





**Andreas Holzinger VO 709.049 Medical Informatics** 01.02.2017 11:15-12:45



### **Lecture 12 Course Summary** and Future Outlook (Reflection Lecture)

a.holzinger@tugraz.at

Tutor: markus.plass@student.tugraz.at

http://hci-kdd.org/biomedical-informatics-big-data









#### ... fasten your seat belts and be prepared for questions!







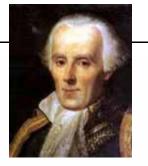
# Lecture 1: Computer Science meets Life Sciences

#### Repetition of Bayes - on the work of Laplace

HCI-KDD &

What is the simplest mathematical operation for us?

$$p(x) = \sum_{x} (p(x, y))$$



(1)

How do we call repeated adding?

$$p(x,y) = p(y|x) * p(y)$$
(2)

Laplace (1773) showed that we can write:

$$p(x,y) * p(y) = p(y|x) * p(x)$$
 (3)

Now we introduce a third, more complicated operation:

$$\frac{p(x,y) * p(y)}{p(y)} = \frac{p(y|x) * p(x)}{p(y)}$$
(4)

We can reduce this fraction by p(y) and we receive what is called Bayes rule:

$$p(x,y) = \frac{p(y|x) * p(x)}{p(y)}$$
  $p(h|d) = \frac{p(d|h)p(h)}{p(d)}$  (5)

04

d ... data

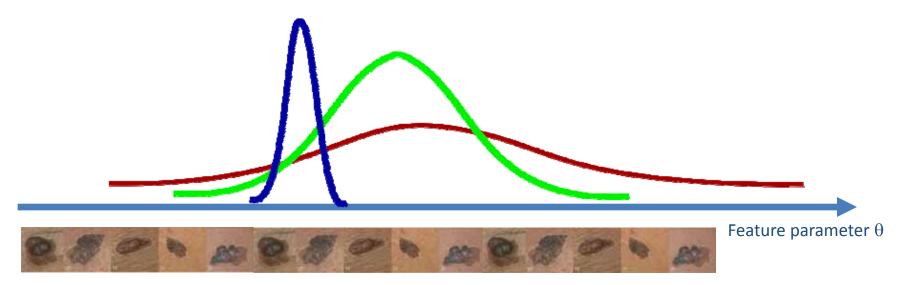
$$\mathcal{H} .... \{H_1, H_2, ..., H_n\} \quad \forall h, d ....$$

h ... hypotheses

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

**Posterior Probability** 

Evidence = marginal likelihood = Normalization





- Your MD has bad news and good news for you.
- Bad news first: You are tested positive for a serious disease D, and this test T is 99% accurate



- Good news: It is a rare disease, striking only 1 in 10,000 (D)
- How worried would you now be or: what is the posterior?

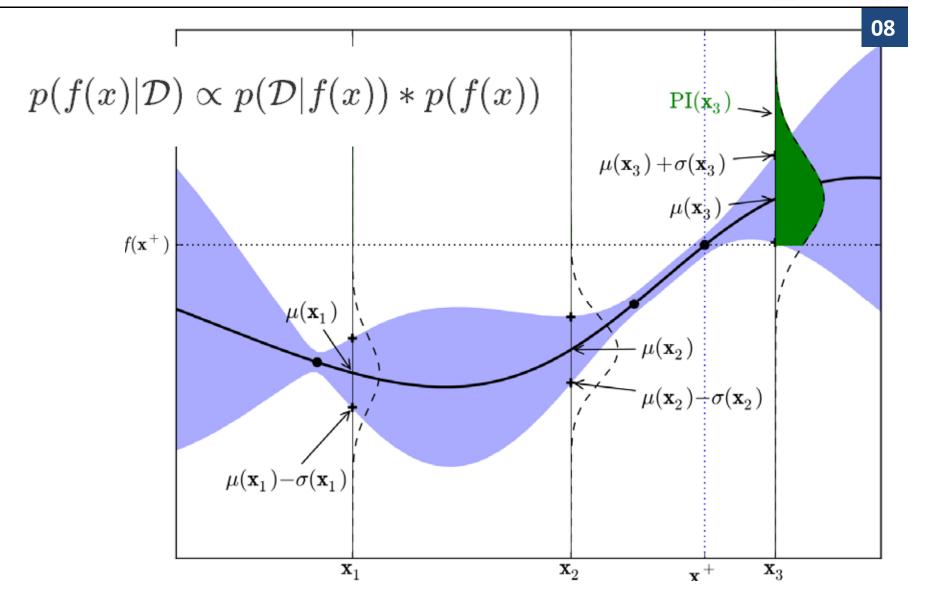
$$posterior = \frac{likelihood*prior}{evidence} \qquad p(h|d) = \frac{p(d|h)*p(h)}{\sum (p(d|\bar{h})*p(\bar{h}))}$$

$$p(T = 1|D = 1) = p(d|h) = 0,99$$
 and  $p(D = 1) = p(h) = 0,0001$  and  $p(T = 0|D = 0) = 0,99$ 

$$p(D=1 \mid T=1) = \frac{(0,99)*(0,0001)}{(1-0,99)*(1-0,0001)+0,99*0,0001} =$$

= 0,0098 = 0,9%





Brochu, E., Cora, V. M. & De Freitas, N. 2010. A tutorial on Bayesian optimization of expensive cost functions, with application to active user modeling and hierarchical reinforcement learning. arXiv:1012.2599.

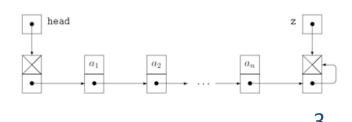


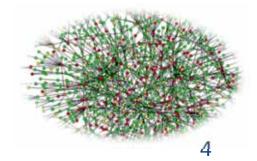
# Lecture 2: Data, Information, Knowledge; **Entropy and Kullback-**Leibler Divergence

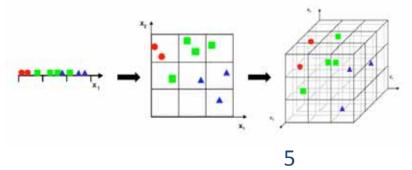


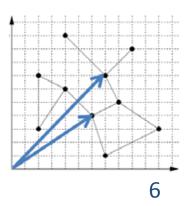












$$H(X) = -\sum_{i=1}^{n} P(x_i) \log_b P(x_i)$$

7

$$D_{\mathrm{KL}}(P\|Q) = \int_{-\infty}^{\infty} p(x) \, \log rac{p(x)}{q(x)} \, \mathrm{d}x$$



9



#### What data do we have in biomedical informatics?



Electronic health record data Physiological data Laboratory results

Imaging data
X-Ray, ultrasound, MR, CT, PET,
cams, observation (e.g. sleep

laboratory), gait (walking)

Genomics

**Proteomics** 

**Protein-Protein Interactions** 

Metabolomics

Chemical processes

Cellular reactions

**Enzymatic reactions** 

Transcriptomics RNA, mRNA, rRNA, tRNA

**Epigenetics** 

Epigenetic modifications

Foodomics, Lipidomics

Nutrition data (Nutrigenomics)

Diet data (allergenics)
Holzinger Group

Exposome
Environmental data
Air pollution
Exposure (toxicants)

Collective data

Social data

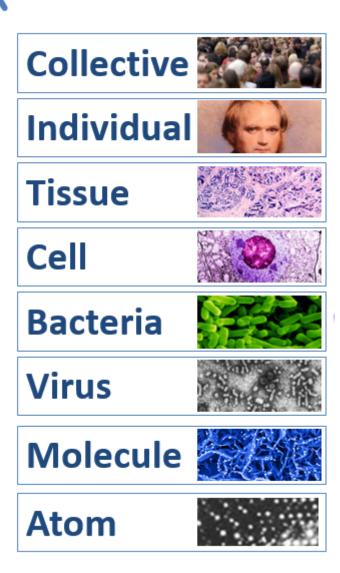
10<sup>-12</sup>

Fitness, Wellness data

Ambient Assisted Living data

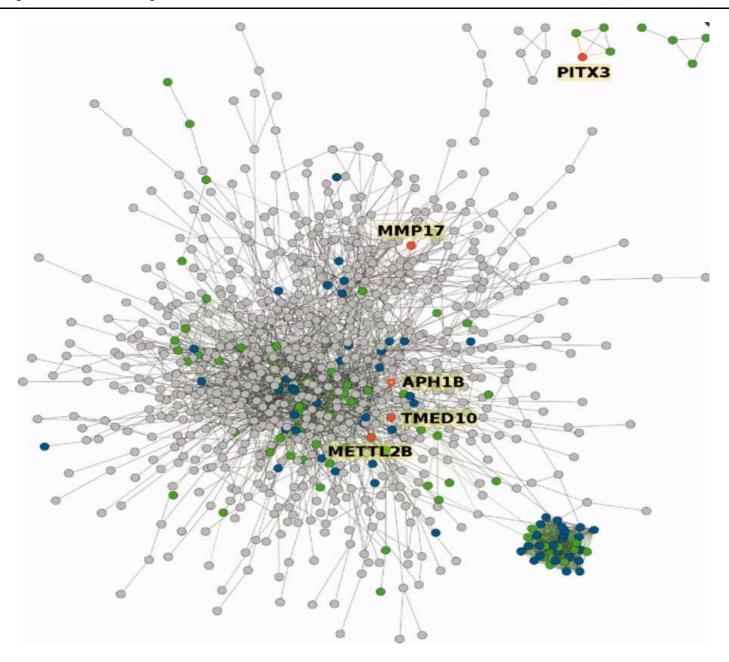
(Non-medical) personal data

11





Winterhalter, C., Widera, P. & Krasnogor, N. 2014. JEPETTO: a Cytoscape plugin for gene set enrichment and topological analysis based on interaction networks. Bioinformatics, 30, (7), 1029-1030, doi:10.1093/bioinformatics/btt732.

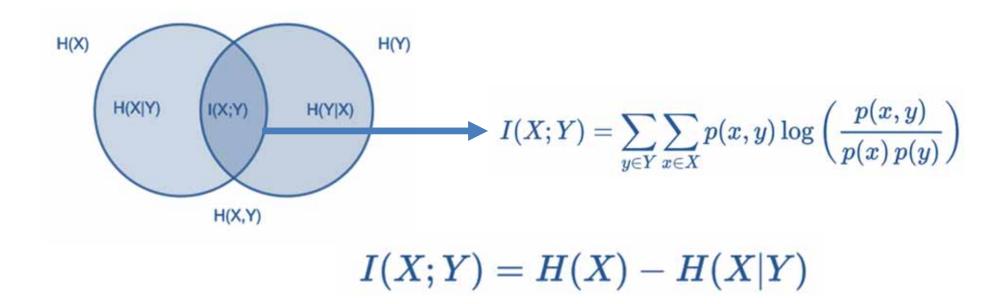




$$H(X) = -\sum_{i=1}^{n} P(x_i) \log_b P(x_i)$$

• Measuring uncertainty, complexity, randomness, surprise, ..., = information!





 In ML we need often to measure the difference between two probability distributions



For discrete distributions

$$D_{ ext{KL}}(P\|Q) = \sum_i P(i) \, \log rac{P(i)}{Q(i)}$$

For continuous distributions

$$D_{\mathrm{KL}}(P\|Q) = \int_{-\infty}^{\infty} p(x) \, \log rac{p(x)}{q(x)} \, \mathrm{d}x$$

$$\mathrm{KL}(p||q) \geqslant 0$$

$$\mathrm{KL}(p||q) \not\equiv \mathrm{KL}(q||p)$$

#### KL-divergence can also be used to measure the distance between two distributions

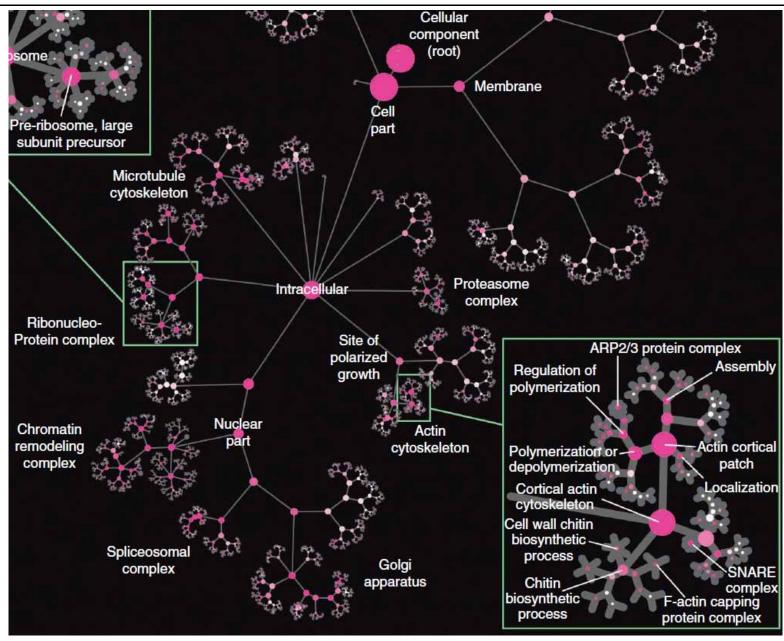
Kullback, S. & Leibler, R. A. 1951. On information and sufficiency. The annals of mathematical statistics, 22, (1), 79-86, doi:http://www.jstor.org/stable/2236703



## Lecture 3: Knowledge Representation, Ontologies & Classifications







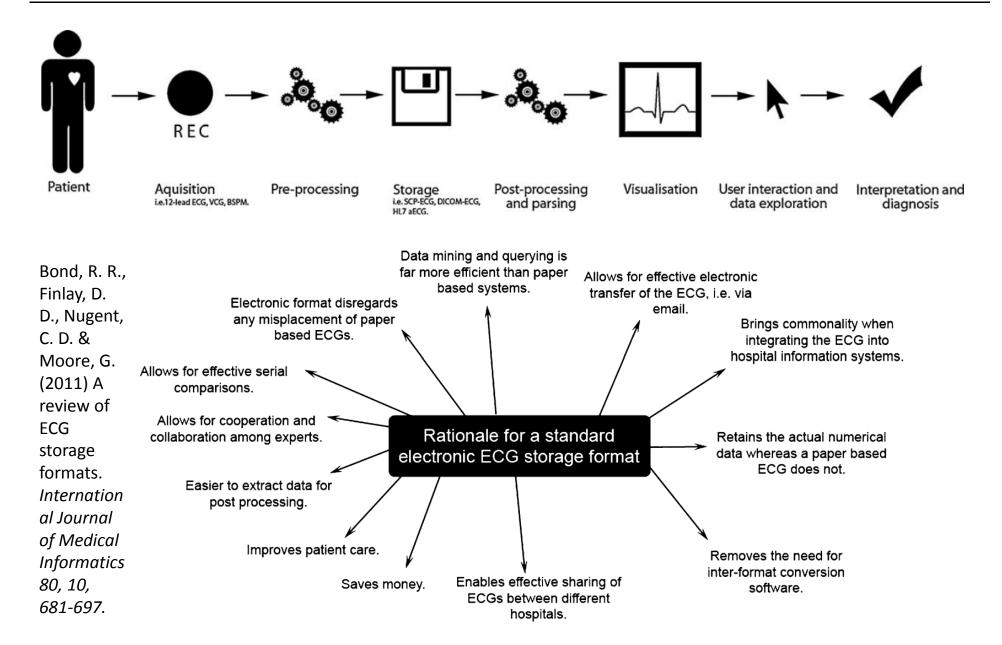
http://www.kurzweilai.net/images/cell-model.png

(Credit: UC San Diego School of Medicine)



#### Slide 3-7: Standardized workflow of ECG data processing







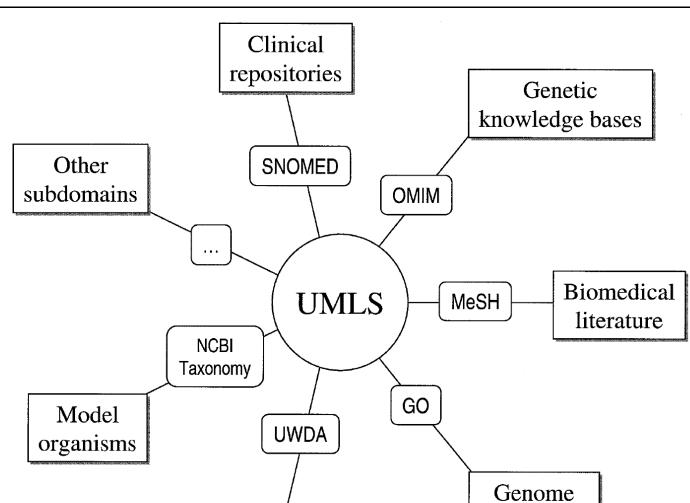
#### What is a knowledge representation?



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

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





Anatomy

annotations



## Lecture 4: Decision, Cognition, Uncertainty, Bayesian Statistics, **Probabilistic Modelling**





#### When is the human \*) better?

\*) human intelligence/natural intelligence/human mind/human brain/ learning

- Natural Language Translation/Curation
   Computers cannot understand the context of sentences [3]
- Unstructured problem solving

Without a pre-set of rules, a machine has trouble solving the problem, because it lacks the creativity required for it [1]

#### NP-hard Problems

Processing times are often exponential and makes it almost impossible to use machines for it, but human make heuristic decisions which are often not perfect but sufficiently good [4]

## When is the computer \*\*) better?

- \*\*) Computational intelligence, Artificial Intelligence/soft computing/ML
- High-dimensional data processing

Humans are very good at dimensions less or equal than 3, but computers can process data in arbitrarily high dimensions

Rule-Based environments

Difficulties for humans in rule-based environments often come from not recognizing the correct goal in order to select the correct procedure or set of rules [2]

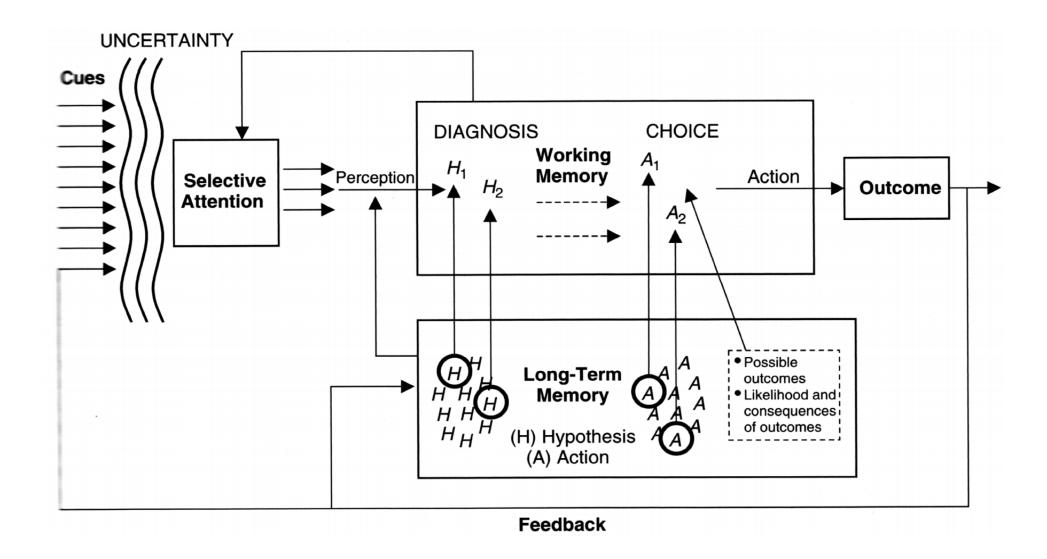
Image optimization

Machine can look at each pixel and apply changes without human personal biases, and with more speed [1]

- biases, and with more speed [1] [1] Kipp, M. 2006. Creativity Meets Automation: Combining Nonverbal Action Authoring with Rules and Machine Learning. In: LNCS 4133, pp. 230-242, doi:10.1007/11821830\_19.
- [2] Cummings, M. M. 2014. Man versus Machine or Man + Machine? IEEE Intelligent Systems, 29, (5), 62-69, doi:10.1109/MIS.2014.87. [3 Pizlo, Z., Joshi, A. & Graham, S. M. 1994. Problem Solving in Human Beings and Computers. Purdue TR 94-075.
- [4] Griffiths, T. L. Connecting human and machine learning via probabilistic models of cognition. Interspeech, 2009, ISCA, 9-12
  See also: Holzinger, A., Plass, M., Holzinger, K., Crisan, G., Pintea, C. & Palade, V. 2016. Towards interactive Machine Learning (iML):
  Applying Ant Colony Algorithms to solve the Traveling Salesman Problem with the Human-in-the-Loop approach. Springer Lecture Notes in
  Computer Science LNCS 9817. Heidelberg, Berlin, New York: Springer, pp. 81-95, doi:10.1007/978-3-319-45507-56.

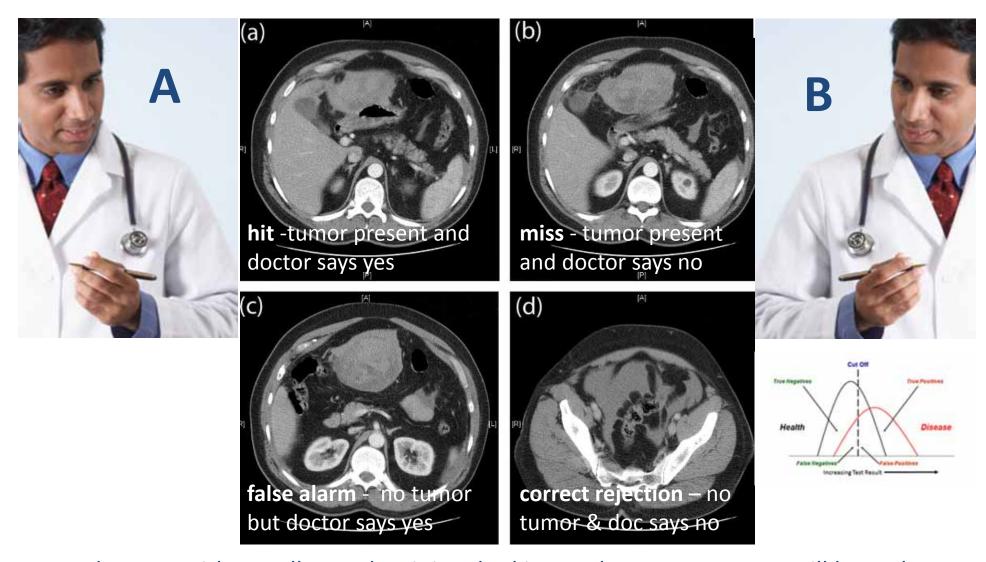
  709.049 12





Wickens, C. D. (1984) Engineering psychology and human performance. Columbus (OH), Charles Merrill.





Two doctors, with equally good training, looking at the same CT scan, will have the same information ... but they may have a different bias/criteria!



For a single decision variable an agent can select D = d for any  $d \in dom(D)$ .

The expected utility of decision D = d is



http://www.eoht.info/page/Oskar+Morgenstern

$$E(U \mid d) = \sum_{x_1, \dots, x_n} P(x_1, \dots, x_n \mid d) U(x_1, \dots, x_n, d)$$

An optimal single decision is the decision D = dmax whose expected utility is maximal:

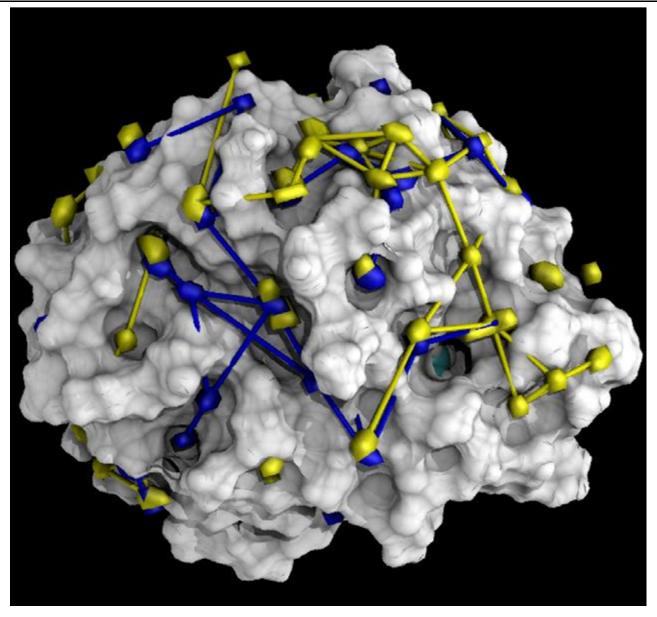
$$d_{\max} = \arg \max_{d \in \text{dom}(D)} E(U \mid d)$$

Von Neumann, J. & Morgenstern, O. 1947. Theory of games and economic behavior, Princeton university press.



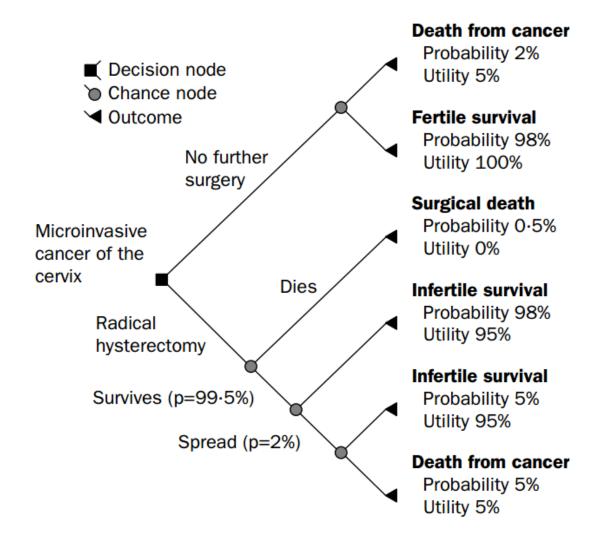
# Lecture 5: **Probabilistic Graphical Models I:** From Knowledge Representation to **Graph Learning**





http://sbcb.bioch.ox.ac.uk/users/oliver/software/









Physician treating a patient approx. 480 B.C.
Beazley (1963), Attic Red-figured Vase-Painters, 813, 96.
Department of Greek, Etruscan and Roman Antiquities, Sully, 1st floor, Campana Gallery, room 43 Louvre, Paris

Elwyn, G., Edwards, A., Eccles, M. & Rovner, D. 2001. Decision analysis in patient care. The Lancet, 358, (9281), 571-574.





- PGM can be seen as a combination between
- Graph Theory + Probability Theory + Machine Learning
- One of the most exciting AI advances in the last decades
- Compact representation for exponentially-large probability distributions
- Example Question: "Is there a path connecting two proteins?"
- Path(X,Y) := edge(X,Y)
- Path(X,Y) := edge(X,Y), path(Z,Y)
- This can NOT be expressed in first-order logic
- Need a Turing-complete fully-fledged language

Friedman, N. 2004. Inferring cellular networks using probabilistic graphical models. Science, 303, (5659), 799-805.

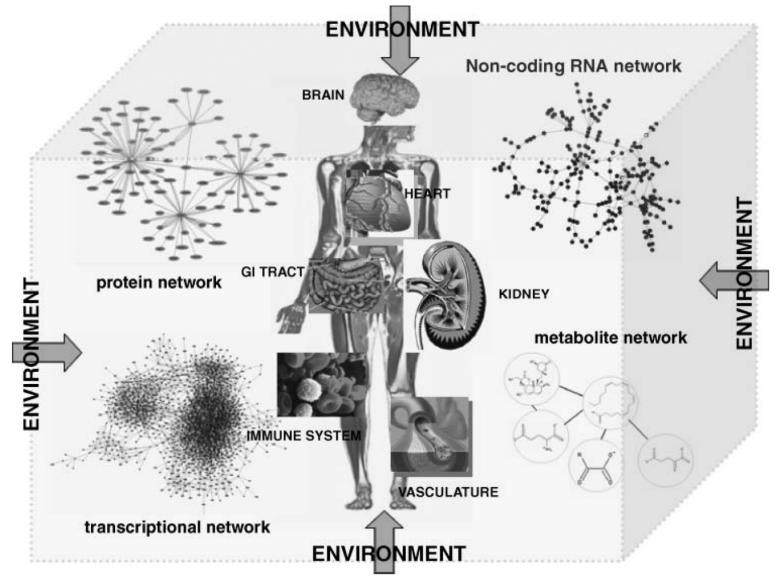
Koller, D. & Friedman, N. 2009. Probabilistic graphical models: principles and techniques, MIT press.



- Take patient information, e.g., observations, symptoms, test results, -omics data, etc. etc.
- Reach conclusions, and predict into the future,
   e.g. how likely will the patient be re-admissioned
- Prior = belief before making a particular observation
- Posterior belief after making the observation and is the prior for the next observation – intrinsically incremental

$$p(x_i|y_j) = \frac{p(y_j|x_i)p(x_i)}{\sum p(x_i, y_j)p(x_i)}$$

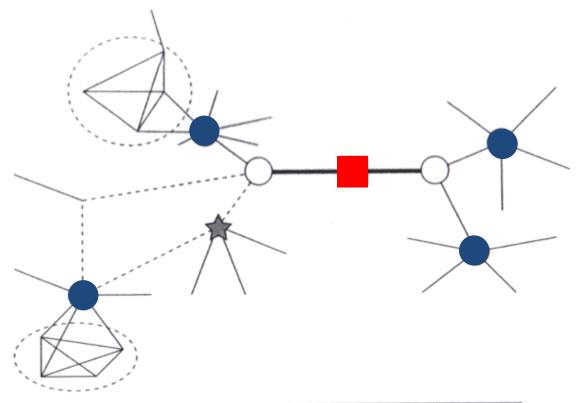




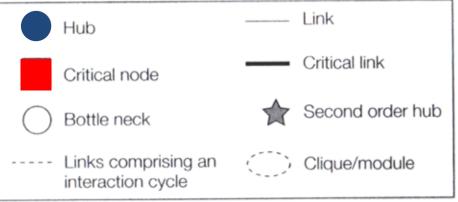
Schadt, E. E. & Lum, P. Y. (2006) Reverse engineering gene networks to identify key drivers of complex disease phenotypes. *Journal of lipid research*, 47, 12, 2601-2613.



G(V, E) Graph  $V \dots vertex$   $E \dots edge \{a, b\}$  $a, b \in V; a \neq b$ 



Hodgman, C. T., French, A. & Westhead, D. R. (2010) Bioinformatics. Second Edition. New York, Taylor & Francis.

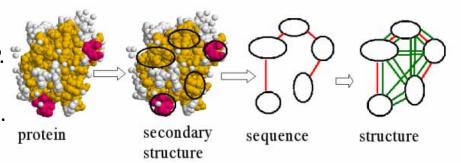




# Lecture 6: Probabilistic **Graphical Models II:** From Bayesian **Networks to Graph Bandits**



Borgwardt, K. M., Ong, C. S., Schönauer, S., Vishwanathan, S., Smola, A. J. & Kriegel, H.-P. 2005. Protein function prediction via graph kernels. Bioinformatics, 21, (suppl 1), i47-i56.



- Important for health informatics: Discovering relationships between biological components
- Unsolved problem in computer science:
- Can the graph isomorphism problem be solved in polynomial time?
  - So far, no polynomial time algorithm is known.
  - It is also not known if it is NP-complete
  - We know that subgraph-isomorphism is NP-complete





- is a probabilistic model, consisting of two parts:
- 1) a dependency structure and
- 2) local probability models.

$$p(x_1, ..., x_n) = \prod_{i=1}^n p(x_i | Pa(x_i))$$

Where  $Pa(x_i)$  are the parents of  $x_i$ 

BN inherently model the <u>uncertainty in the data.</u> They are a successful marriage between probability theory and graph theory; allow to model a multidimensional probability distribution in a sparse way by searching independency relations in the data. Furthermore this model allows different strategies to integrate two data sources.

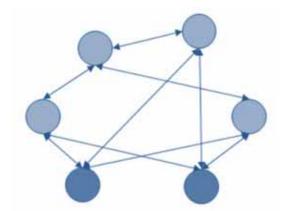
Pearl, J. (1988) Probabilistic reasoning in intelligent systems: networks of plausible inference. San Francisco, Morgan Kaufmann.



				Gene 1				
				P(on)	8.0			
				P(off)	0.2			
				Gene 1	160			
Gen	ne 2	Gene 1	Gene 1			Gene 2	Gene 1	Gene 1
-		on	off		\.		on	off
P(or	n)	0.3	0.6	Gene 2	Gene 3	P(on)	0.3	0.6
P(of	ff)	0.7	0.4	Gene 2	Gene 3	P(off)	0.7	0.4
				Prognosis	,			
	Prognosis		Gene 2 on	Gene 2 on	Ger	ne 2 off	Gene 2 off	
			Gene 3 on	Gene 3 off	Ger	ne 2 on	Gene 3 off	
	P(go	ood)	0.6	0.1	0.9		0.5	
P(poor)		0.4	0.9	0.1		0.5		

Gevaert, O., Smet, F. D., Timmerman, D., Moreau, Y. & Moor, B. D. (2006) Predicting the prognosis of breast cancer by integrating clinical and microarray data with Bayesian networks. *Bioinformatics*, 22, 14, 184-190.

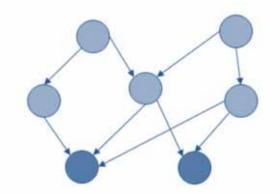




**Undirected:** Markov random fields, useful e.g. for computer vision (Details: Murphy 19)

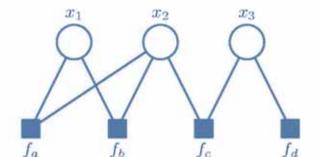
$$P(X) = \frac{1}{Z} \exp\left(\sum_{ij} W_{ij} x_i x_j + \sum_i x_i b_i\right)$$





**Directed:** Bayes Nets, useful for designing models (Details: Murphy 10)

$$p(\mathbf{x}) = \prod_{k=1}^{K} p(x_k | \mathbf{pa}_k)$$



Factored: useful for inference/learning

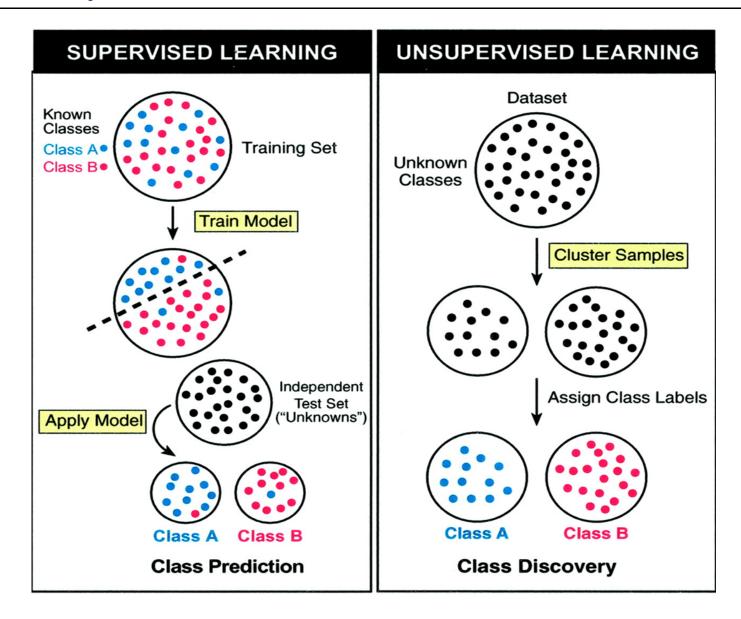
$$p(\mathbf{x}) = \prod_{s} f_s(\mathbf{x}_s)$$



# Lecture 7: Dimensionality Reduction and **Subspace Clustering** with the Doctor-in-the-Loop



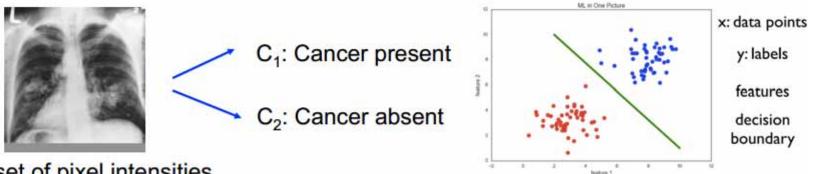




Ramaswamy, S. & Golub, T. R. (2002) DNA Microarrays in Clinical Oncology. Journal of Clinical Oncology, 20, 7, 1932-1941.



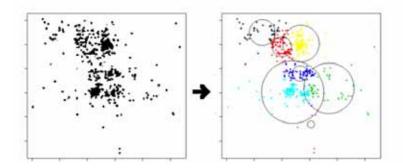




- x -- set of pixel intensities
- Typical questions include:
  - Is this protein functioning as an enzyme?
  - Does this gene sequence contain a splice site?
  - Is this melanoma malign?
- Given object x predict the class label y
  - If  $y \in \{0,1\} \rightarrow$  binary classification problem
  - If  $y \in \{1, ..., n\}$  and is  $n \in \mathbb{N} \to \text{multiclass problem}$
  - If  $y \in \mathbb{R} \to \text{regression problem}$

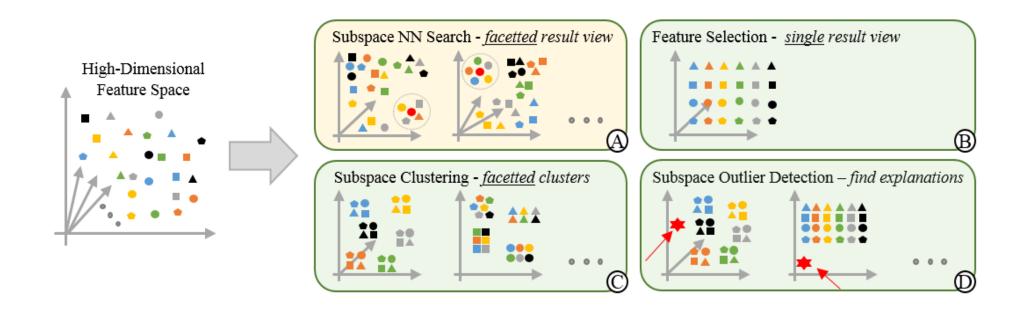


 Group similar objects into clusters together, e.g.



- For image segmentation
- Grouping genes similarly affected by a disease
- Clustering patients with similar diseases
- Cluster biological samples for category discovery
- Finding subtypes of diseases
- Visualizing protein families
- Inference: given  $x_i$ , predict  $y_i$  by learning f
- No training data set learn model and apply it





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: Guo, Y., Friston, K., Aldo, F., Hill, S. & Peng, H. (eds.) Brain Informatics and Health, Lecture Notes in Artificial Intelligence LNAI 9250. Cham: Springer International Publishing, pp. 358-368, doi:10.1007/978-3-319-23344-4\_35.



# Lecture 8: **Decision Making** under Uncertainty: **Decision Support** Systems





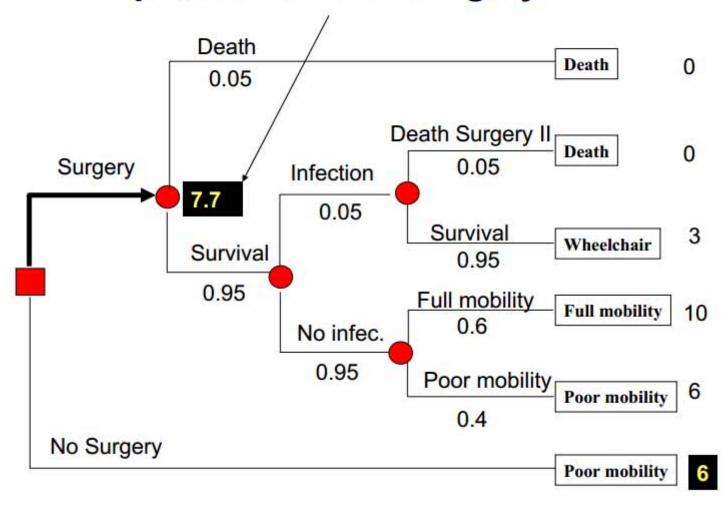
- Type 1 Decisions: related to the diagnosis, i.e. computers are used to assist in diagnosing a disease on the basis of the individual patient data. Questions include:
  - What is the probability that this patient has a myocardial infarction on the basis of given data (patient history, ECG, ...)?
  - What is the probability that this patient has acute appendices, given the signs and symptoms concerning abdominal pain?
- Type 2 Decisions: related to therapy, i.e. computers are used to select the best therapy on the basis of clinical evidence, e.g.:
  - What is the best therapy for patients of age x and risks y, if an obstruction of more than z % is seen in the left coronary artery?
  - What amount of insulin should be prescribed for a patient during the next 5 days, given the blood sugar levels and the amount of insulin taken during the recent weeks?

Bemmel, J. H. V. & Musen, M. A. 1997. Handbook of Medical Informatics, Heidelberg, Springer.





### **Expected Value of Surgery**





 $h_1$  = 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

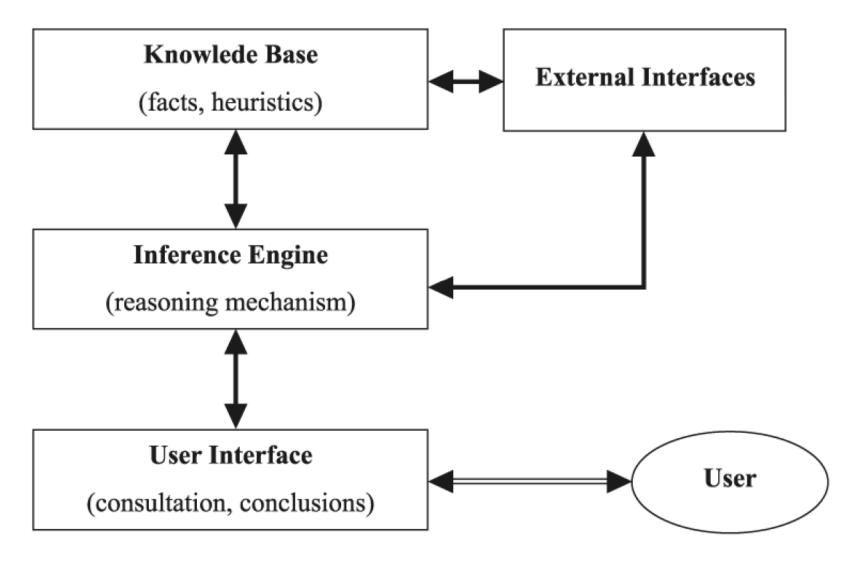
PATIENT-1 is not febrile

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

John Jones

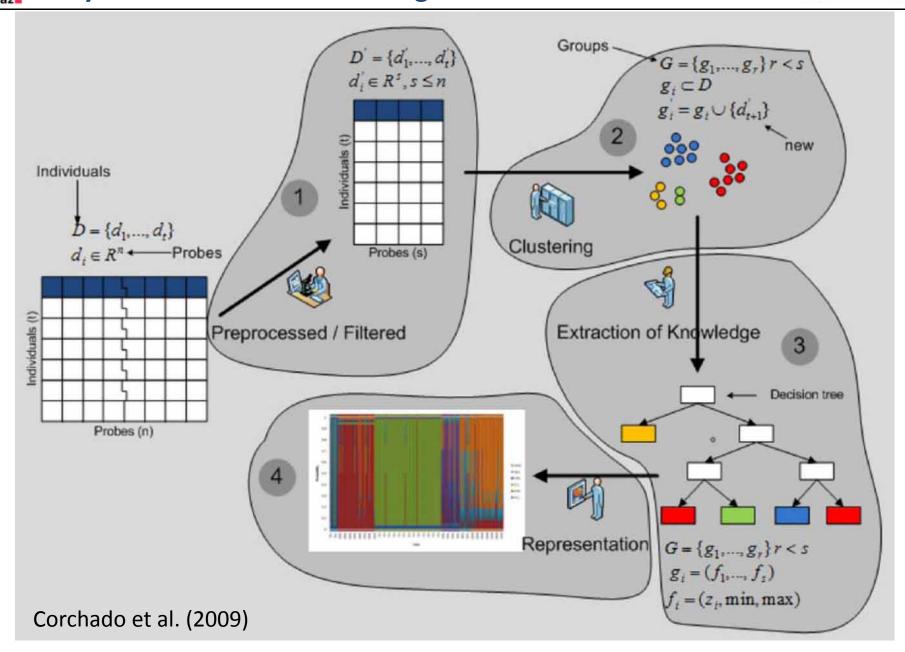
Shortliffe, E. H. & Buchanan, B. G. (1984) Rule-based expert systems: the MYCIN experiments of the Stanford Heuristic Programming Project. Addison-Wesley.





Metaxiotis, K. & Psarras, J. (2003) Expert systems in business: applications and future directions for the operations researcher. *Industrial Management & Data Systems*, 103, 5, 361-368.

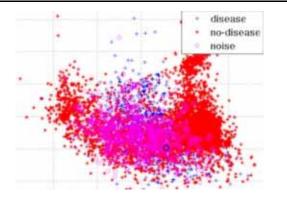






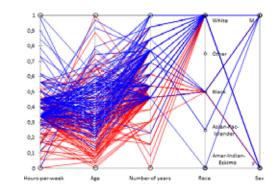
# Lecture 9: Interactive Visualization and Visual Analytics

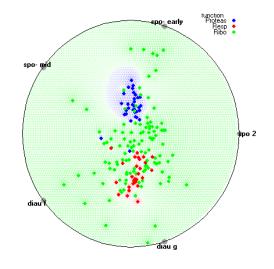




**Scatterplot** = oldest, point-based technique, projects data from n-dim space to an arbitrary k-dim display space;

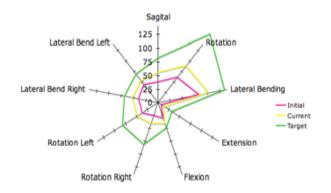
**Parallel coordinates** = (PCP), originally for the study of high-dimensional geometry, data point plotted as polyline;





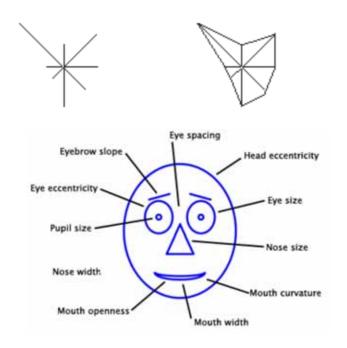
**RadViz** = Radial Coordinate visualization, is a "force-driven" point layout technique, based on Hooke's law for equilibrium;

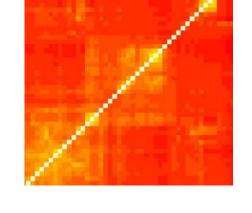




Radar chart (star plot, spider web, polar graph, polygon plot) = radial axis technique;

**Heatmap** = a tabular display technique using color instead of figures for the entries;

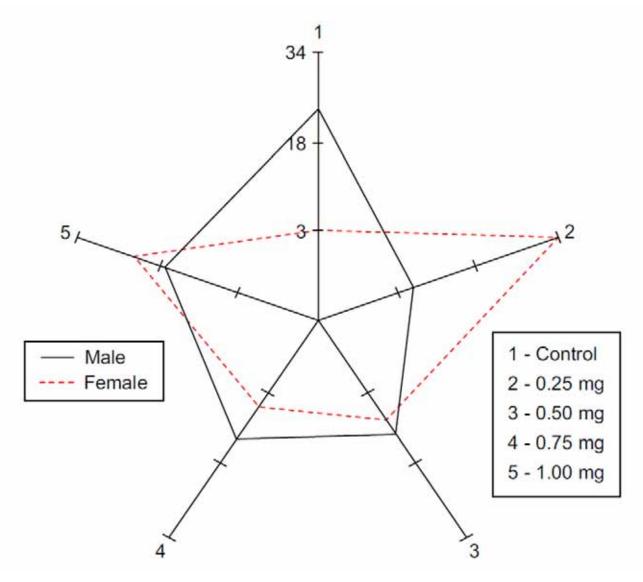




**Glyph** = a visual representation of the entity, where its attributes are controlled by data attributes;

**Chernoff face** = a face glyph which displays multivariate data in the shape of a human face



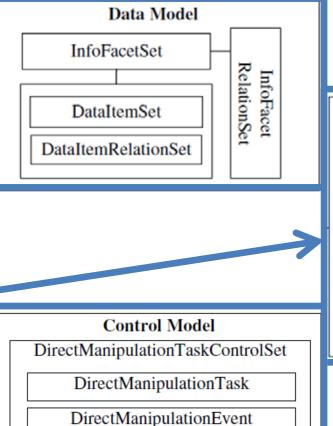


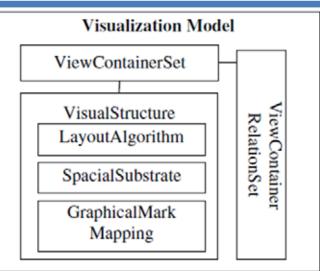
Saary, M. J. (2008) Radar plots: a useful way for presenting multivariate health care data. *Journal Of Clinical Epidemiology, 61, 4, 311-317.* 

### Slide 9-40 Design of Interactive Information Visualization



- 1) What facets of the target information should be visualized?
- 2) What data source should each facet be linked to and what relationships these facets have?
- 3) What layout algorithm should be used to visualize each facet?
- 4) What interactive techniques should be used for each facet and for which infovis tasks?





Ren, L., Tian, F., Zhang, X. & Zhang, L. (2010) DaisyViz: A model-based user interface toolkit for interactive information visualization systems. *Journal of Visual Languages & Computing, 21, 4, 209-229.* 

InDirectManipulationTaskControlSet

**DynamicQueryControl** 

KeywordSearchControl

FilterbyLegendsControl

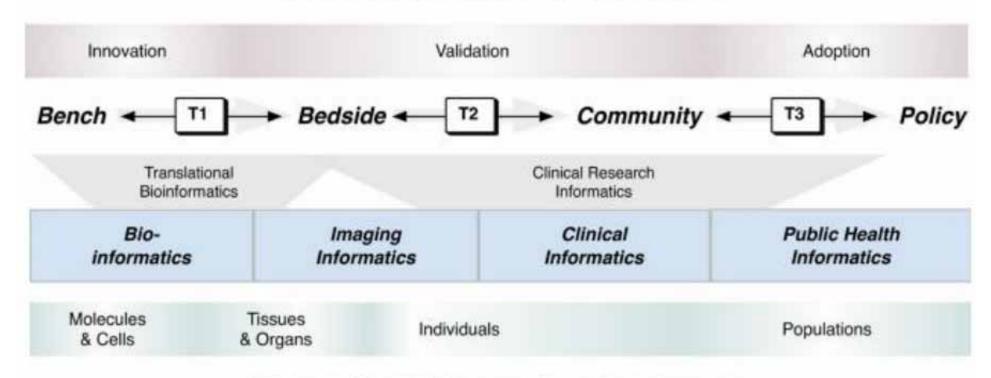


# Lecture 10: Biomedical Information Systems and Knowledge Management





### Translational Medicine Continuum



### **Biomedical Informatics Continuum**

Sarkar, I. 2010. Biomedical informatics and translational medicine. Journal of Translational Medicine, 8, (1), 2-12.

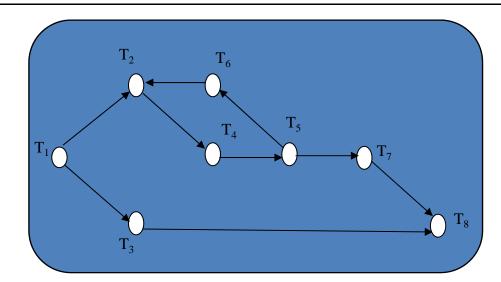




- A workflow is defined as a process that contains tasks T, and the respective rules on how those tasks are executed:
- Workflow W:=  $(T, P, C, A, S_0)$  where
  - $T = \{T_1, T_2, ... T_m\}$  A set of tasks,  $m \ge 1$
  - $P = (p_{ii})_{m \times m}$  Precedence matrix of the task set
  - $C = (c_{ij})_{m \times m}$  Conflict matrix of the task set
  - $A = (A(T_1), A(T_2), ..., A(T_m))$  Pre-Condition set for each task
  - $S_0 \in \{0, 1, 2, 3\}_m$  is the initial state

J. Wang, D. Rosca, W. Tepfenhart & A. Milewski (2006) Dynamic Workflow Modeling and Analysis, Monmouth University





$$T = \{T_1, T_2, ..., T_8\},\$$

$$A(T_1) = \emptyset, A(T_2) = \{\{T_1\}, \{T_6\}\}, A(T_3) = \{\{T_1\}\},\$$

$$A(T_4) = \{\{T_2\}\}, A(T_5) = \{\{T_4\}\},\$$

$$A(T_6) = A(T_7) = \{\{T_5\}\}, A(T_8) = \{\{T_3, T_7\}\}.\$$

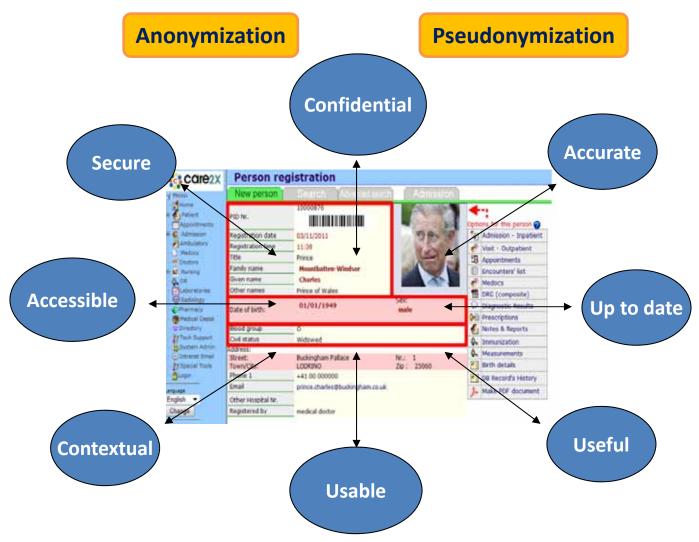
$$S_0 = (1, 0, 0, 0, 0, 0, 0, 0).$$

J. Wang, D. Rosca, W. Tepfenhart & A. Milewski (2006) Dynamic Workflow Modeling and Analysis, Monmouth University



## Lecture 11: Privacy, Data Protection, Safety, Security & Privacy Aware **Machine Learning**





Anonymization: Personal data cannot be re-identified (e.g. k-Anonymization)

Pseudonymization: The personal data is replaced by a "pseudonym", which allows later tracking back to the source data (re-identification)





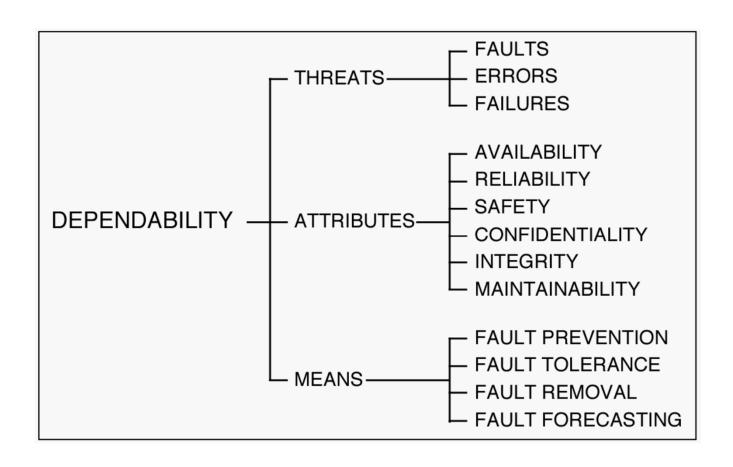
damage;



- Data Protection = all measures to ensure availability and integrity of data
- Privacy = (US pron. "prai ..."; UK pron. "pri ..."; from Latin: privatus "separated from the rest", are the individual rights of people to protect their personal life and matters Confidentiality = secrecy ("ärztliche Schweigepflicht")

Mills, K. S., Yao, R. S. & Chan, Y. E. (2003) Privacy in Canadian Health Networks: challenges and opportunities. Leadership in Health Services, 16, 1, 1-10.





Avizienis, A., Laprie, J. C. & Randell, B. (2001) Fundamental concepts of dependability. *Technical Report Computing Science University of Newcastle, 1145, CS-TR-739, 7-12.* 





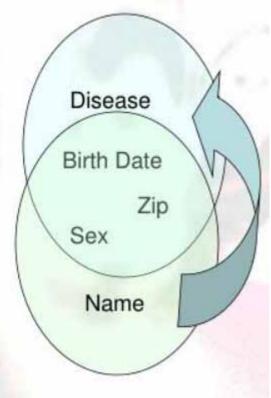
87 % of the population in the USA can be uniquely re-identified by Zip-Code, Gender and date of birth

### Hospital Patient Data

Birthdate	Sex	Zipcode	Disease
1/21/76	Male	53715	Flu
4/13/86	Fernole	53715	Hepatitis
2/28/76	Male	53703	Brochitis
1/21/76	Male	53703	Broken Arm
4/13/86	Female	53706	Sprained Ankle
2/28/76	Female	53706	Hang Nail

#### Voter Registration Data

Name	Birthdate	Sex	Zipcode
Andre 4	1/21/76	Male	53715
Beth	1/10/81	Female	55410
Carol	10/1/44	Female	90210
Dan	2/21/84	Male	02174
Eller:	4/19/72	Female	02237



Samarati, P. 2001. Protecting respondents identities in microdata release. IEEE Transactions on Knowledge and Data Engineering, 13, (6), 1010-1027, doi:10.1109/69.971193.

Sweeney, L. 2002. Achieving k-anonymity privacy protection using generalization and suppression. International Journal of Uncertainty, Fuzziness and Knowledge-Based Systems, 10, (05), 571-588.





- K-Anonymity ... a release of data is said to have the k-anonymity property if the information for each person contained in the release cannot be distinguished from at least k-1 individuals whose information also appear in the release.
- L-Diversity ... extension requiring that the values of all confidential attributes within a group of *k* sets contain at least *L* clearly distinct values
- t-Closeness ... extension requiring that the distribution of the confidential attribute within a group of *k* records is similar to the confidential attribute's distribution in the whole data set (local distribution must resemble the global distribution)



#### The Right to Be Forgotten: Towards Machine Learning on Perturbed Knowledge Bases

Bernd Malle<sup>1,2</sup>, Peter Kieseberg<sup>1,2</sup>, Edgar Weippl<sup>2</sup>, and Andreas Holzinger<sup>1(⊠)</sup>

<sup>1</sup> Holzinger Group HCI-KDD, Institute for Medical Informatics, Statistics and Documentation, Medical University Graz, Graz, Austria {b.malle,a.holzinger}@hci-kdd.org
<sup>2</sup> SBA Research gGmbH, Favoritenstrae 16, 1040 Vienna, Austria PKieseberg@sba-research.org

Abstract. Today's increasingly complex information infrastructures represent the basis of any data-driven industries which are rapidly becoming the 21st century's economic backbone. The sensitivity of those infrastructures to disturbances in their knowledge bases is therefore of crucial interest for companies, organizations, customers and regulating bodies. This holds true with respect to the direct provisioning of such information in crucial applications like clinical settings or the energy industry, but also when considering additional insights, predictions and personalized services that are enabled by the automatic processing of those data. In the light of new EU Data Protection regulations applying from 2018 onwards which give customers the right to have their data deleted on request, information processing bodies will have to react to these changing jurisdictional (and therefore economic) conditions. Their choices include a re-design of their data infrastructure as well as preventive actions like anonymization of databases per default. Therefore, insights into the effects of perturbed/anonymized knowledge bases on

Malle, B., Kieseberg, P., Weippl, E. & Holzinger, A. 2016. The right to be forgotten: Towards Machine Learning on perturbed knowledge bases. Springer Lecture Notes in Computer Science LNCS 9817. Heidelberg, Berlin, New York: Springer, pp. 251-256, doi:10.1007/978-3-319-45507-5\_17.



#### Europäischer Datenschutz in der Big-Data-Welt



(Bild: Håkan Dahlström CC BY 2.0<br>)

Datensparsamkeit ist schwierig in Big Data-Zeiten. Der Beirat der Datenschutzkonvention des Europarats hat eine Reihe von Richtlinien für Dataminer vorgelegt. Derweil warnt der SAP-Finanzchef vor Risiken von EU-Datenschutzregeln.

Der Beirat der Datenschutzkonvention des Europarat legte zum Internationalen Datenschutztag "Richtlinien zum Schutz persönlicher Daten in einer Big Data-Welt" vor.

**Holzinger Group** 65



