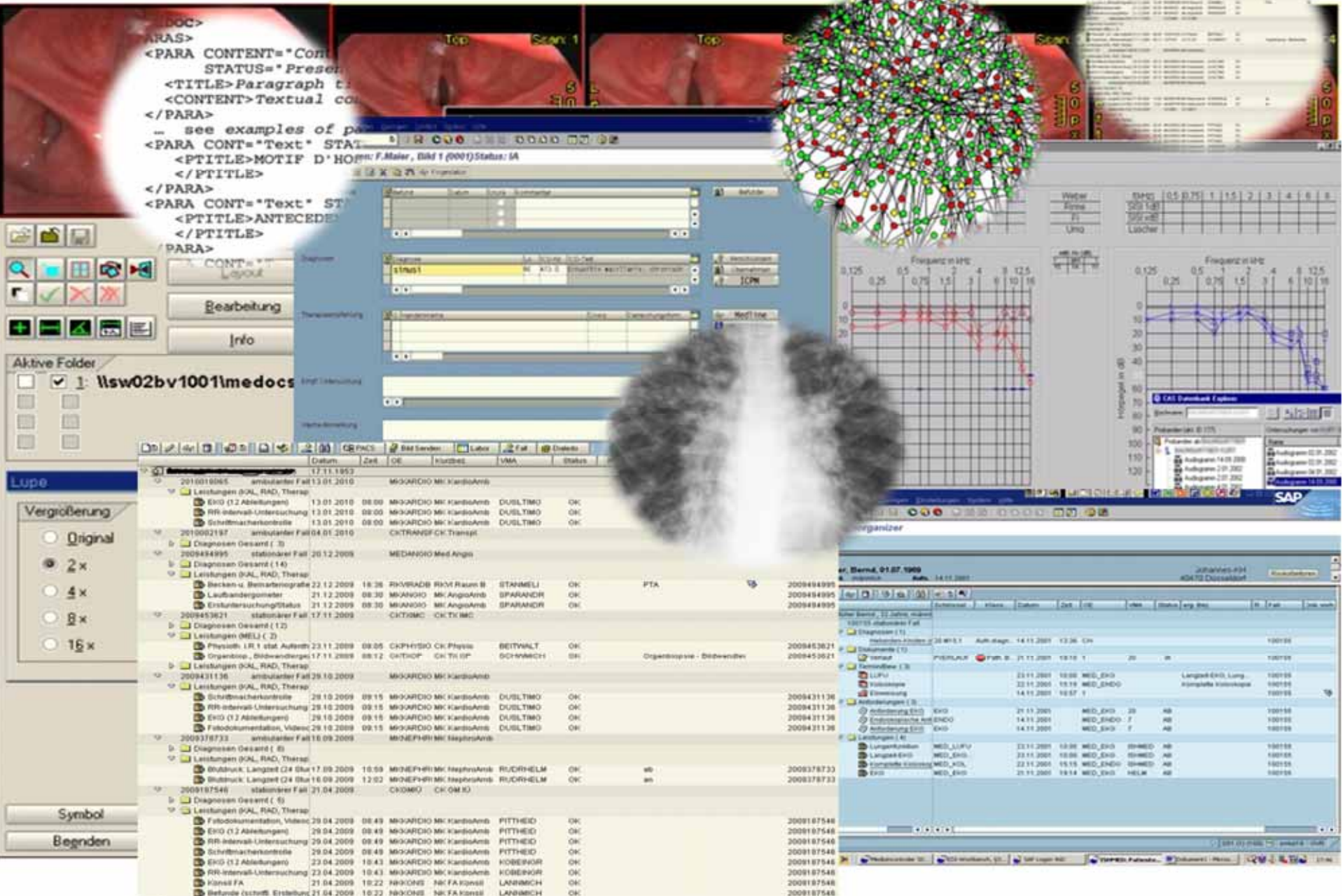
Translational Medicine Continuum



Biomedical Informatics Continuum

Indra N. Sarkar 2010. Biomedical informatics and translational medicine.
Journal of Translational Medicine, 8, (1), 2-12, doi:10.1186/1479-5876-8-22

What are the key problems in medical data management ?





Biomedical R&D data
(e.g. clinical trial data)

Clinical patient data
(e.g. EPR, lab, reports etc.)

The combining link is text

Health business data
(e.g. costs, utilization, etc.)

Private patient data
(e.g. AAL, monitoring, etc.)

Manyika, J., Chui, M., Brown, B., Bughin, J., Dobbs, R., Roxburgh, C. & Byers, A. H. (2011) *Big data: The next frontier for innovation, competition, and productivity*. Washington (DC), McKinsey Global Institute.

**Radiologischer Befund**

angelegt am 06.05.2006/20:21
geschr. von
gedruckt am 17.11.2006/08:21
Anlo: NCHB

Kurzanamnese: St.p. SHT

Fragestellung: -

Untersuchung: Thorax eine Ebene liegend

SB

Bewegungsartefakte. Zustand nach Schädelhirntrauma.

Das Cor in der Größennorm, keine akuten Stauungszeichen.
Fragliches Infiltrat parahilär li. im UF, RW-Erguss li.

Zustand nach Anlage eines ET, die Spitze ca. 5cm cranial der Bifurkation, lieg. MS, orthot.
positioniert. ZVK über re., die Spitze in Proj. auf die VCS. Kein Hinweis auf Pneumothorax.
Der re. Rezessus frei.

Mit kollegialen Grüßen

*** Elektronische Freigabe durch am 09.05.2006 ***

Holzinger, A., Geierhofer, R. & Errath, M. 2007. Semantische Informationsextraktion in medizinischen Informationssystemen. *Informatik Spektrum*, 30, (2), 69-78.

Digression: Medical Communication

- ... and requires a lot of communication and information exchange ...



Image Source: Andreas Holzinger

Holzinger, A., Geierhofer, R., Ackerl, S. & Searle, G. (2005). *CARDIAC@VIEW: The User Centered Development of a new Medical Image Viewer*. Central European Multimedia and Virtual Reality Conference, Prague, Czech Technical University (CTU), 63-68.

Radiologischer Befund		angelegt am 06.05.2006/20:26 geschr. von [REDACTED] gedruckt am 17.11.2006/08:24 Anfo: NCHIN
Kurzanamnese:	St.p. SHT	
Fragestellung:	-	
Untersuchung:	Thorax eine Ebene liegend [REDACTED]	
SB		
Bewegungsartefakte. Zustand nach Schädelhirntrauma.		
Das Cor in der Größennorm, keine akuten Stauungszeichen. Fragliches Infiltrat parahilär li. im UF, RW-Erguss li.		
Zustand nach Anlage eines ET, die Spitze ca. 5cm cranial der Bifurkation, lieg. MS, orthotop positioniert. ZVK über re., die Spitze in Proj. auf die VCS. Kein Hinweis auf Pneumothorax. Der re. Rezessus frei.		
Mit kollegialen Grüßen		
[REDACTED]		
*** Elektronische Freigabe durch [REDACTED] am 09.05.2006 ***		

Special Words
Language Mix
Abbreviations
Errors ...

Holzinger, A., Geierhofer, R. & Errath, M. 2007. Semantische Informationsextraktion in medizinischen Informationssystemen. *Informatik Spektrum*, 30, (2), 69-78.

Untersuchungsbefund / Beschwerden: *perf. Antrumschleimhaut für histol. Untersuchung*
Leber 1/3 große Ds in a. b. d. in unklare Schlingen nach
in Leber verlaufend & östlich & colicisch & sang.
& Antrumschleimhaut & U.S. & Antrumschleimhaut & M. b. d. in Leber 2/3
Leber 2/3: Antrumschleimhaut
in Leber 2/3: C.P. < 0,5 Leber 2/3

Diagnose: *subakutes Antrum, DD: Gastritis*

Empfehlung / Therapie: *histol. Sch. in unklare Antrumschleimhaut*
Antrum 1/3 Ds in U.S. & U.S.
Py. 1/3 Ds in U.S. & U.S.

Mit freundlichen kollegialen Grüßen

[Signature]
-Unterschrift-

NR 1091502

„die Antrumschleimhaut ist durch Lymphozyten infiltriert“

„lymphozytäre Infiltration der Antrum mukosa“

„Lymphozyteninfiltration der Magenschleimhaut im Antrumbereich“

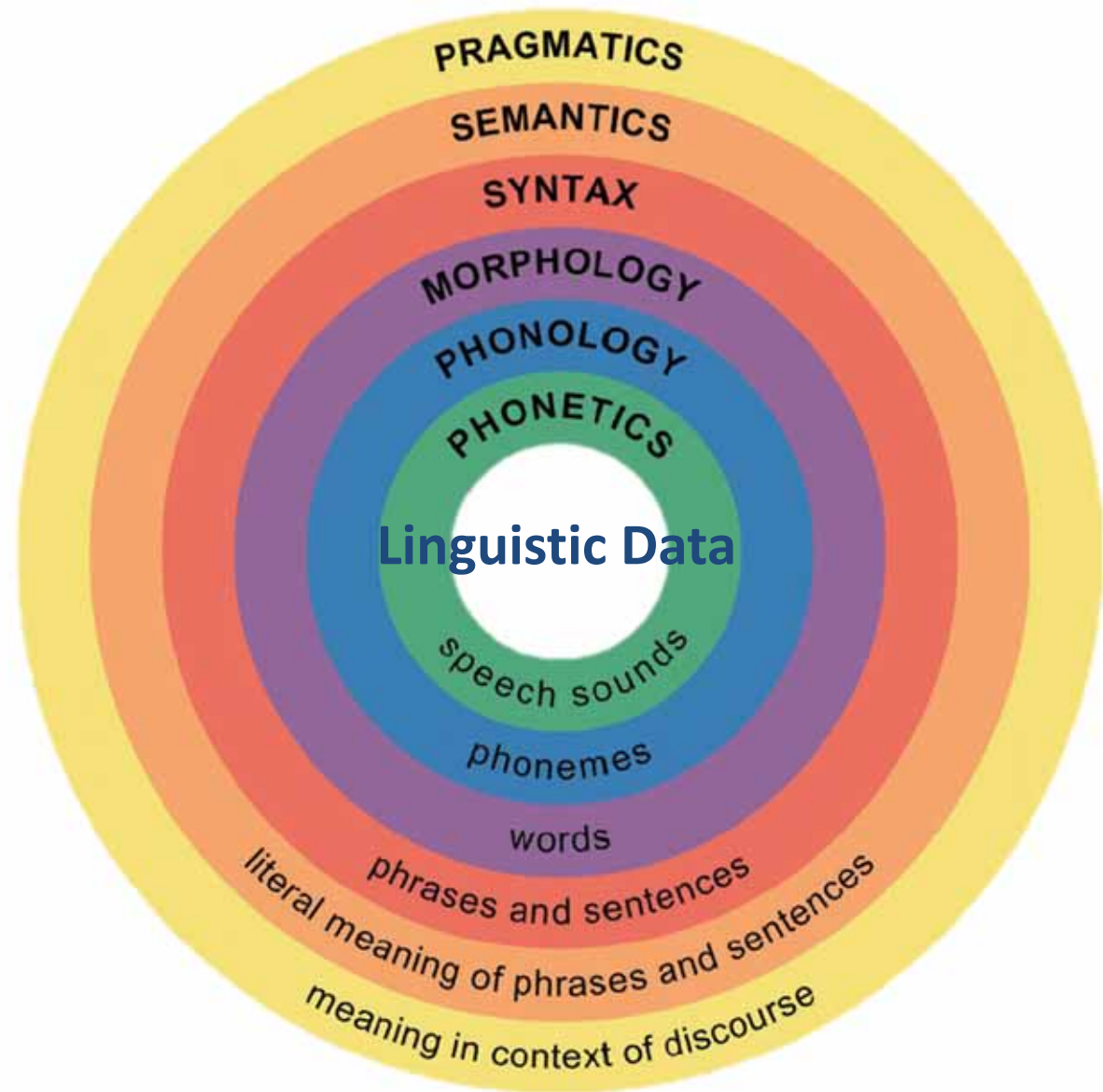
- Syntax
- Semantics
- Pragmatics
- Context
- (Emotion)



"a young boy is holding a
baseball bat."

Andrej Karpathy & Li Fei-Fei. Deep visual-semantic alignments for generating image descriptions. Proceedings of the IEEE conference on computer vision and pattern recognition, 2015. 3128-3137.

Image Source: <https://cs.stanford.edu/people/karpathy/deepimagesent/>



Thomas, J. J. & Cook, K. A.
2005. *Illuminating the path:
The research and
development agenda for
visual analytics*, New York,
IEEE Computer Society Press.

- Increasingly large data sets due to **data-driven medicine** [1]
- Increasing amounts of **non-standardized** data and **un-structured information** (e.g. “free text”)
- Data **quality**, data **integration**, universal **access**
- **Privacy**, security, safety, data protection, data ownership, fair use of data [2]
- **Time** aspects in databases [3]

[1] Shah, N. H. & Tenenbaum, J. D. 2012. The coming age of data-driven medicine: translational bioinformatics' next frontier. Journal of the American Medical Informatics Association, 19, (E1), E2-E4.

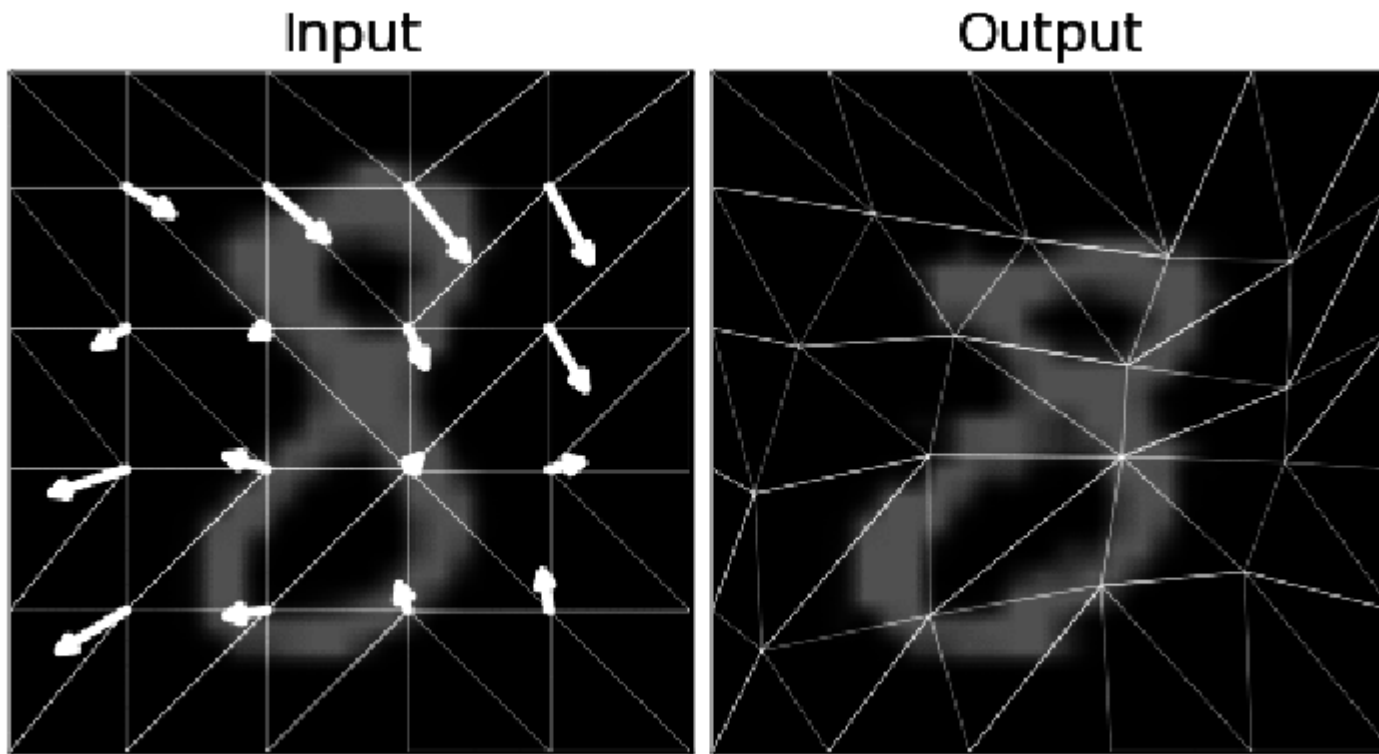
[2] Kieseberg, P., Hobel, H., Schrittwieser, S., Weippl, E. & Holzinger, A. 2014. Protecting Anonymity in Data-Driven Biomedical Science. In: LNCS 8401. Berlin Heidelberg: Springer pp. 301-316..

[3] Gschwandtner, T., Gärtner, J., Aigner, W. & Miksch, S. 2012. A taxonomy of dirty time-oriented data. In: LNCS 7465. Heidelberg, Berlin: Springer, pp. 58-72.

Digression: Data Augmentation

- Generation of artificial data via expansion of your dataset
- Why ?
- Neural networks require “big data” so augmentation is now basically part of most all deep learning projects
- It is also used to address issues with class imbalance
- It is a cheap and relatively easy way to get more data, which will almost certainly improve the accuracy of a trained model
- It improves model generalisation, model accuracy, and can control overfitting
- Image augmentation is most common, because text augmentation is much harder, and DL is applied to images
- done by making label-preserving transformations to the original images (e.g. rotation, zooming, cropping, ...)

Marcus D. Bloice, Peter M. Roth & Andreas Holzinger 2019. Biomedical image augmentation using Augmentor. Oxford Bioinformatics, 35, (1), 4522-4524, doi:10.1093/bioinformatics/btz259.



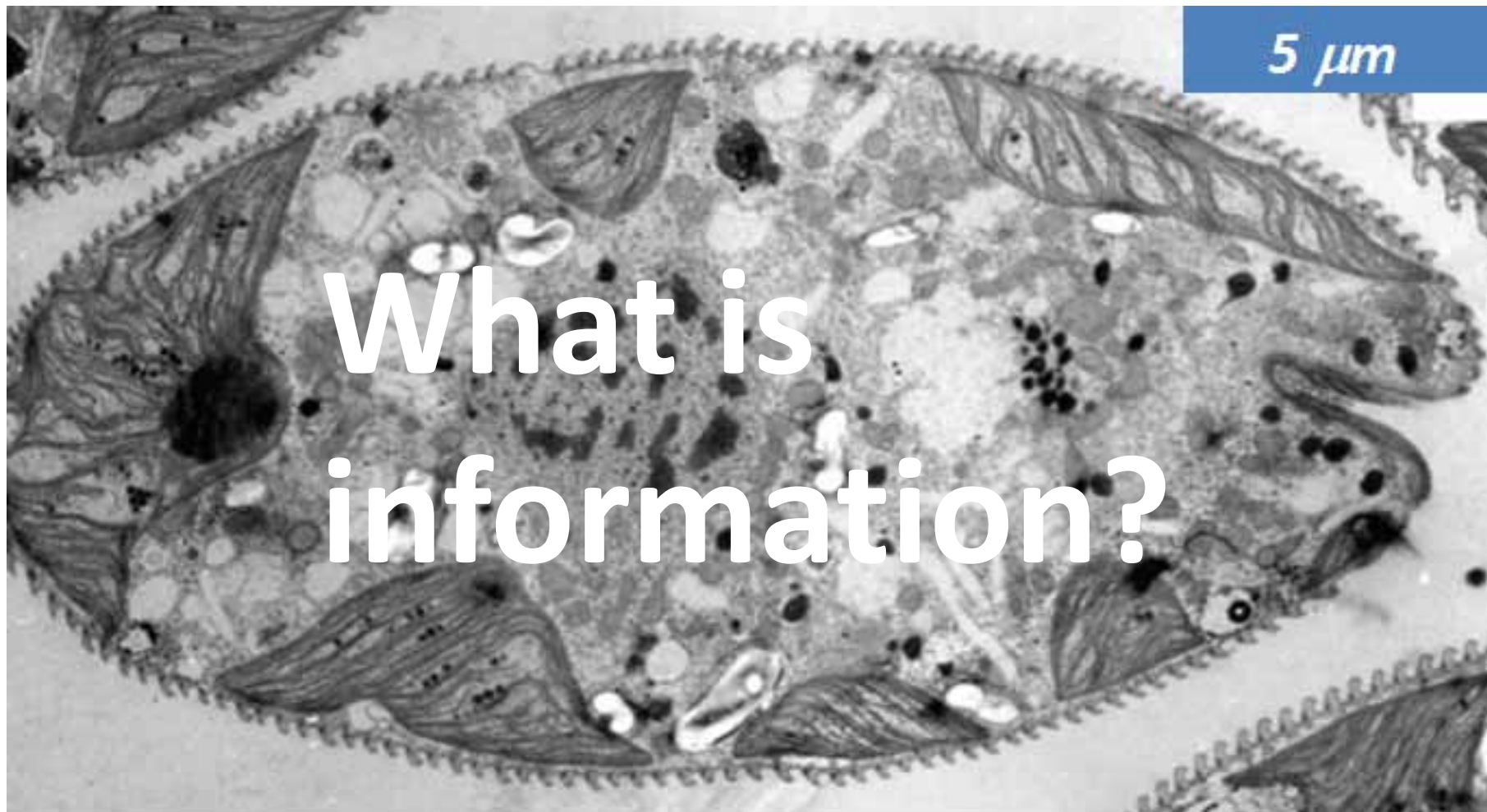
Marcus D Bloice, Christof Stocker & Andreas Holzinger 2017. Augmentor: an image augmentation library for machine learning. arXiv preprint arXiv:1708.04680.

04 Information Theory & Entropy

- Boolean models
- Algebraic models
- Probabilistic models *)

*) Our probabilistic models describes data which we can observe from our environment – and if we use the mathematics of probability theory , in order to express the uncertainties around our model then the inverse probability allows us to infer unknown unknowns ... learning from data and making predictions – the core essence of machine learning and of vital importance for health informatics

Ghahramani, Z. 2015. Probabilistic machine learning and artificial intelligence. Nature, 521, (7553), 452-459, doi:10.1038/nature14541.



Lane, N. & Martin, W. (2010) The energetics of genome complexity.
Nature, 467, 7318, 929-934.

Bayes' Rule in words

d ... data; h ... hypothesis

$H = \{H_1, H_2, \dots, H_n\}$... Hypothesis space

Posterior
Probability

$\forall h, d \dots$

Likelihood

Prior
Probability

$$p(h|d) = \frac{p(d|h)p(h)}{\sum_{h \in H} p(d|h') p(h')}$$

Sum over space of
alternative hypotheses

Evidence =
marginal
likelihood

- Information is the reduction of uncertainty
- If something is 100 % certain its uncertainty = 0
- Uncertainty is max. if all choices are equally probable (I.I.D)
- Uncertainty (as information) sums up for independent sources



low entropy
low complexity

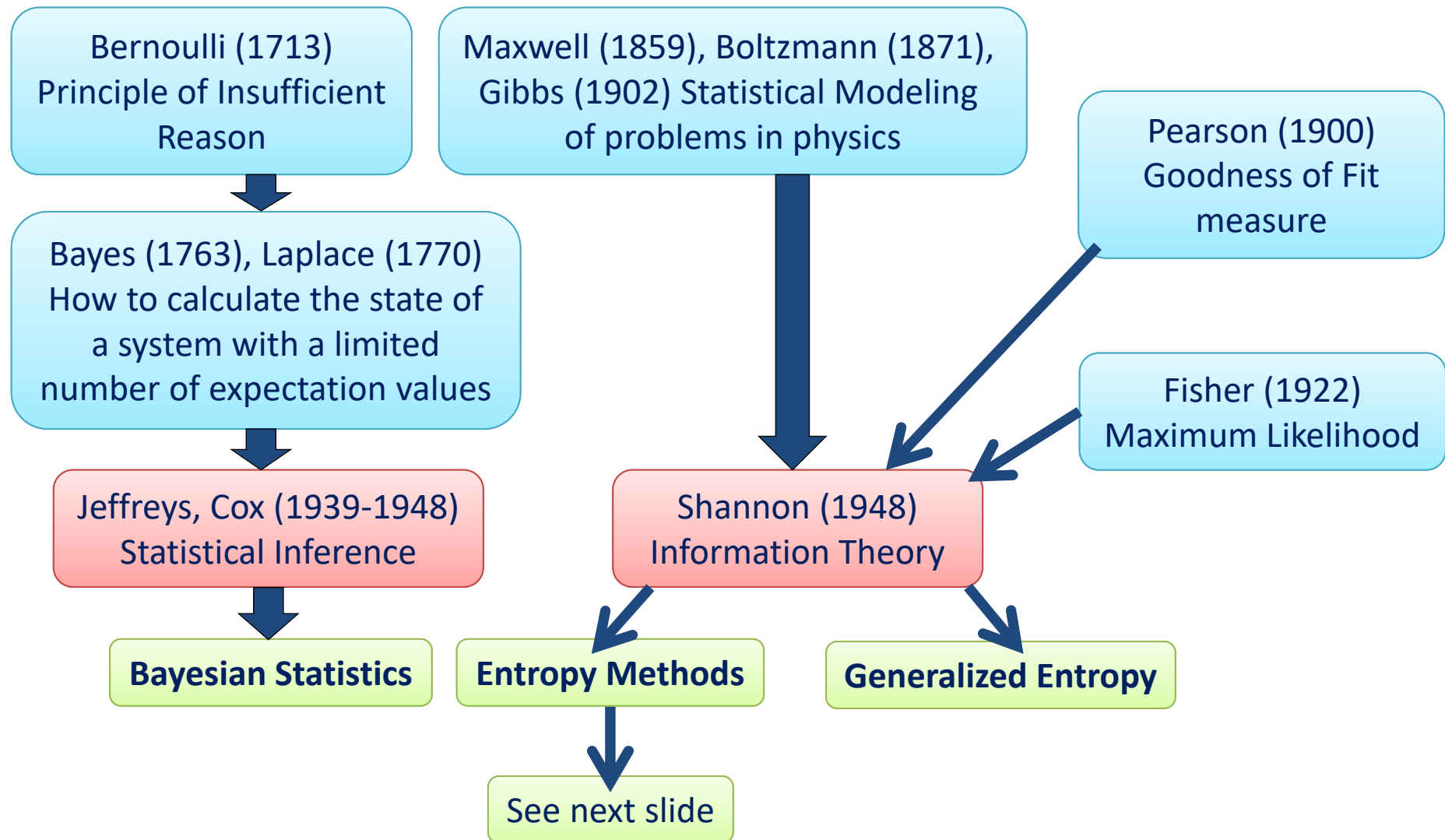


medium entropy
high complexity



high entropy
low complexity

<http://www.scottaaronson.com>



confer also with: Golan, A. (2008) Information and Entropy Econometric: A Review and Synthesis. *Foundations and Trends in Econometrics*, 2, 1-2, 1-145.

Entropic Methods

Jaynes (1957)
Maximum Entropy (MaxEn)

Adler et al. (1965)
Topology Entropy (TopEn)

Pincus (1991)
Approximate Entropy (ApEn)

Richman (2000)
Sample Entropy (SampEn)

Mowshowitz (1968)
Graph Entropy (MinEn)

Posner (1975)
Minimum Entropy (MinEn)

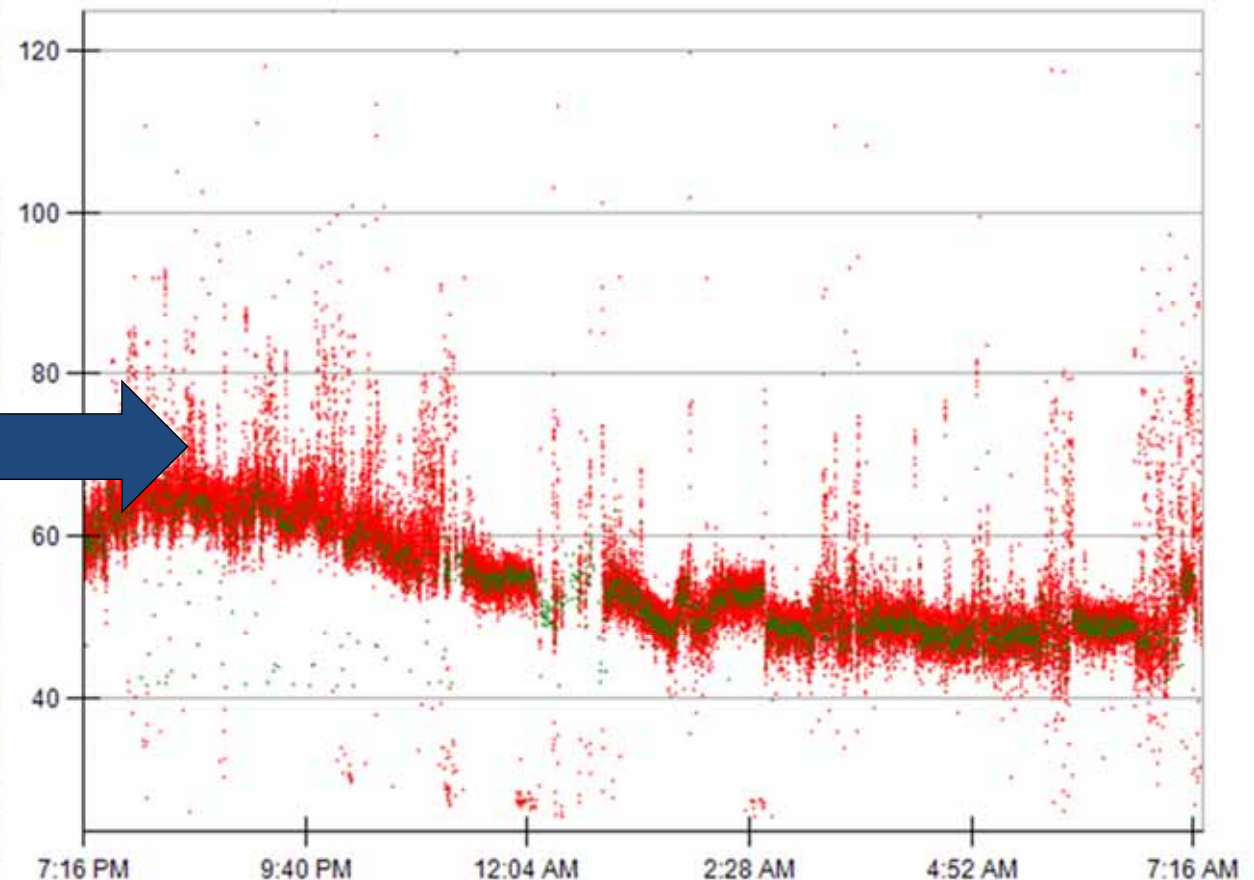
Rubinstein (1997)
Cross Entropy (CE)

Generalized Entropy

Renyi (1961)
Renyi-Entropy

Tsallis (1980)
Tsallis-Entropy

Holzinger, A., Hörtenhuber, M., Mayer, C., Bachler, M., Wassertheurer, S., Pinho, A. & Koslicki, D. 2014. On Entropy-Based Data Mining. In: Holzinger, A. & Jurisica, I. (eds.) Lecture Notes in Computer Science, LNCS 8401. Berlin Heidelberg: Springer, pp. 209-226.



Holzinger, A., Stocker, C., Bruschi, M., Auinger, A., Silva, H., Gamboa, H. & Fred, A. 2012. On Applying Approximate Entropy to ECG Signals for Knowledge Discovery on the Example of Big Sensor Data. In: Huang, R., Ghorbani, A., Pasi, G., Yamaguchi, T., Yen, N. & Jin, B. (eds.) *Active Media Technology, Lecture Notes in Computer Science, LNCS 7669*. Berlin Heidelberg: Springer, pp. 646-657.

EU Project EMERGE (2007-2010)

Let: $\langle x_n \rangle = \{x_1, x_2, \dots, x_N\}$

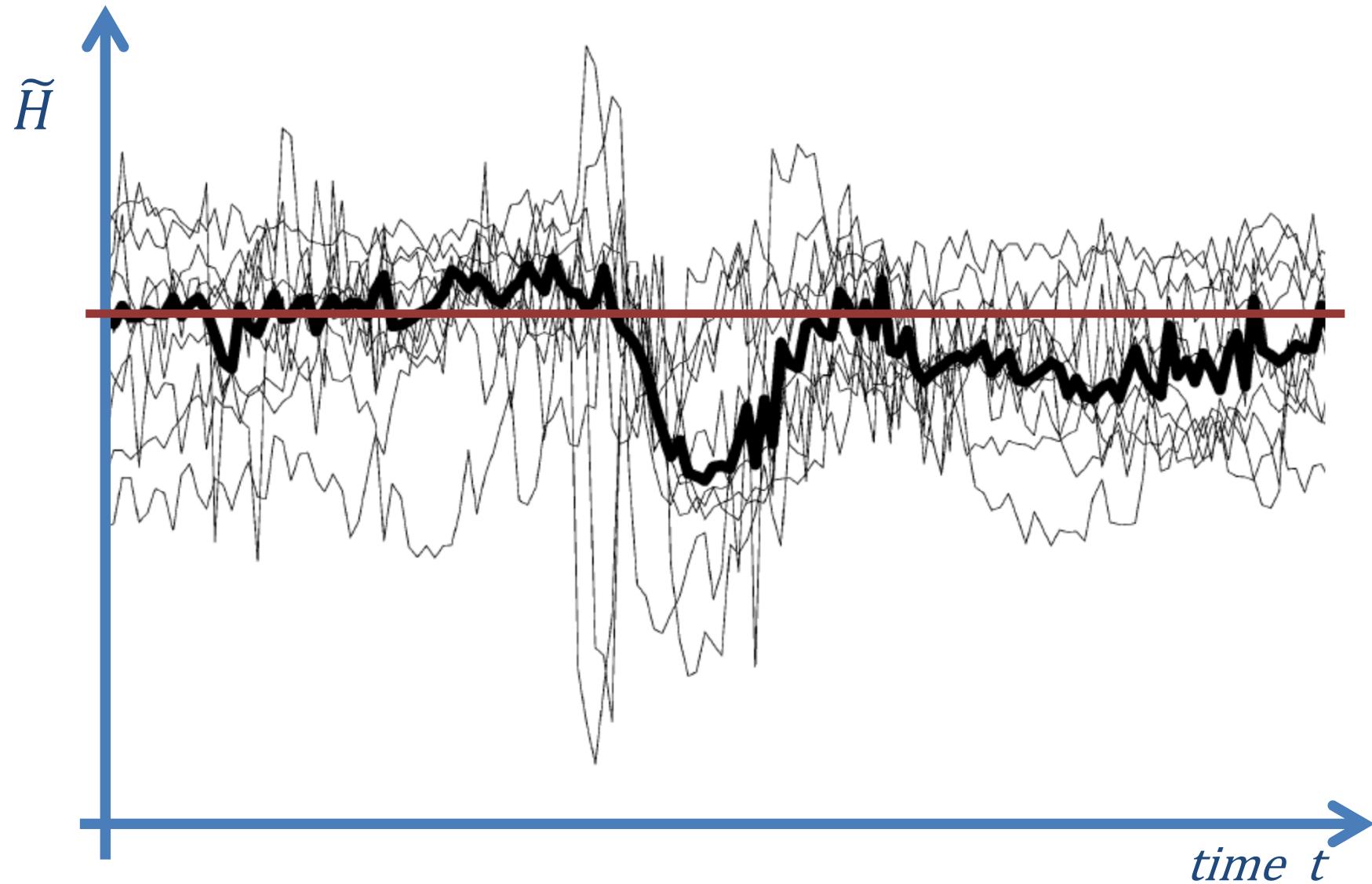
$$\vec{X}_i = (x_i, x_{(i+1)}, \dots, x_{(i+m-1)})$$

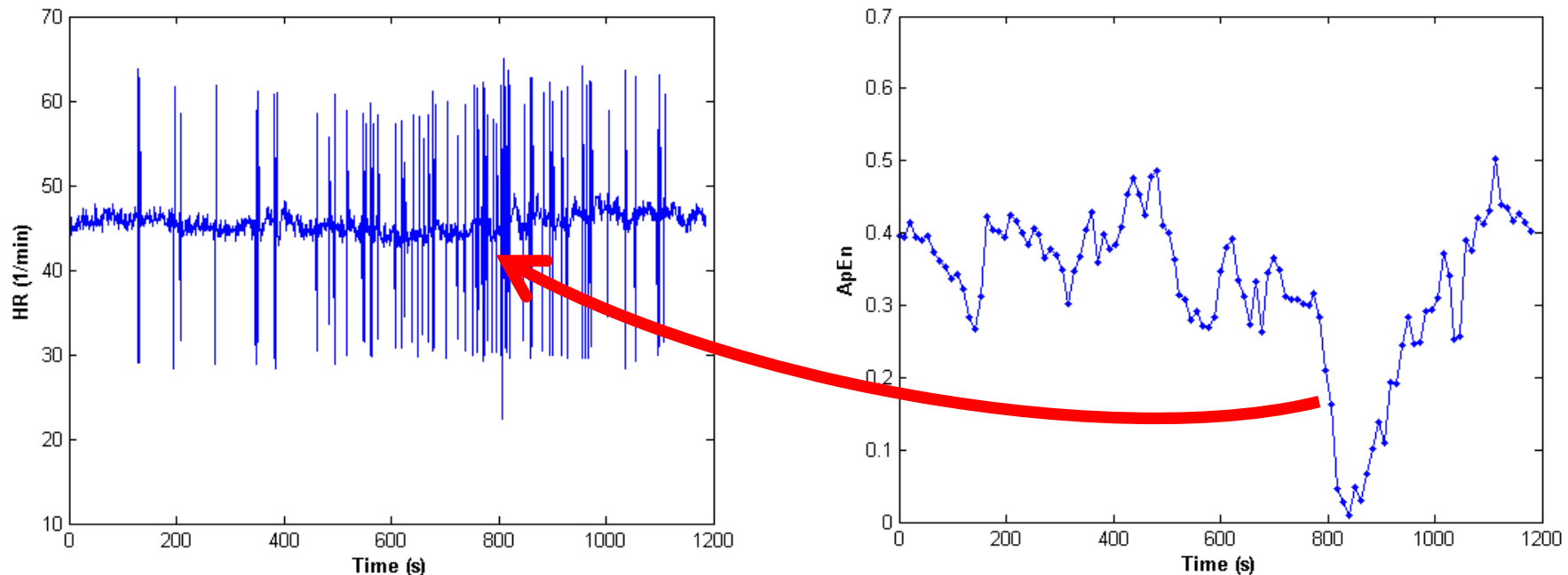
$$\|\vec{X}_i, \vec{X}_j\| = \max_{k=1,2,\dots,m} (|x_{(i+k-1)} - x_{(j+k-1)}|)$$

$$\tilde{H}(m, r) = \lim_{N \rightarrow \infty} [\phi^m(r) - \phi^{m+1}(r)]$$

$$C_r^m(i) = \frac{N^m(i)}{N - m + 1} \quad \phi^m(r) = \frac{1}{N - m + 1} \sum_{t=1}^{N-m+1} \ln C_r^m(i)$$

Pincus, S. M. (1991) Approximate Entropy as a measure of system complexity. *Proceedings of the National Academy of Sciences of the United States of America*, 88, 6, 2297-2301.





Holzinger, A., Hörtenhuber, M., Mayer, C., Bachler, M., Wassertheurer, S., Pinho, A. & Koslicki, D. 2014. On Entropy-Based Data Mining. In: Holzinger, A. & Jurisica, I. (eds.) Interactive Knowledge Discovery and Data Mining in Biomedical Informatics, Lecture Notes in Computer Science, LNCS 8401. Berlin Heidelberg: Springer, pp. 209-226.

Cross-Entropy Kullback-Leibler Divergence

- Entropy:
 - Measure for the **uncertainty** of random variables
- Kullback-Leibler divergence:
 - **comparing two distributions**
- Mutual Information:
 - measuring the **correlation** of two random variables

ON INFORMATION AND SUFFICIENCY

BY S. KULLBACK AND R. A. LEIBLER

The George Washington University and Washington, D. C.

1. Introduction. This note generalizes to the abstract case Shannon's definition of information [15], [16]. Wiener's information (p. 75 of [18]) is essentially the same as Shannon's although their motivation was different (cf. footnote 1, p. 95 of [16]) and Shannon apparently has investigated the concept more completely. R. A. Fisher's definition of information (intrinsic accuracy) is well known (p. 709 of [6]). However, his concept is quite different from that of Shannon and Wiener, and hence ours, although the two are not unrelated as is shown in paragraph 2.

R. A. Fisher, in his original introduction of the *criterion of sufficiency*, required "that the statistic chosen should summarize the whole of the relevant information supplied by the sample," (p. 316 of [5]). Halmos and Savage in a recent paper, one of the main results of which is a generalization of the well known Fisher-Neyman theorem on sufficient statistics to the abstract case, conclude, "We think that confusion has from time to time been thrown on the subject by . . . , and (c) the assumption that a sufficient statistic contains all the information in only the technical sense of 'information' as measured by variance," (p. 241 of [8]). It is shown in this note that the information in a sample as defined herein, that is, in the Shannon-Wiener sense cannot be increased by any statistical operations and is invariant (not decreased) if and only if sufficient statistics are employed. For a similar property of Fisher's information see p. 717 of [6], Doob [19].

We are also concerned with the statistical problem of discrimination ([3], [17]), by considering a measure of the "distance" or "divergence" between statistical populations ([1], [2], [13]) in terms of our measure of information. For the statistician two populations differ more or less according as to how difficult it is to discriminate between them with the best test [14]. The particular measure of divergence we use has been considered by Jeffreys ([10], [11]) in another connection. He is primarily concerned with its use in providing an invariant density of *a priori* probability. A special case of this divergence is Mahalanobis' generalized distance [13].



Solomon Kullback 1907-1994



Richard Leibler 1914-2003

Kullback, S. & Leibler, R. A.
1951. On information and
sufficiency. The annals of
mathematical statistics, 22, (1),
79-86,
www.jstor.org/stable/2236703

$$H[x] = - \sum_x p(x) \log_2 p(x)$$

Shannon, C. E. 1948. A Mathematical Theory of Communication. Bell System Technical Journal, 27, 379-423.

Important quantity in

- coding theory
- statistical physics
- machine learning

$$H[\mathbf{y}|\mathbf{x}] = - \iint p(\mathbf{y}, \mathbf{x}) \ln p(\mathbf{y}|\mathbf{x}) \, d\mathbf{y} \, d\mathbf{x}$$

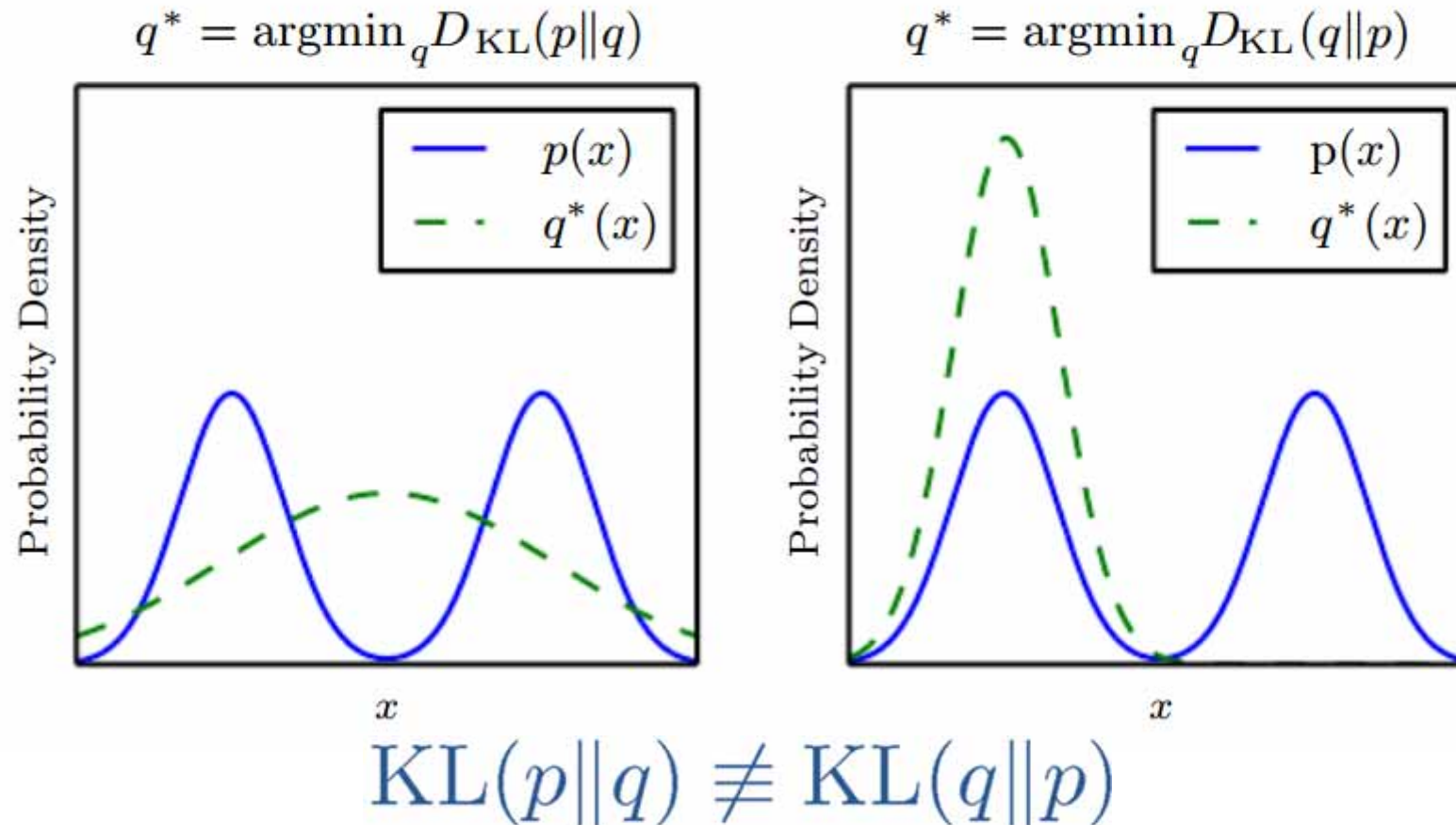
$$H[\mathbf{x}, \mathbf{y}] = H[\mathbf{y}|\mathbf{x}] + H[\mathbf{x}]$$

$$\begin{aligned}\text{KL}(p\|q) &= - \int p(\mathbf{x}) \ln q(\mathbf{x}) \, d\mathbf{x} - \left(- \int p(\mathbf{x}) \ln p(\mathbf{x}) \, d\mathbf{x} \right) \\ &= - \int p(\mathbf{x}) \ln \left\{ \frac{q(\mathbf{x})}{p(\mathbf{x})} \right\} \, d\mathbf{x}\end{aligned}$$

$$\text{KL}(p\|q) \simeq \frac{1}{N} \sum_{n=1}^N \{ -\ln q(\mathbf{x}_n|\boldsymbol{\theta}) + \ln p(\mathbf{x}_n) \}$$

$$\text{KL}(p\|q) \geq 0$$

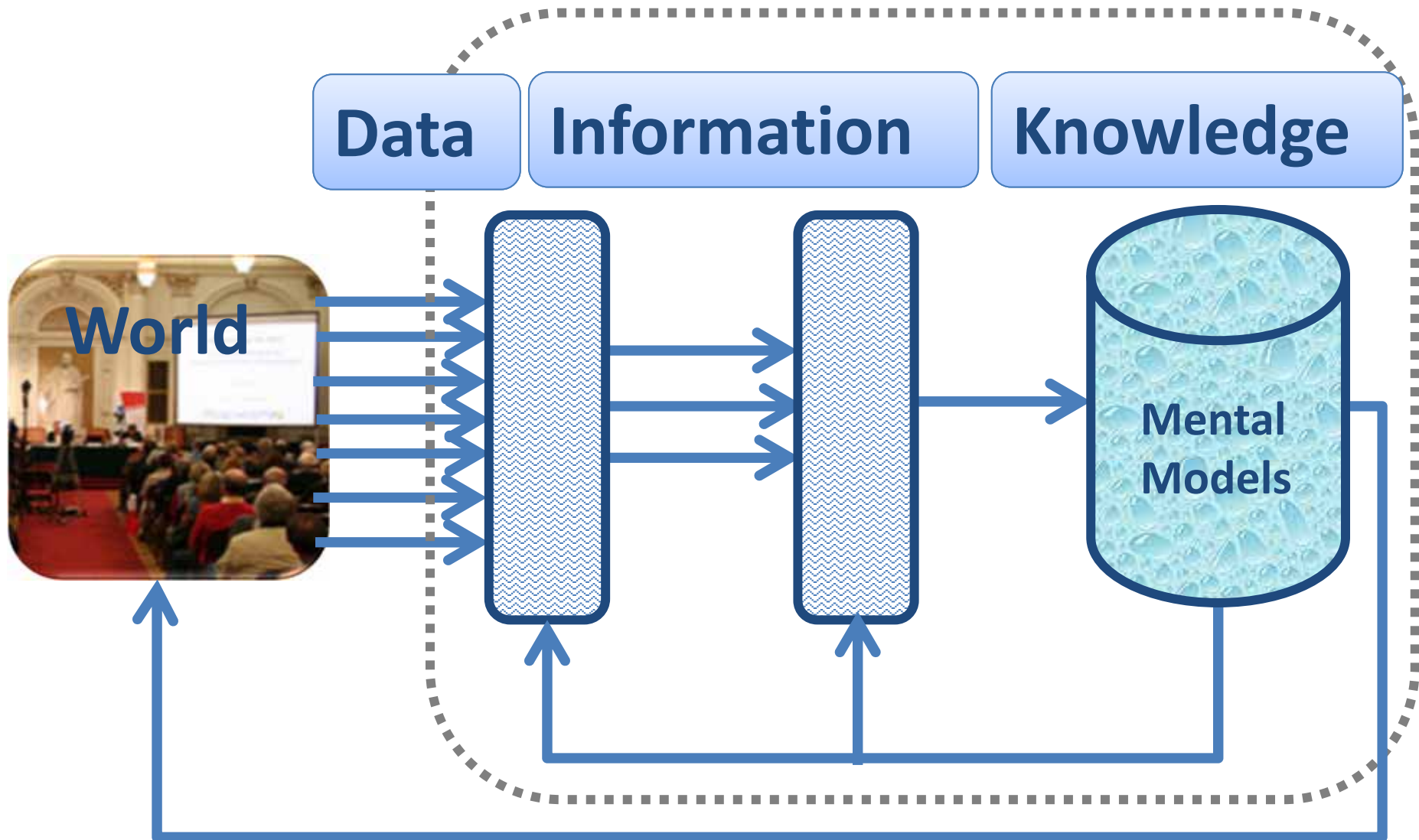
KL-divergence is often used to measure the distance between two distributions



Goodfellow, I., Bengio, Y. & Courville, A. 2016. Deep Learning, Cambridge (MA), MIT Press.

- ... are **robust** against noise;
- ... can be applied to **complex time series** with good replication;
- ... is **finite** for stochastic, noisy, composite processes;
- ... the values correspond directly to irregularities – good for detecting **anomalies**

05 Knowledge Representation

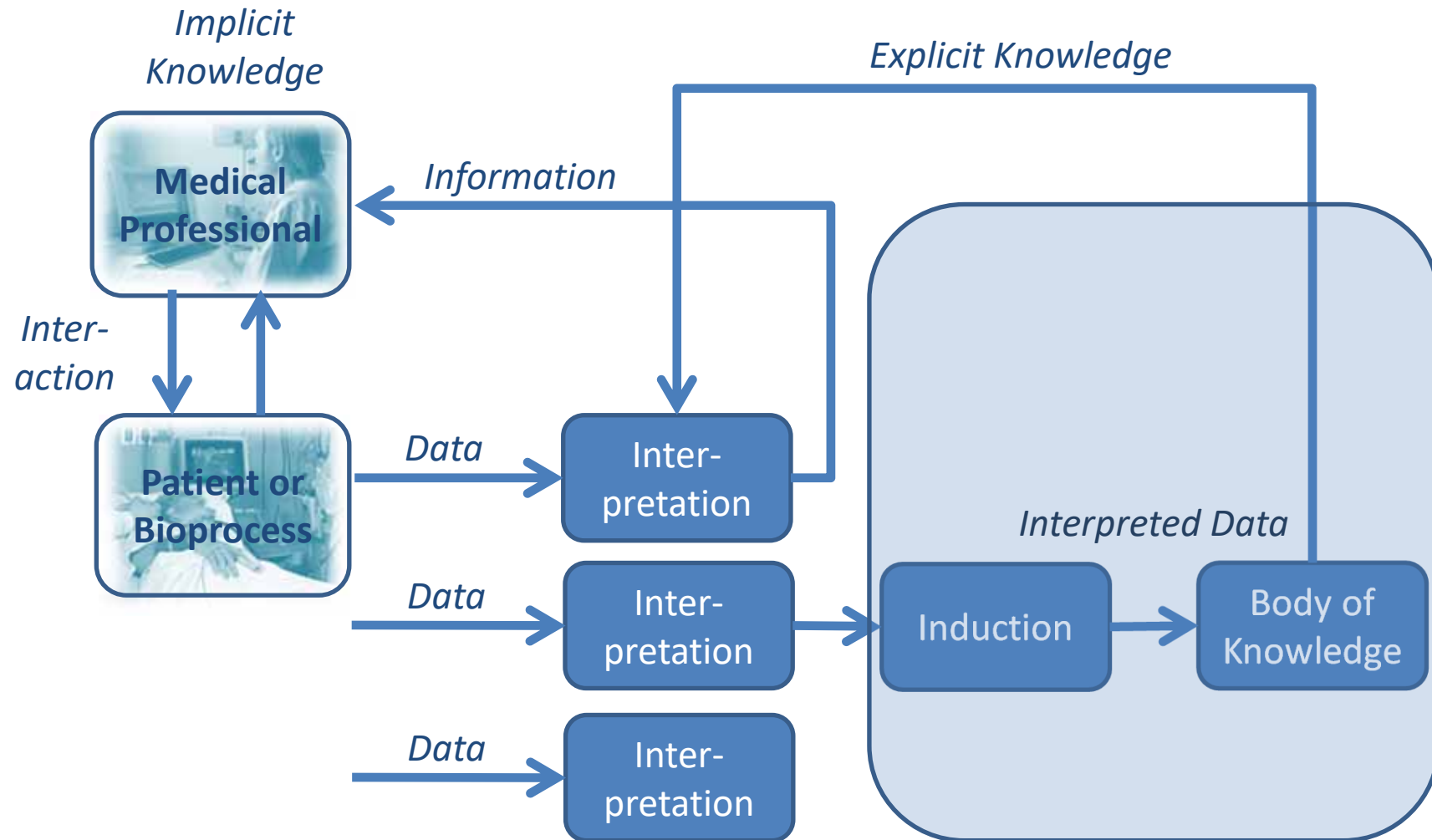


Knowledge := a set of expectations



Biomedical informatics (BMI) is the interdisciplinary field that studies and pursues the effective use of biomedical data, information, and knowledge for scientific problem solving, and decision making, motivated by efforts to improve human health

Edward H. Shortliffe 2011. Biomedical Informatics: Defining the Science and its Role in Health Professional Education. In: Holzinger, Andreas & Simon, Klaus-Martin (eds.) Information Quality in e-Health. Lecture Notes in Computer Science LNCS 7058. Heidelberg, New York: Springer, pp. 711-714.

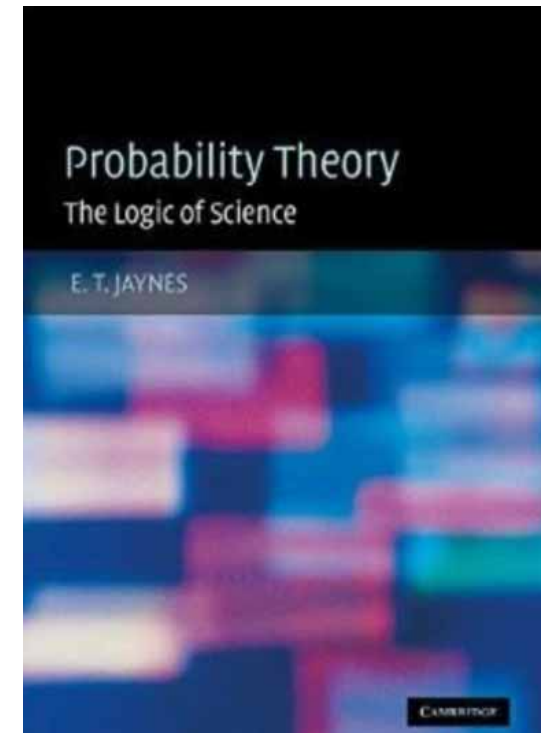


Bemmel, J. H. v. & Musen,
M. A. (1997) *Handbook of
Medical Informatics*.
Heidelberg, Springer.

• •
• •
• •

- Logical representations are based on
 - Facts about the world (true or false)
 - These facts can be combined with logical operators
 - Logical inference is based on certainty

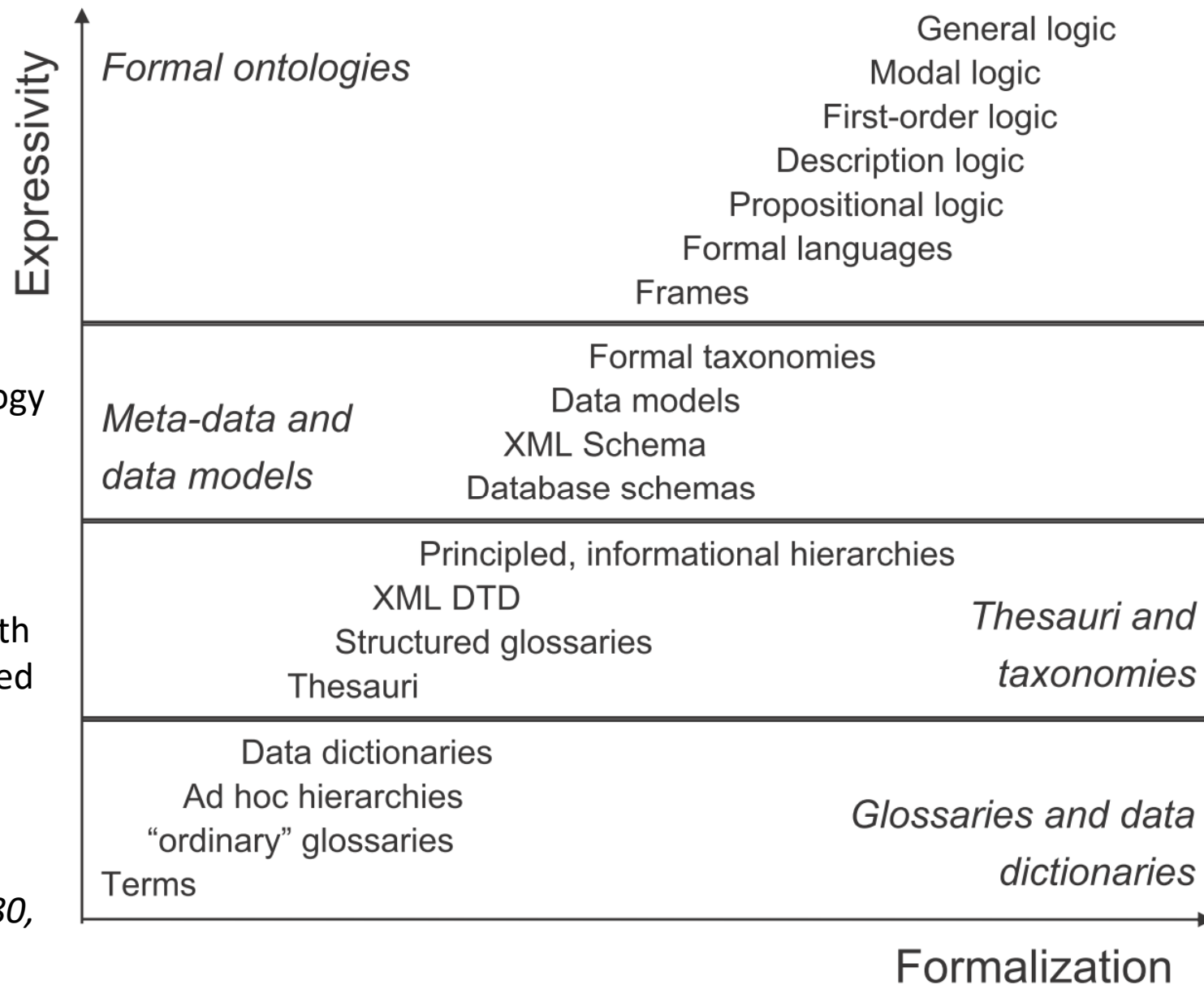
Edwin T. Jaynes 2003. Probability theory: The logic of science, Cambridge, Cambridge University Press.

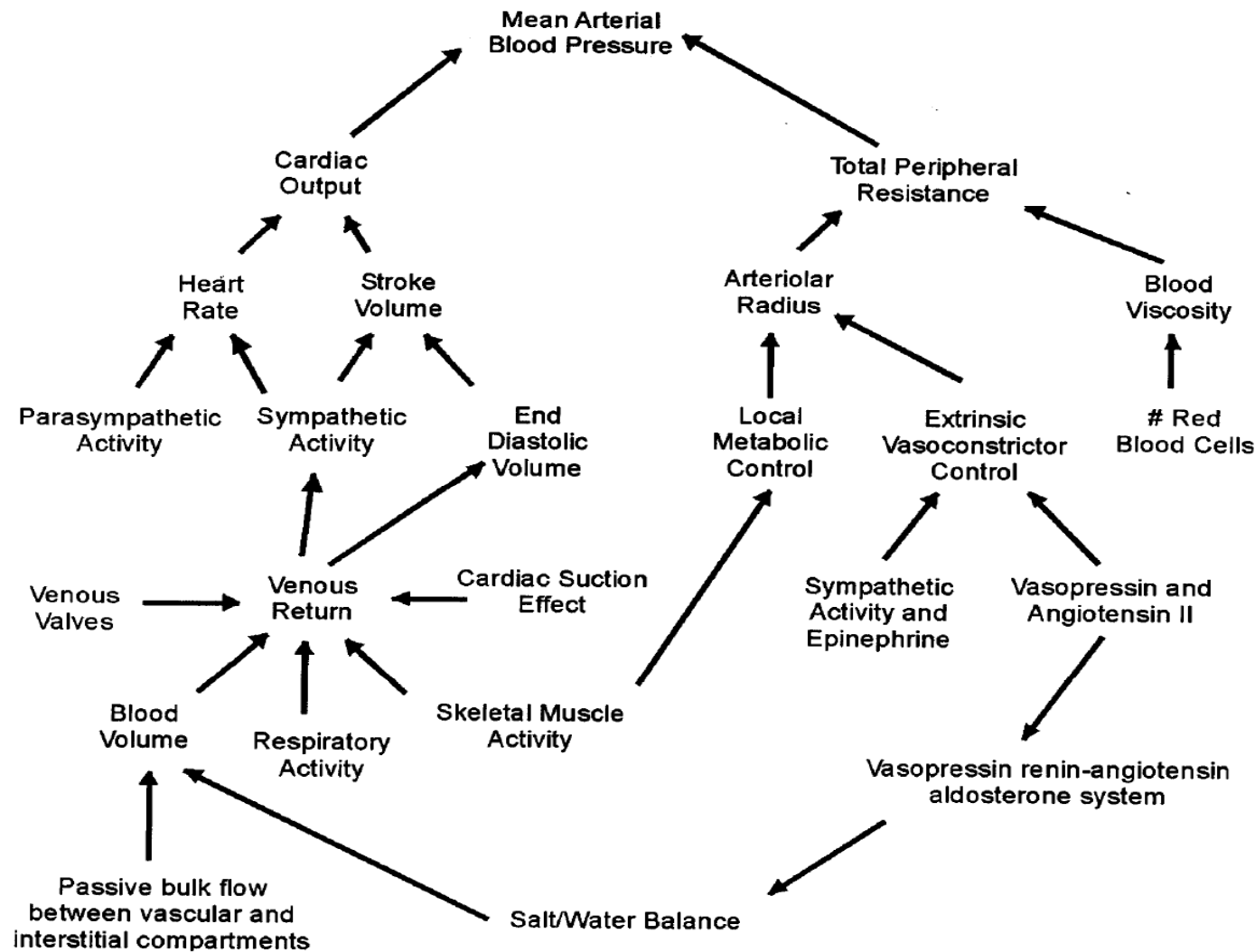


Mathematical Logic	Psychology	Biology	Statistics	Economics
Aristotle				
Descartes				
Boole	James		Laplace	Bentham Pareto
Frege Peano			Bernoullii	Friedman
Goedel	Hebb	Lashley	Bayes	
Post	Bruner	Rosenblatt		
Church	Miller	Ashby	Tversky, Kahneman	Von Neumann
Turing	Newell, Simon	Lettvin		Simon
Davis		McCulloch, Pitts		Raiffa
Putnam		Heubel, Weisel		
Robinson				
Logic PROLOG	SOAR KBS, Frames	Connectionism	Causal Networks	Rational Agents

Davis, R., Shrobe, H. , Szolovits, P. 1993 What is a knowledge representation? AI Magazine, 14, 1, 17-33.

Blobel, B.
(2011) Ontology
driven health
information
systems
architectures
enable pHealth
for empowered
patients.
*International
Journal of
Medical
Informatics*, 80,
2, e17-e25.





Hajdukiewicz, J. R., Vicente, K. J., Doyle, D. J., Milgram, P. & Burns, C. M. (2001) Modeling a medical environment: an ontology for integrated medical informatics design. *International Journal of Medical Informatics*, 62, 1, 79-99.

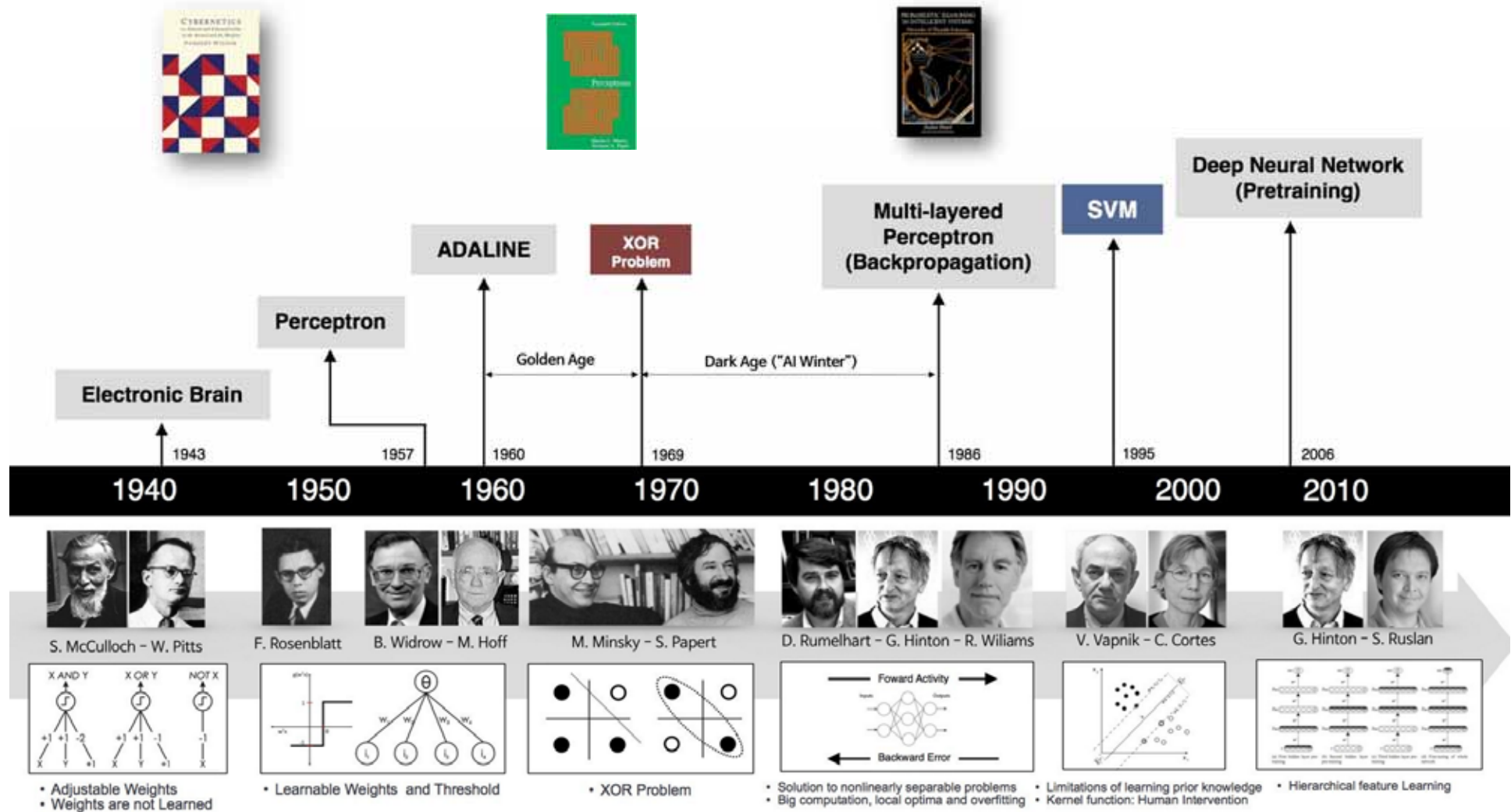
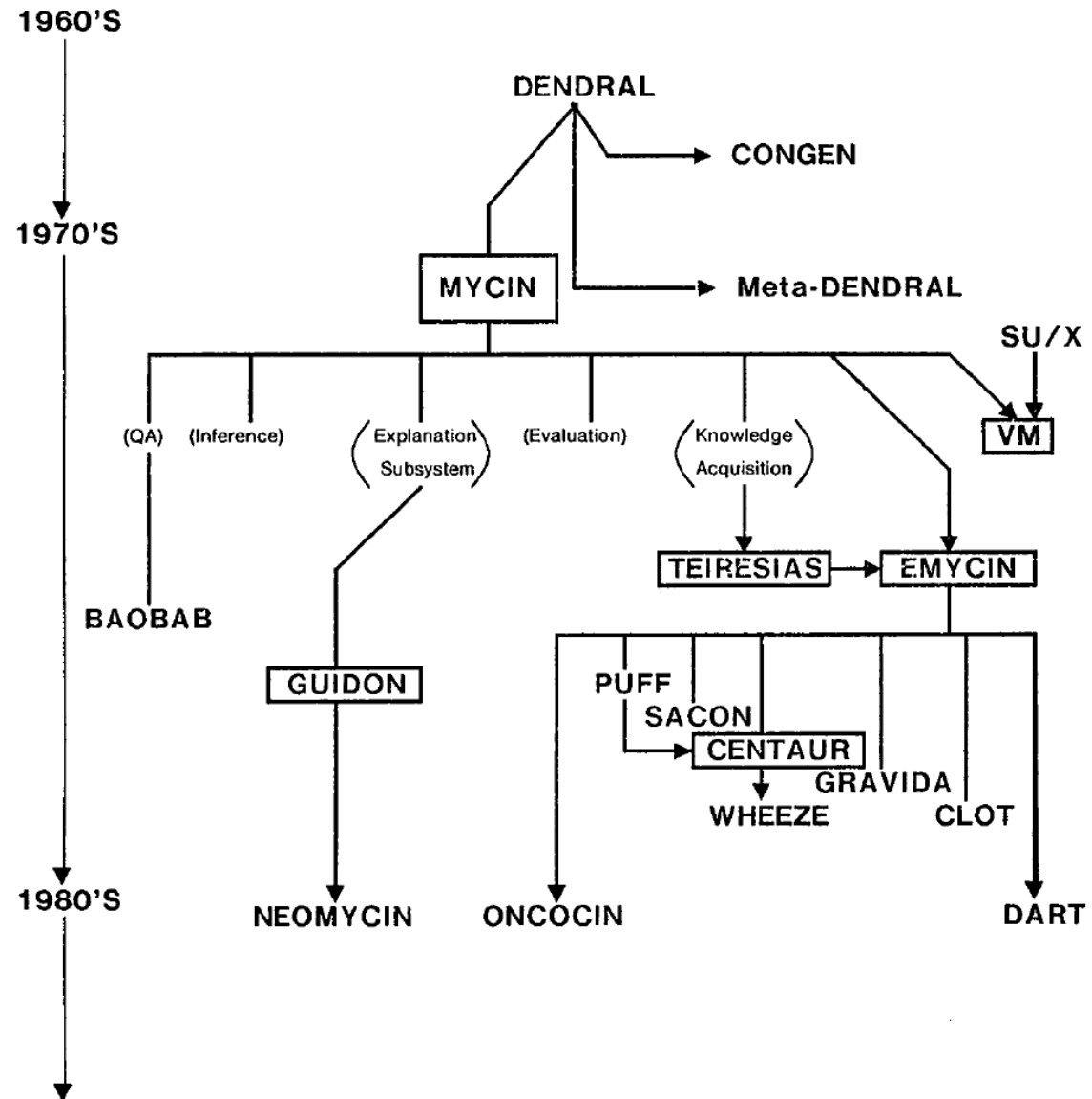


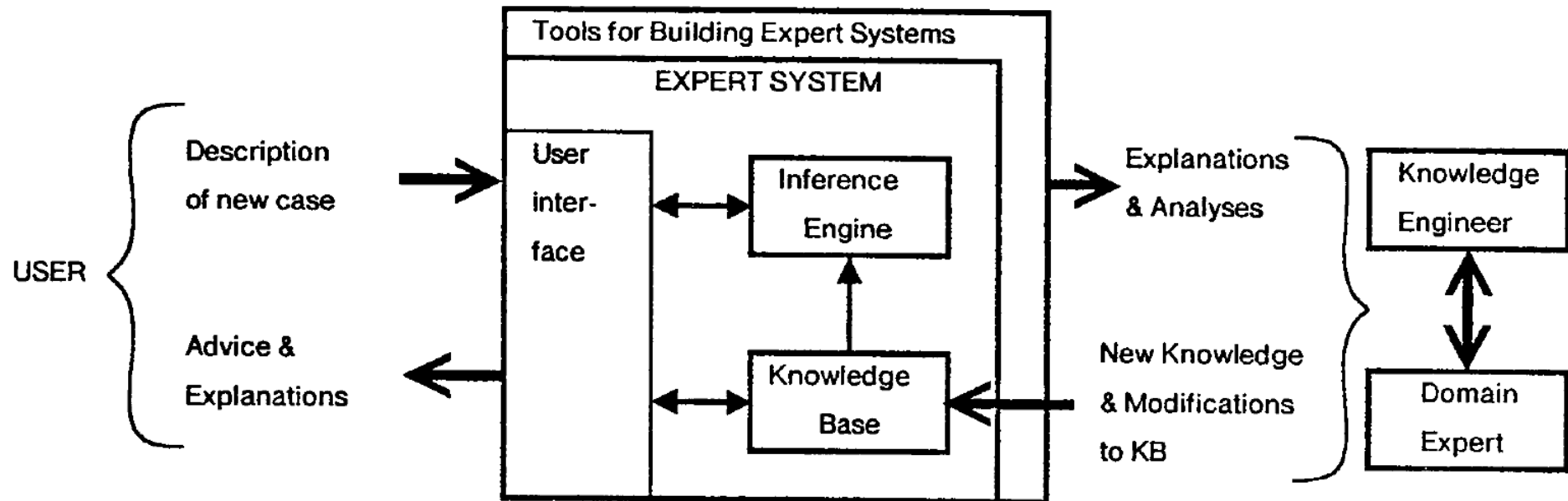
Image source: Andrew Beam, Department of Biomedical Informatics, Harvard Medical School

<https://slides.com/beamandrew/deep-learning-101/#/12>

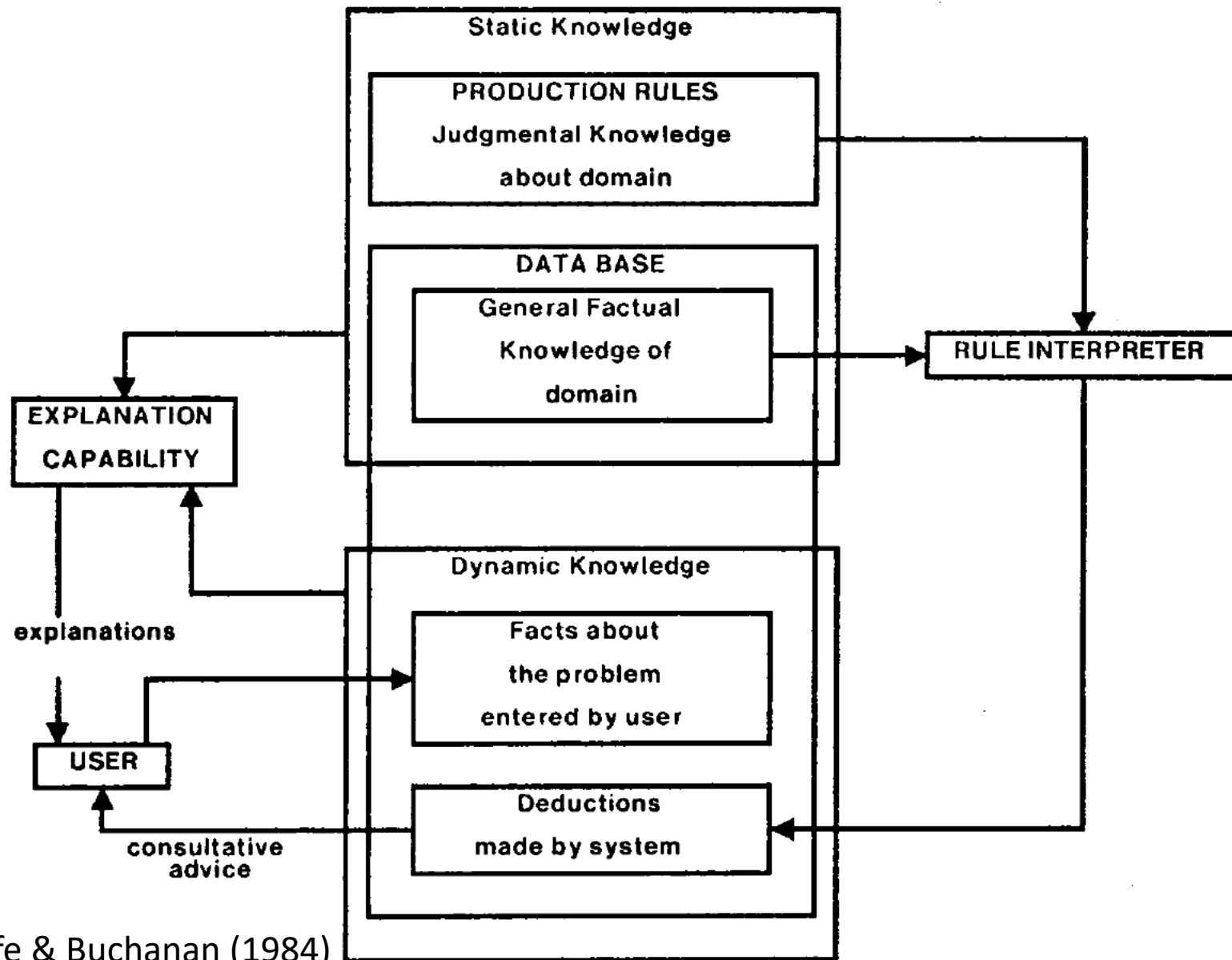
This image is used according UrhG §42 lit. f Abs 1 as “Belegfunktion” for discussion with students

Shortliffe, E. H. &
Buchanan, B. G. (1984)
*Rule-based expert
systems: the MYCIN
experiments of the
Stanford Heuristic
Programming Project.*
Addison-Wesley.





Shortliffe, T. & Davis, R. (1975) Some considerations for the implementation of knowledge-based expert systems *ACM SIGART Bulletin*, 55, 9-12.



Shortliffe & Buchanan (1984)

- MYCIN is a rule-based Expert System, which is used for therapy planning for patients with bacterial infections
- Goal oriented strategy (“Rückwärtsverkettung”)
- To every rule and every entry a certainty factor (CF) is assigned, which is between 0 und 1
- Two measures are derived:
 - MB: measure of belief
 - MD: measure of disbelief
- Certainty factor – CF of an element is calculated by:
$$CF[h] = MB[h] - MD[h]$$
- CF is positive, if more evidence is given for a hypothesis, otherwise CF is negative
- $CF[h] = +1 \rightarrow h$ is 100 % true
- $CF[h] = -1 \rightarrow h$ is 100% false

h_1 = The identity of ORGANISM-1 is streptococcus

h_2 = PATIENT-1 is febrile

h_3 = The name of PATIENT-1 is John Jones

$CF[h_1, E] = .8$: There is strongly suggestive evidence (.8) that the identity of ORGANISM-1 is streptococcus

$CF[h_2, E] = -.3$: There is weakly suggestive evidence (.3) that PATIENT-1 is not febrile

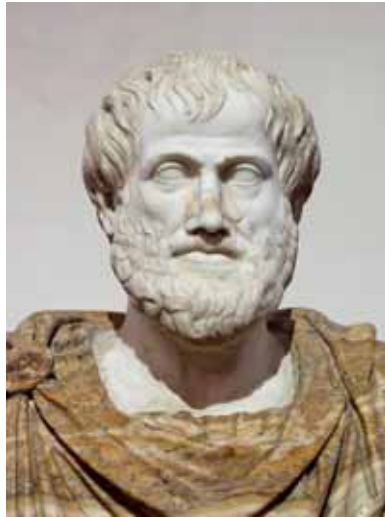
$CF[h_3, E] = +1$: It is definite (1) that the name of PATIENT-1 is John Jones

Shortliffe, E. H. & Buchanan, B. G. (1984) *Rule-based expert systems: the MYCIN experiments of the Stanford Heuristic Programming Project*. Addison-Wesley.

Ontologies

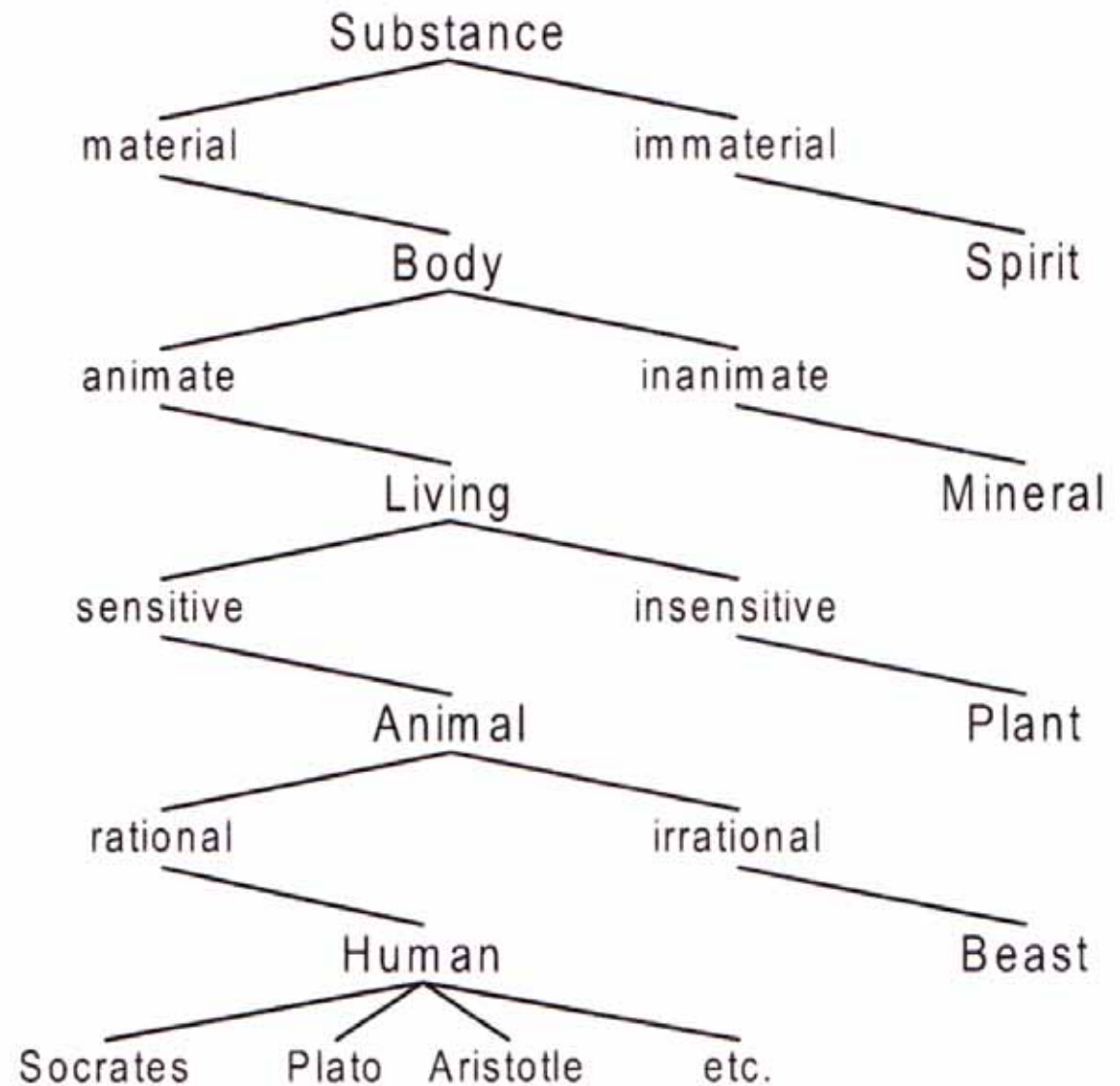


Image Sources: The images are in the public domain and are used according UrhG §42 lit. f Abs 1 as “Belegfunktion” for discussion with students



* 384 BC † 322 BC

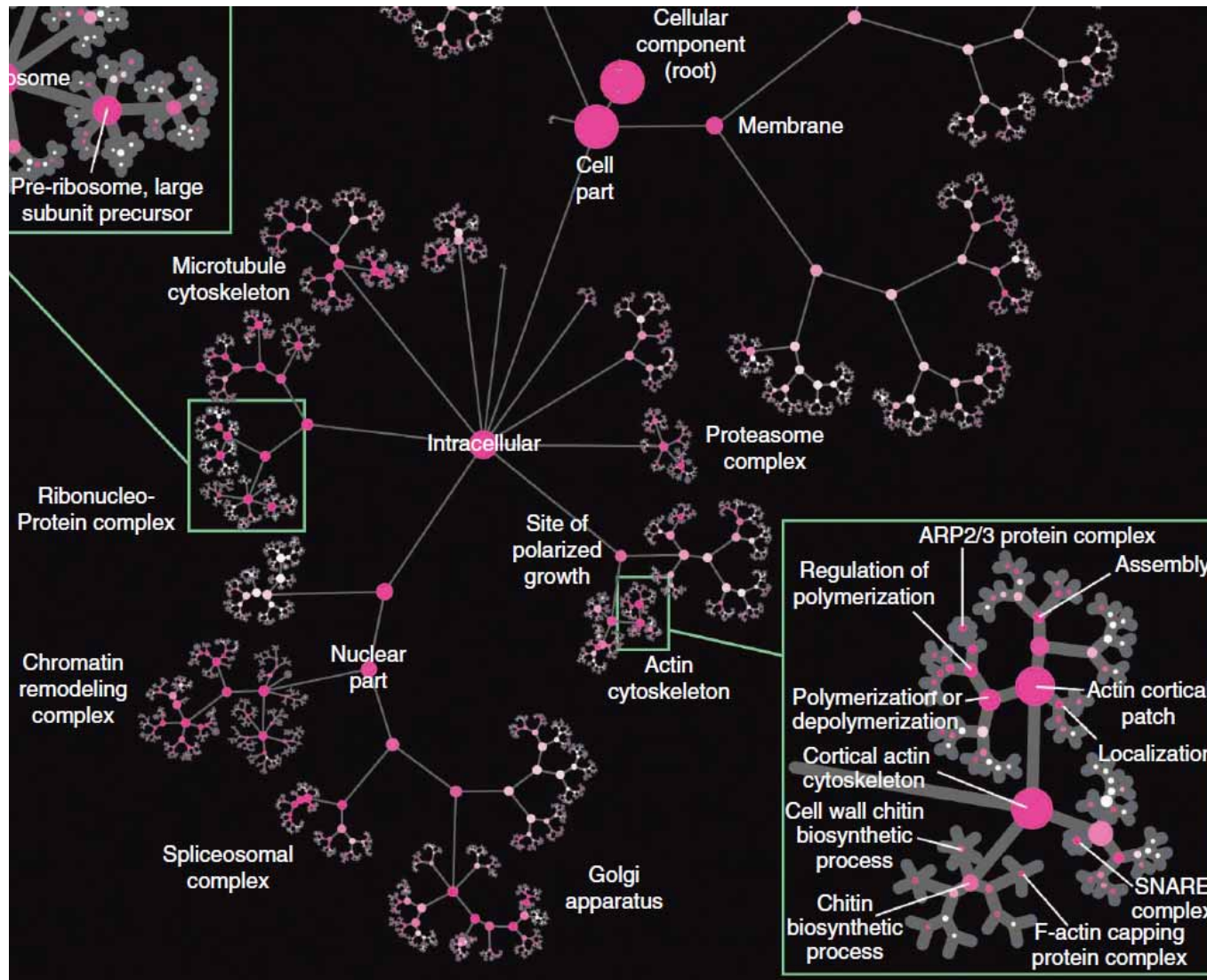
Simonet, M., Messai, R., Diallo, G. & Simonet, A. (2009) Ontologies in the Health Field. In: Berka, P., Rauch, J. & Zighed, D. A. (Eds.) *Data Mining and Medical Knowledge Management: Cases and Applications*. New York, Medical Information Science Reference, 37-56.



Later: Porphyry (≈ 234-305) tree

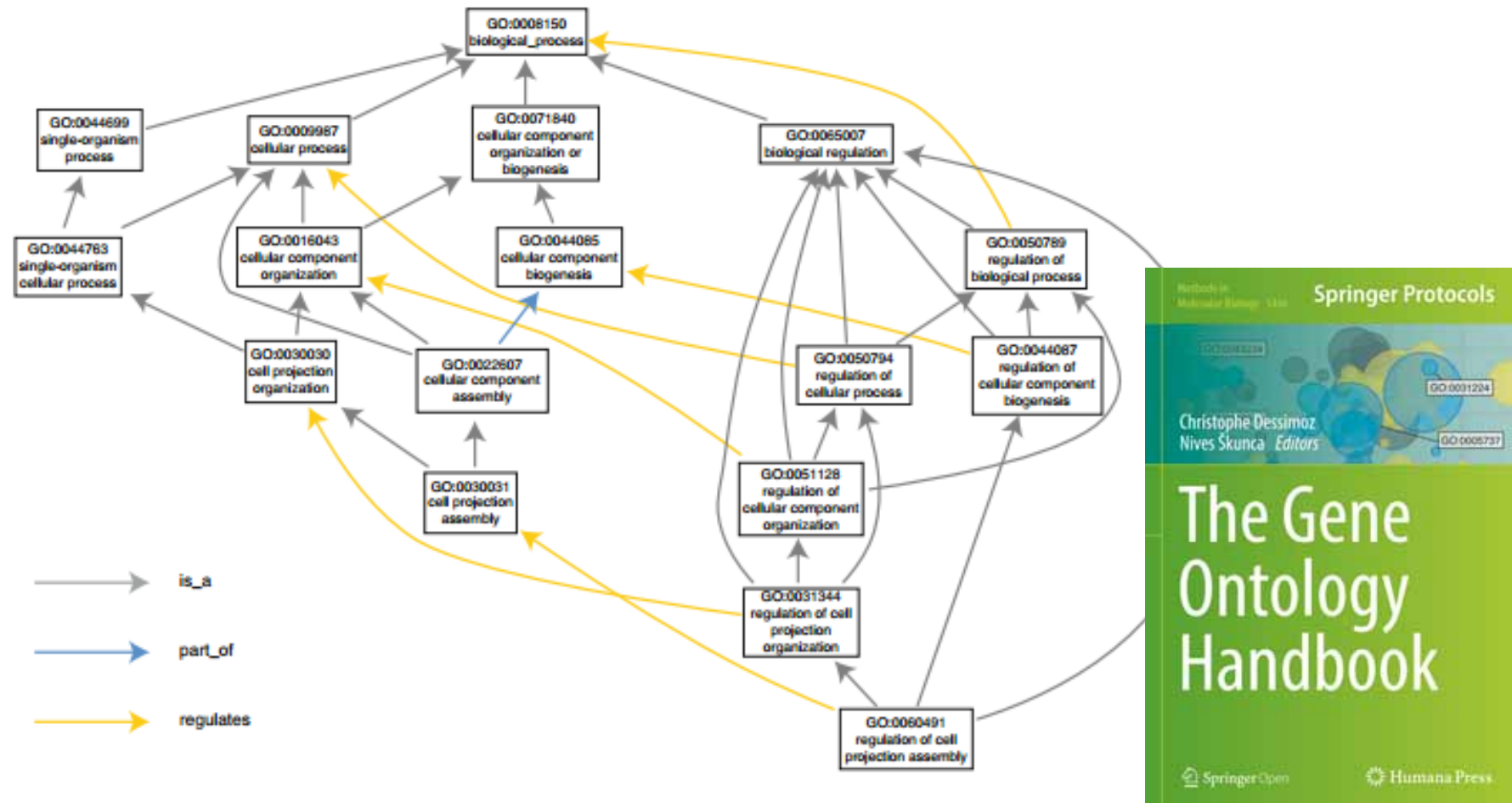
- Aristotle attempted to **classify the things in the world** - where it is employed to describe the existence of beings in the world;
- Artificial Intelligence and Knowledge Engineering deals also with **reasoning about models of the world**.
- Therefore, AI researchers adopted the term 'ontology' to describe **what can be computationally represented** of the world within a program.
- **“An ontology is a formal, explicit specification of a shared conceptualization”.**
 - A 'conceptualization' refers to an **abstract model** of some phenomenon in the world by having identified the relevant concepts of that phenomenon.
 - 'Explicit' means that the type of concepts used, and the constraints on their use are **explicitly defined**.

Studer, R., Benjamins, V. R. & Fensel, D. (1998) Knowledge Engineering: Principles and methods. *Data & Knowledge Engineering*, 25, 1-2, 161-197.



Janusz Dutkowski, Michael Kramer, Michal A Surma, Rama Balakrishnan, J Michael Cherry, Nevan J Krogan & Trey Ideker
2013. A gene ontology inferred from molecular networks. Nature biotechnology, 31, (1), 38.

<http://geneontology.org/>

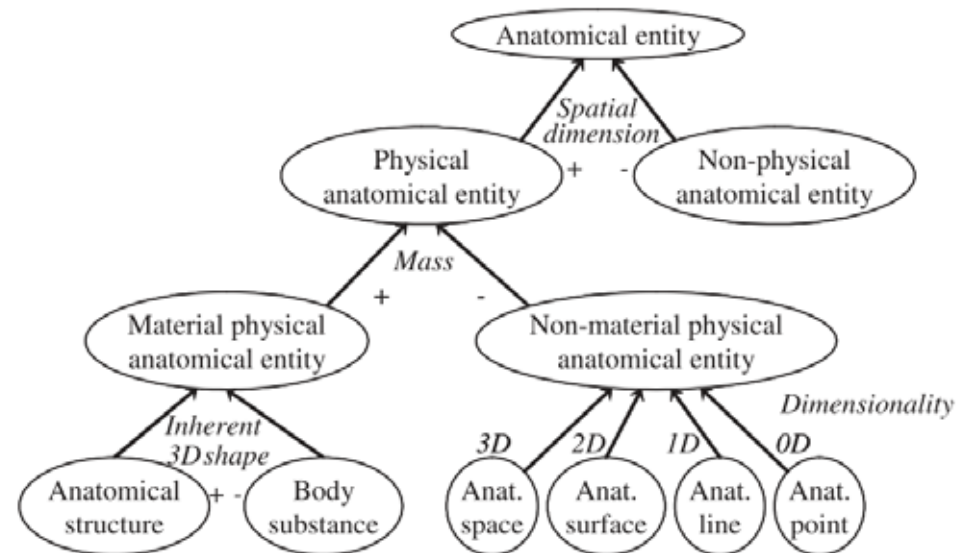


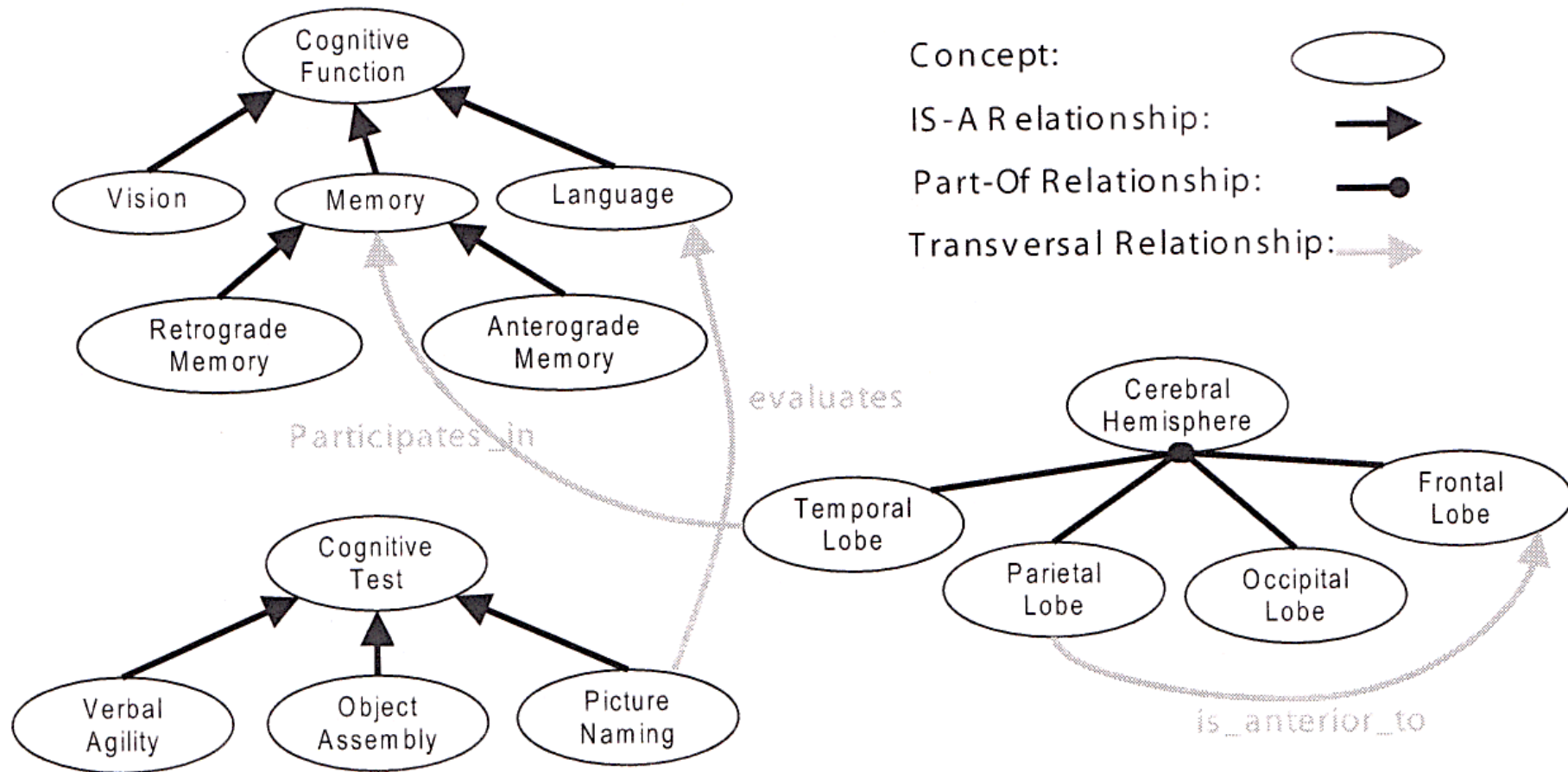
Hastings, J. 2017. Primer on Ontologies. In: Dessimoz, C. & Škunca, N. (eds.) *The Gene Ontology Handbook*. New York, NY: Springer New York, pp. 3-13, doi:10.1007/978-1-4939-3743-1_1.

- Ontology = a structured description of a domain in form of **concepts** \leftrightarrow **relations**;
- The **IS-A relation** provides a taxonomic skeleton;
- Other relations reflect the **domain semantics**;
- Formalizes the **terminology** in the domain;
- Terminology = terms definition and usage in the specific **context**;
- Knowledge base = **instance classification** and **concept classification**;
- Classification provides the **domain terminology**
- ...

- (1) In addition to the IS-A relationship, partitive (meronomic) relationships may hold between concepts, denoted by PART-OF. Every PART-OF relationship is irreflexive, asymmetric and transitive. IS-A and PART-OF are also called hierarchical relationships.
- (2) In addition to hierarchical relationships, associative relationships may hold between concepts. Some associative relationships are domain-specific (e.g., the branching relationship between arteries in anatomy and rivers in geography).
- (3) Relationships r and r' are inverses if, for every pair of concepts x and y , the relations $\langle x, r, y \rangle$ and $\langle y, r', x \rangle$ hold simultaneously. A symmetric relationship is its own inverse. Inverses of hierarchical relationships are called INVERSE-IS-A and HAS-PART, respectively.
- (4) Every non-taxonomic relation of x to z , $\langle x, r, z \rangle$, is either inherited ($\langle y, r, z \rangle$) or refined ($\langle y, r, z' \rangle$ where z' is more specific than z) by every child y of x . In other words, every child y of x has the same properties (z) as its parent or more specific properties (z').

Zhang, S. & Bodenreider, O. 2006. Law and order: Assessing and enforcing compliance with ontological modeling principles in the Foundational Model of Anatomy. *Computers in Biology and Medicine*, 36, (7-8), 674-693.





Simonet, M., Messai, R., Diallo, G. & Simonet, A. (2009) Ontologies in the Health Field. In: Berka, P., Rauch, J. & Zighed, D. A. (Eds.) *Data Mining and Medical Knowledge Management: Cases and Applications*. New York, Medical Information Science Reference, 37-56.

Name	Ref.	Scope	# concepts	# concept names				Subs. Hier.	Version / Notes
				Min	Max	Med	Avg		
SNOMED CT	[21]	Clinical medicine (patient records)	310,314	1	37	2	2.57	yes	July 31, 2007
LOINC	[24]	Clinical observations and laboratory tests	46,406	1	3	3	2.85	no	Version 2.21 (no “natural language” names)
FMA	[25]	Human anatomical structures	~72,000	1	?	?	~1.50	yes	(not yet in the UMLS)
Gene Ontology	[28]	Functional annotation of gene products	22,546	1	24	1	2.15	yes	Jan. 2, 2007
RxNorm	[31]	Standard names for prescription drugs	93,426	1	2	1	1.10	no	Aug. 31, 2007
NCI Thesaurus	[34]	Cancer research, clinical care, public information	58,868	1	100	2	2.68	yes	2007_05E
ICD-10	[36]	Diseases and conditions (health statistics)	12,318	1	1	1	1.00	no	1998 (tabular)
MeSH	[38]	Biomedicine (descriptors for indexing the literature)	24,767	1	208	5	7.47	no	Aug. 27, 2007
UMLS Meta.	[41]	Terminology integration in the life sciences	1,4 M	1	339	2	3.77	n/a	2007AC (English only)

Bodenreider, O. (2008) Biomedical ontologies in action: role in knowledge management, data integration and decision support. *Methods of Information In Medicine*, 47, Supplement 1, 67-79.

- **1) Graph notations**
 - Semantic networks
 - Topic Maps (ISO/IEC 13250)
 - Unified Modeling Language (UML)
 - Resource Description Framework (RDF)
- **2) Logic based**
 - Description Logics (e.g., OIL, DAML+OIL, OWL)
 - Rules (e.g. RuleML, LP/Prolog)
 - First Order Logic (KIF – Knowledge Interchange Format)
 - Conceptual graphs
 - (Syntactically) higher order logics (e.g. LBase)
 - Non-classical logics (e.g. Flogic, Non-Mon, modalities)
- **3) Probabilistic/fuzzy**

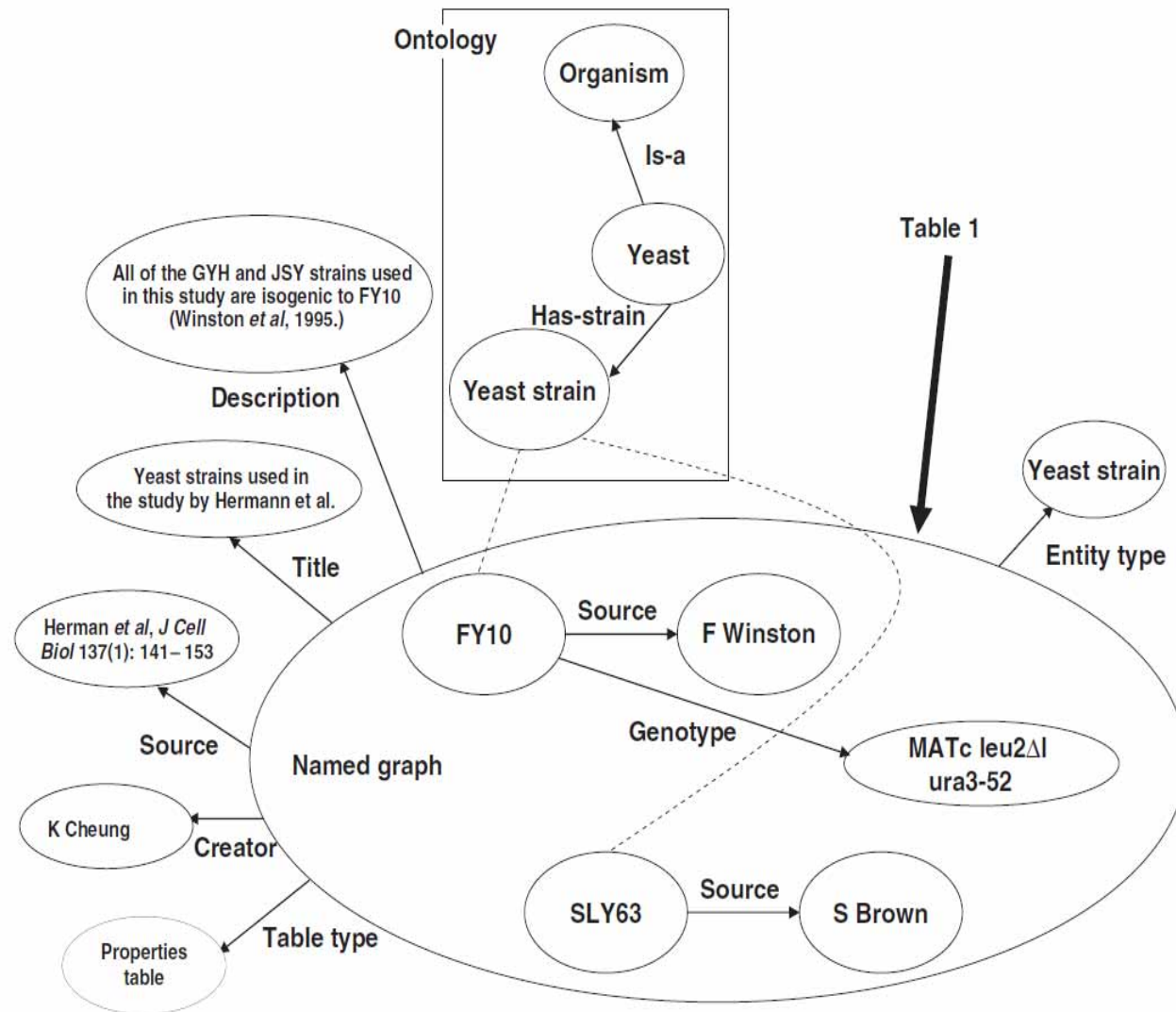


Table 1 Yeast strains used in the study by Hermann et al (1997)

Name	Genotype*	Source
FY10	MAT α leu2 Δ 1 ura3-52	F Winston
FY22	MAT α his3 Δ 200 ura3-52	F Winston
GHY1	MAT α leu2 Δ 1 his3 Δ 200 ura3-52 mdm20-1	This study
JSY707	MAT α his3 Δ 200 ura3-52 tpm1D::HIS3	This study
JSY948	MAT α leu2 Δ 1/leu2 Δ 1 ura3-52/ura3-52	This study
JSY999	MAT α leu2 Δ 1 his3 Δ 200 ura3-52	This study
JSY1065	MAT α leu2 Δ 1 his3 Δ 200 ura3-52 mdm20D::LEU2	This study
JSY1084	MAT α leu2 Δ 1 his3 Δ 200 ura3-52 tpm1D::HIS3	This study
JSY1138	MAT α leu2 Δ 1/leu2 Δ 1 his3 Δ 200/his3 Δ 200 ura3-52/ura3-52 tpm1D::HIS3/ + mdm20D::LEU2/ +	This study
JSY1285	MAT α leu2 Δ 1 his3 Δ 200 ura3-52 tpm2D::HIS3	This study
JSY1340	MAT α leu2 Δ 1 his3 Δ 200 ura3-52 mdm20D::LEU2	This study
JSY1374	MAT α leu2 Δ 1/leu2 Δ 1 his3 Δ 200/his3 Δ 200 ura3-52/ura3-52 tpm2D::HIS3/ + mdm20D::LEU2/ +	This study
ABY1249	MAT α leu2-3,112 ura3-52 lys2-801 ade2-101 ade3 bem2-10	A Bretscher
IGY4	MAT α leu2-3,112 his3 Δ 200 ura3-52 lys2-801 ade2 sac6D::LEU2	A Adams
SLY63	MAT α leu2-3,112 ura3-52 trp1-1 his6 myo2-66	S Brown

Cheung, K.-H., Samwald, M., Auerbach, R. K. & Gerstein, M. B. 2010. Structured digital tables on the Semantic Web: toward a structured digital literature. *Molecular Systems Biology*, 6, 403.

DL = Description Logic

Axiom	DL syntax	Example
Sub class	$C_1 \sqsubseteq C_2$	Alga \sqsubseteq Plant \sqsubseteq Organism
Equivalent class	$C_1 \equiv C_2$	Cancer \equiv Neoplastic Process
Disjoint with	$C_1 \sqsubseteq \neg C_2$	Vertebrate $\sqsubseteq \neg$ Invertebrate
Same individual	$x_1 \equiv x_2$	Blue_Shark \equiv Prionace_Glauca
Different from	$x_1 \sqsubseteq \neg x_2$	Sea Horse $\sqsubseteq \neg$ Horse
Sub property	$P_1 \sqsubseteq P_2$	has_mother \sqsubseteq has_parent
Equivalent property	$P_1 \equiv P_2$	treated_by \equiv cured_by
Inverse	$P_1 \equiv P_2^-$	location_of \equiv has_location ⁻
Transitive property	$P^+ \sqsubseteq P$	part_of ⁺ \sqsubseteq part_of
Functional property	$\top \sqsubseteq \leq 1P$	$\top \sqsubseteq \leq 1$ has_tributary
Inverse functional property	$\top \sqsubseteq \leq 1P^-$	$\top \sqsubseteq \leq 1$ has_scientific_name ⁻

Concept equivalence
Speak: C1 is equivalent to C2

Concept inclusion,
Speak: All C1 are C2

Bhatt, M., Rahayu, W., Soni, S. P. & Wouters, C. (2009) Ontology driven semantic profiling and retrieval in medical information systems. *Web Semantics: Science, Services and Agents on the World Wide Web*, 7, 4, 317-331.

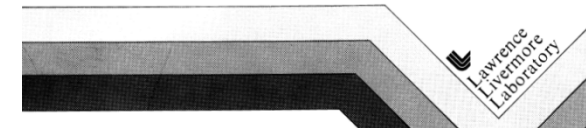
web.efzg.hr/dok/MAT/vkojic/Larrys_speakeasy.pdf

Handbook for
Spoken Mathematics

(Larry's Speakeasy)

Lawrence A. Chang, Ph.D.

With assistance from
Carol M. White
Lila Abrahamson



HELPFUL: https://en.wikipedia.org/wiki/List_of_mathematical_symbols

LaTeX Symbols : <http://www.artofproblemsolving.com/wiki/index.php/LaTeX:Symbols>

Math ML: <http://www.robinlionheart.com/stds/html4/entities-mathml>

The *MathML* Association promotes & funds MathML
implementations



MathML3 is an ISO/IEC International Standard

Constructor	DL syntax	Example
Intersection	$C_1 \sqcap \dots \sqcap C_n$	Anatomical_Abnormality \sqcap Pathological_Function
Union	$C_1 \sqcup \dots \sqcup C_n$	Body_Substance \sqcup Organic_Chemical
Complement	$\neg C$	\neg Invertebrate
One of	$x_1 \sqcup \dots \sqcup x_n$	Oestrogen \sqcup Progesterone
All values from	$\forall P.C$	\forall co_occurs_with.Plant
Some values	$\exists P.C$	\exists co_occurs_with.Animal
Max cardinality	$\leq nP$	≤ 1 has_ingredient
Min cardinality	$\geq nP$	≥ 2 has_ingredient

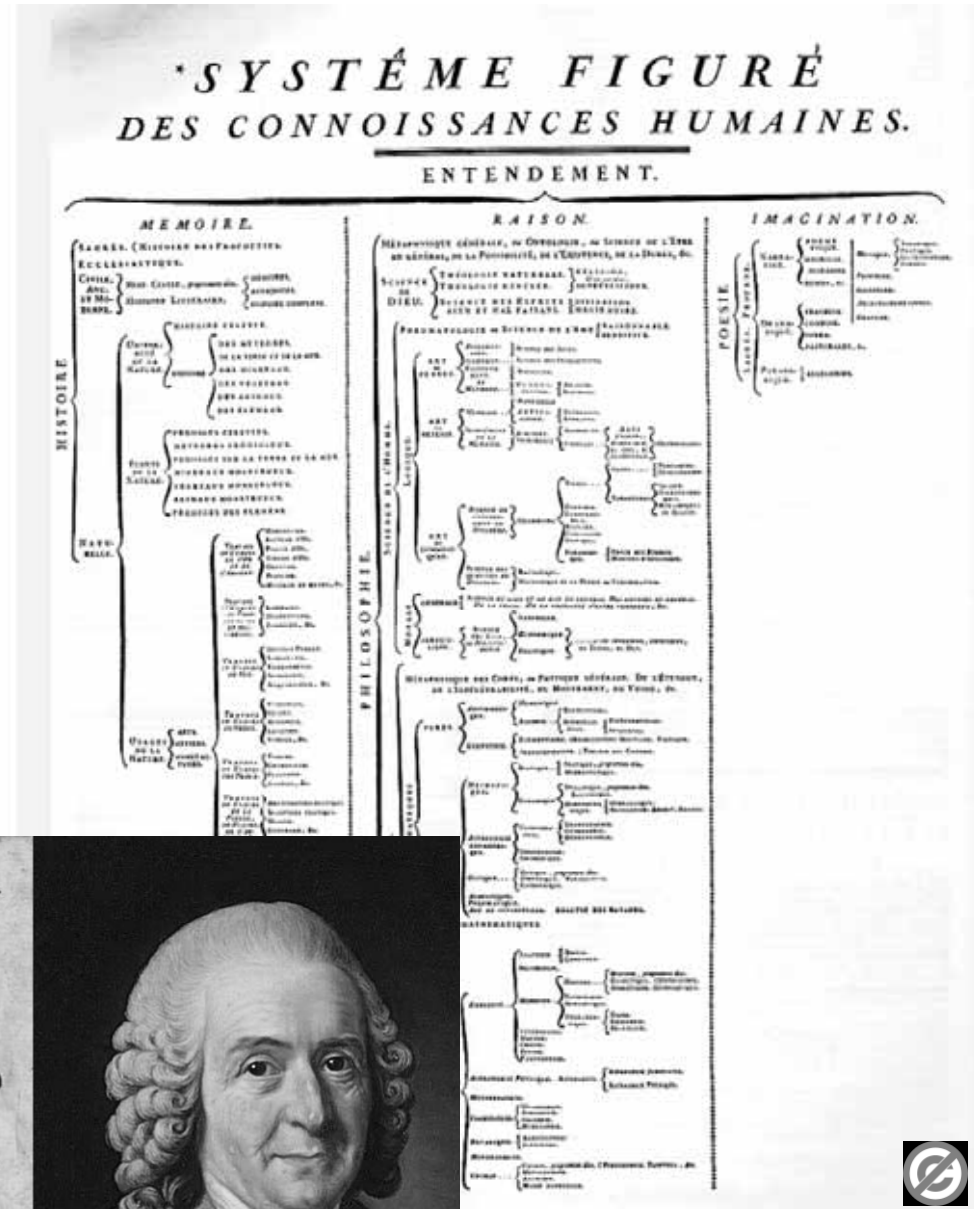
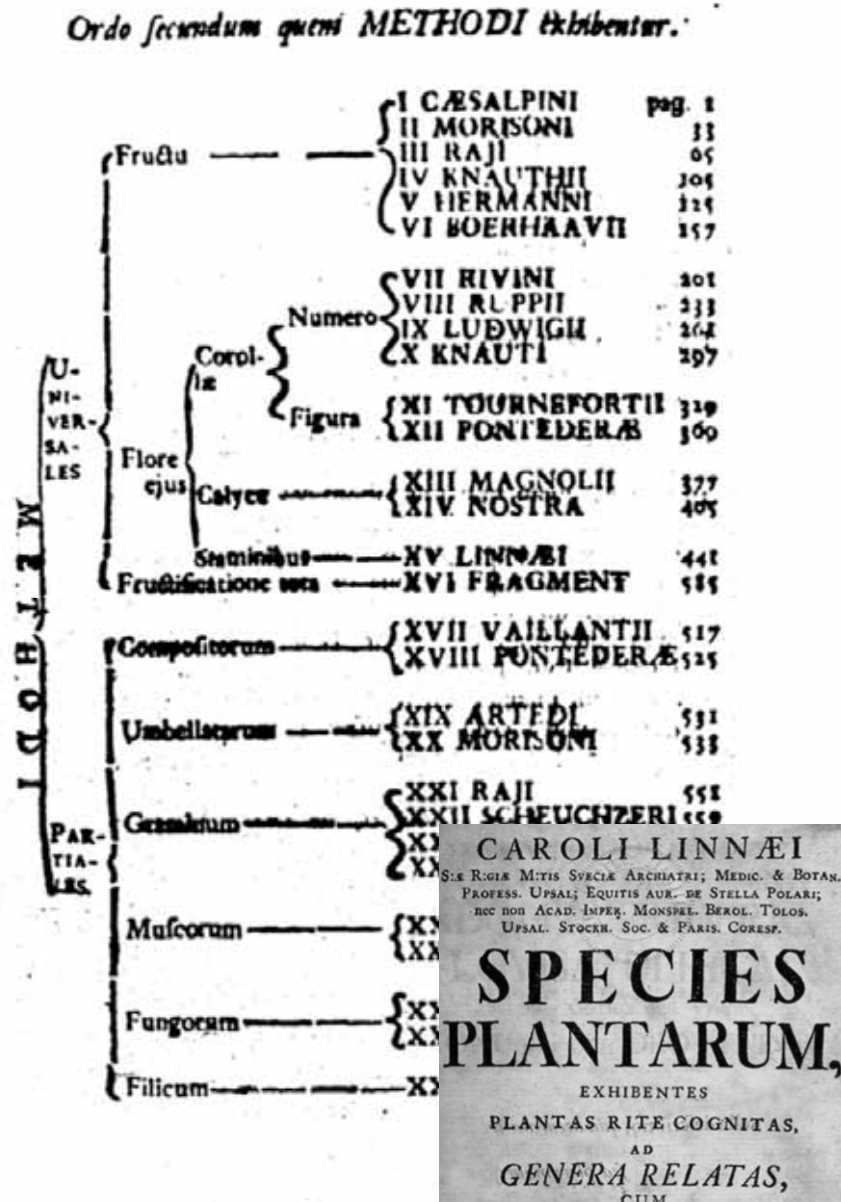
Intersection/conjunction of concepts,
Speak: C1 and ... Cn

Universal Restriction
Speak: All P-successors are in C

Existential Restriction
Speak: An P-successor exists in C

Bhatt et al. (2009)

Medical Classifications



- Since the classification by Carl von Linné (1735) approx. 100+ various classifications in use:
 - International **C**lassification of **D**iseases (ICD)
 - Systematized **N**omenclature of **M**edicine (SNOMED)
 - **M**edical **S**ubject **H**eadings (MeSH)
 - **F**oundational **M**odel of **A**natomy (FMA)
 - **G**ene **O**ntology (GO)
 - **U**nified **M**edical **L**anguage **S**ystem (UMLS)
 - **L**ogical **O**bservation **I**dentifiers **N**ames & **C**odes (LOINC)
 - **N**ational **C**ancer **I**nstitute **T**hesaurus (NCI Thesaurus)



[Home](#) [Health topics](#) [Data and statistics](#) [Media centre](#) [Publications](#) [Countries](#) [Programmes and projects](#) [About](#)

Classifications

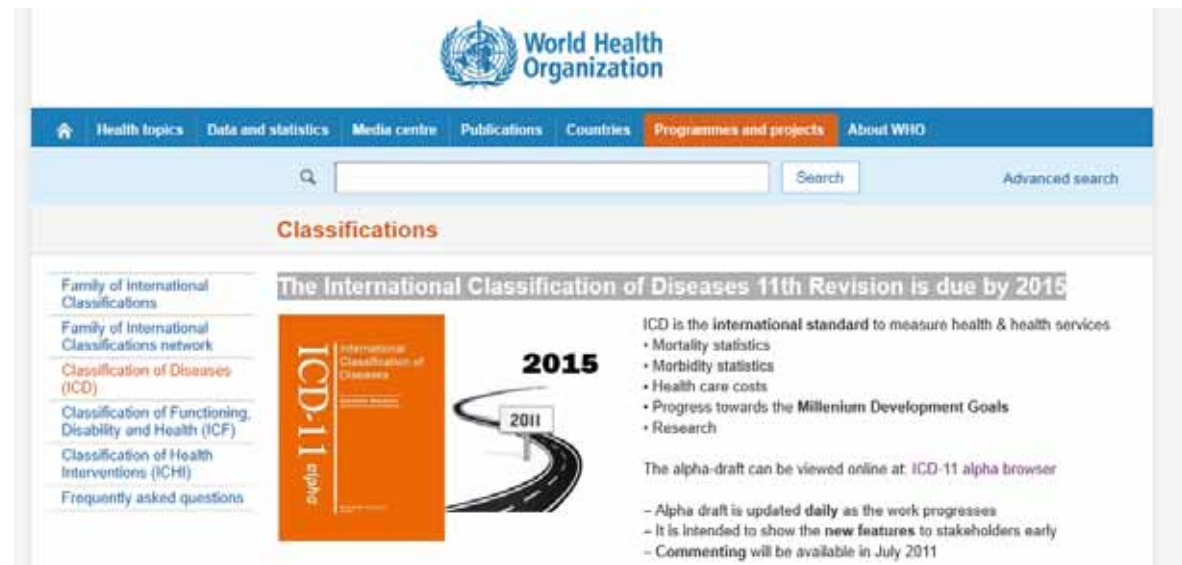
- Family of International Classifications
- Family of International Classifications network
- Classification of Diseases (ICD)**
- Classification of Functioning, Disability and Health (ICF)
- Classification of Health Interventions (CHI)
- Frequently asked questions

International Classification of Diseases (ICD)

ICD-10 was endorsed by the Forty-third World Health Assembly in May 1990 and came into use in WHO Member States as from 1994. The classification is the latest in a series which has its origins in the 1850s. The first edition, known as the International List of Causes of Death, was adopted by the International Statistical Institute in 1893. WHO took over the responsibility for the ICD at its creation in 1948 when the Sixth Revision, which included causes of morbidity for the first time, was published. The World Health Assembly adopted in 1967 the WHO Nomenclature Regulations that stipulate use of ICD in its most current revision for mortality and morbidity statistics by all Member States.

<http://www.who.int/classifications/icd/en>

- 1629 London Bills of Mortality
- 1855 **William Farr** (London, one founder of medical statistics): List of causes of death, list of diseases
- 1893 von Jacques Bertillot: List of causes of death
- 1900 International Statistical Institute (ISI) accepts Bertillot's list
- 1938 5th Edition
- 1948 WHO
- 1965 ICD-8
- 1989 ICD-10
- 2015 ICD-11 due
- 2018 ICD-11 adopt



- 1965 SNOP, 1974 SNOMED, 1979 SNOMED II
- 1997 (Logical Observation Identifiers Names and Codes (LOINC) integrated into SNOMED
- 2000 SNOMED RT, 2002 SNOMED CT

INTERNATIONAL HEALTH TERMINOLOGY
STANDARDS DEVELOPMENT ORGANISATION



239 pages

SNOMED CT[®] Technical Reference Guide

January 2011 International Release
(US English)

<http://www.isb.nhs.uk/documents/isb-0034/amd-26-2006/techrefguid.pdf>

A

24184005|Finding of increased blood pressure (finding) →
38936003|Abnormal blood pressure (finding) AND
roleGroup SOME
(363714003|Interprets (attribute) SOME
75367002|Blood pressure (observable entity))

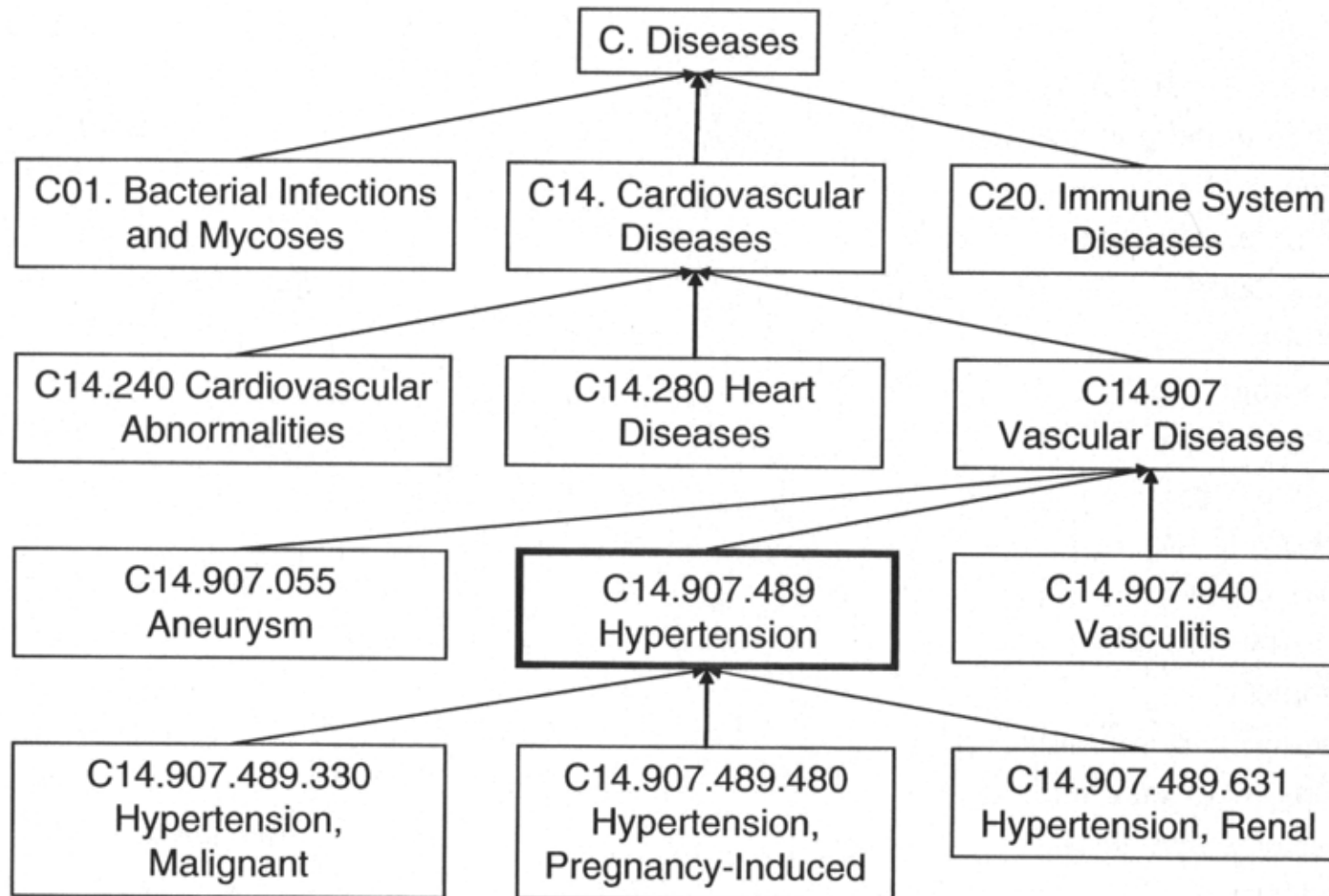
B

12763006|Finding of decreased blood pressure (finding) →
392570002|Blood pressure finding (finding) AND
roleGroup SOME
(363714003|Interprets (attribute) SOME
75367002|Blood pressure (observable entity))

Rector, A. L. & Brandt, S. (2008) Why Do It the Hard Way? The Case for an Expressive Description Logic for SNOMED. *Journal of the American Medical Informatics Association*, 15, 6, 744-751.

- MeSH thesaurus is produced by the National Library of Medicine (NLM) since 1960.
- Used for cataloging documents and related media and as an index to search these documents in a database and is part of the metathesaurus of the Unified Medical Language System (UMLS).
- This thesaurus originates from keyword lists of the Index Medicus (today Medline);
- MeSH thesaurus is polyhierarchical, i.e. every concept can occur multiple times. It consists of the three parts:
 - 1. MeSH Tree Structures,
 - 2. MeSH Annotated Alphabetic List and
 - 3. Permuted MeSH.

1. Anatomy [A]
2. Organisms [B]
3. Diseases [C]
4. Chemicals and Drugs [D]
5. Analytical, Diagnostic and Therapeutic Techniques and Equipment [E]
6. Psychiatry and Psychology [F]
7. Biological Sciences [G]
8. Natural Sciences [H]
9. Anthropology, Education, Sociology, Social Phenomena [I]
10. Technology, Industry, Agriculture [J]
11. Humanities [K]
12. Information Science [L]
13. Named Groups [M]
14. Health Care [N]
15. Publication Characteristics [V]
16. Geographicals [Z]



Hersh, W. (2010) *Information Retrieval: A Health and Biomedical Perspective*. New York, Springer.

National Library of Medicine - Medical Subject Headings

2011 MeSH

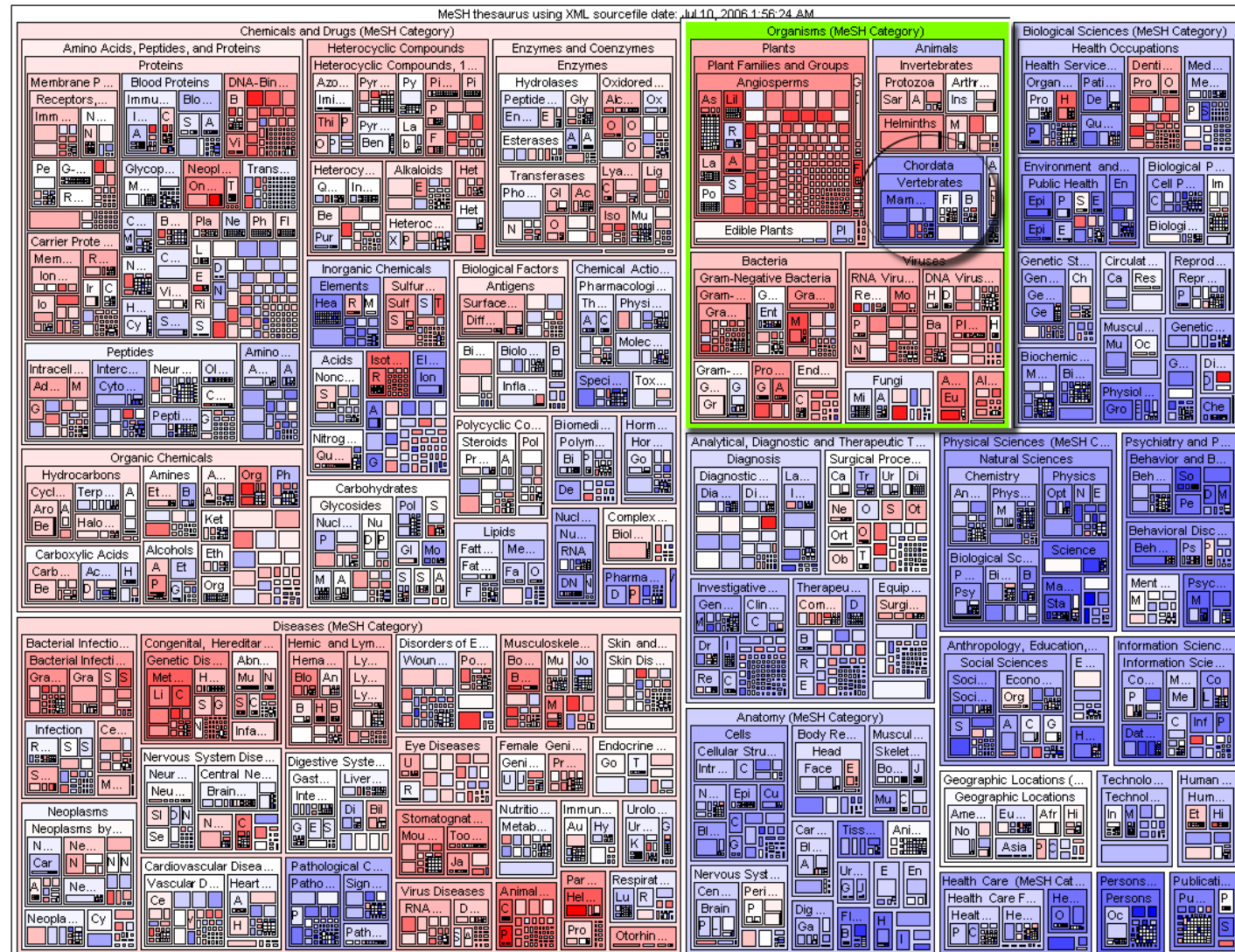
MeSH Descriptor Data

[Return to Entry Page](#)

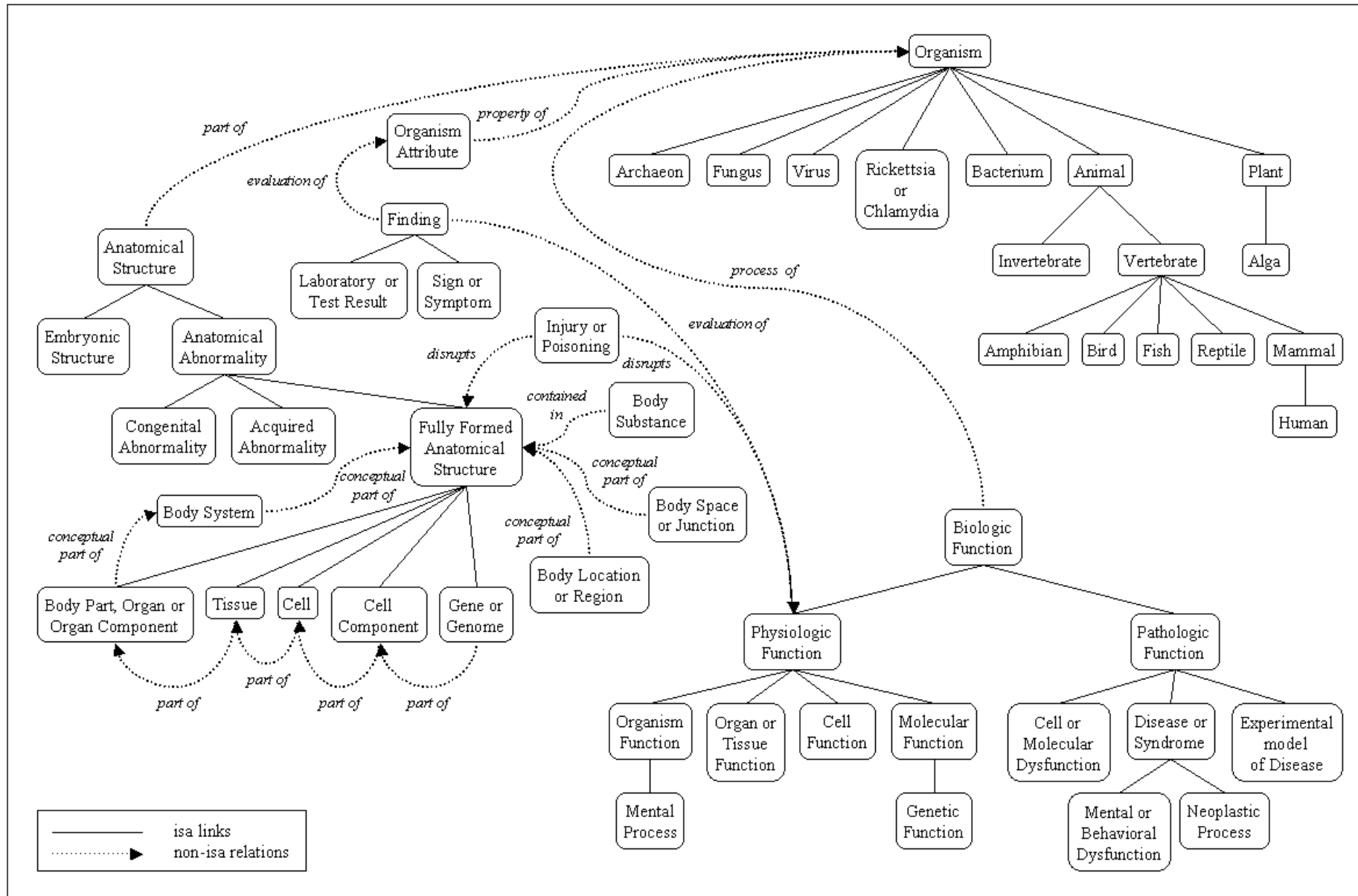
Standard View. [Go to Concept View](#); [Go to Expanded Concept View](#)

MeSH Heading	Hypertension
Tree Number	C14.907.489
Annotation	not for intracranial or intraocular pressure; relation to BLOOD PRESSURE : Manual 23.27 ; Goldblatt kidney is HYPERTENSION, GOLDBLATT see HYPERTENSION, RENOVASCULAR ; hypertension with kidney disease is probably HYPERTENSION, RENAL , not HYPERTENSION ; venous hypertension: index under VENOUS PRESSURE (IM) & do not coordinate with HYPERTENSION ; PREHYPERTENSION is also available
Scope Note	Persistently high systemic arterial BLOOD PRESSURE . Based on multiple readings (BLOOD PRESSURE DETERMINATION), hypertension is currently defined as when SYSTOLIC PRESSURE is consistently greater than 140 mm Hg or when DIASTOLIC PRESSURE is consistently 90 mm Hg or more.
Entry Term	Blood Pressure, High
See Also	Antihypertensive Agents
See Also	Vascular Resistance
Allowable Qualifiers	BL CF CI CL CN CO DH DI DT EC EH EM EN EP ET GE HI IM ME MI MO NU PA PC PP PS PX RA RH RI RT SU TH UR US VE VI
Date of Entry	19990101
Unique ID	D006973

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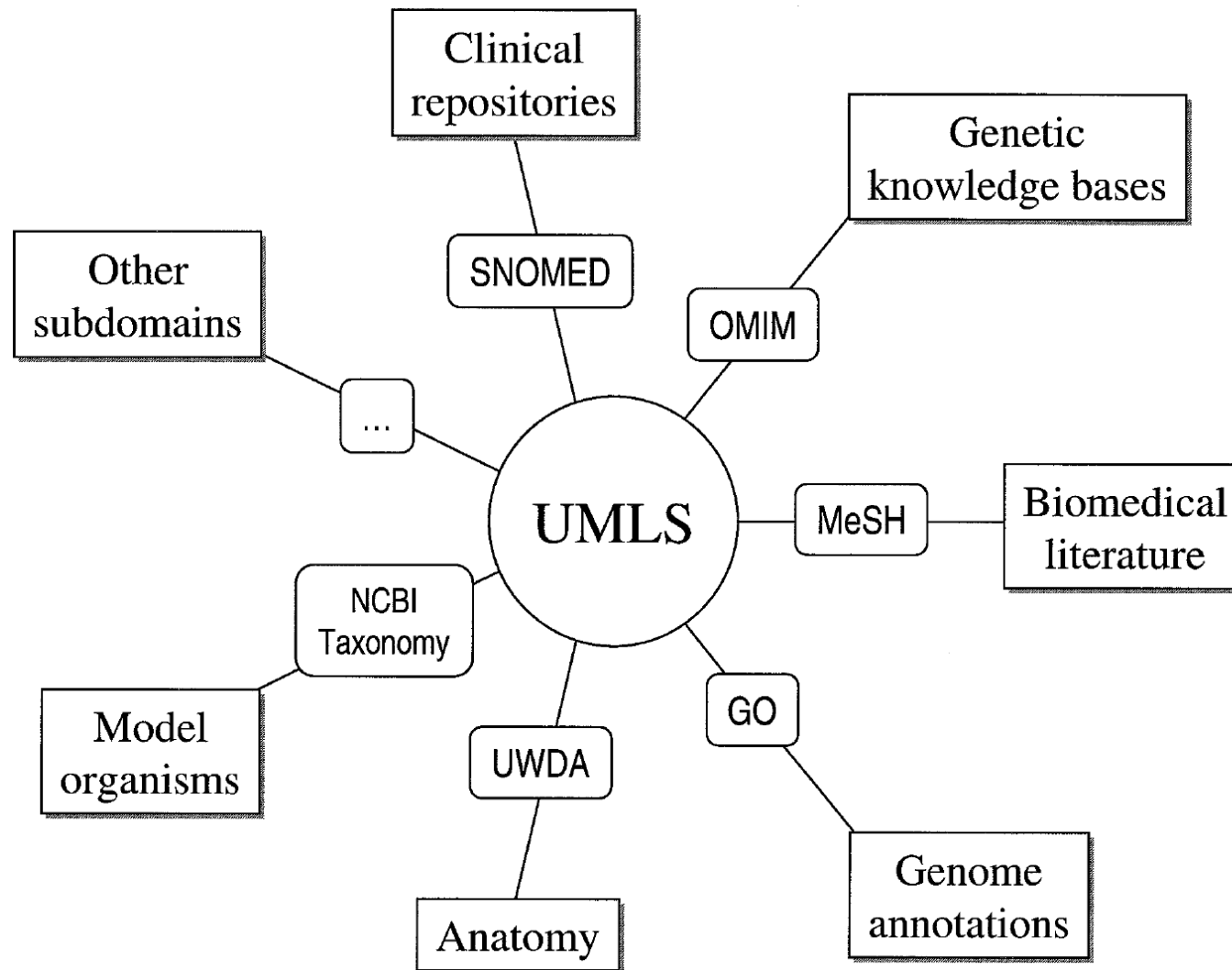
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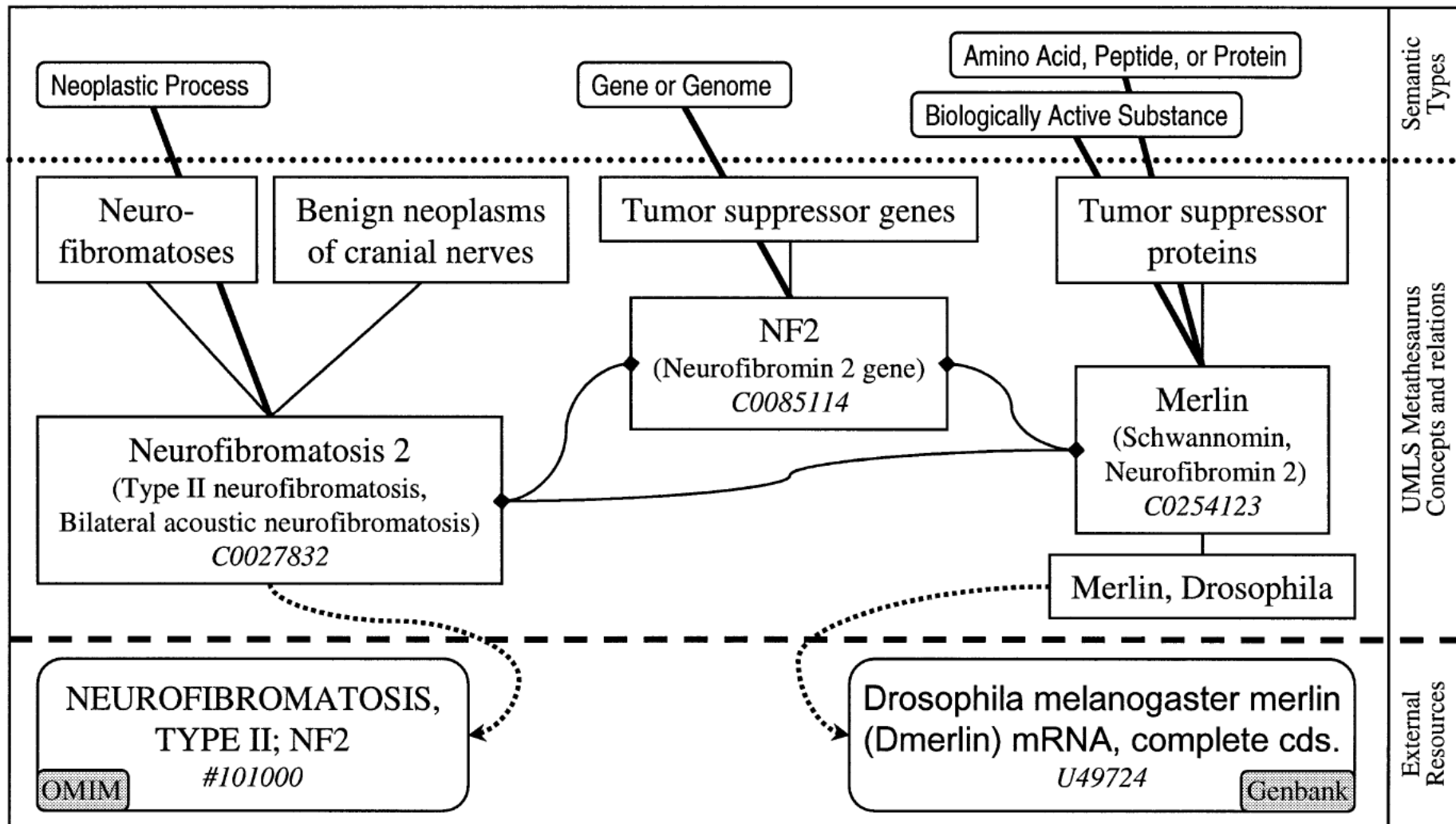
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Written by [Mike Thomas](#)



Thank you!