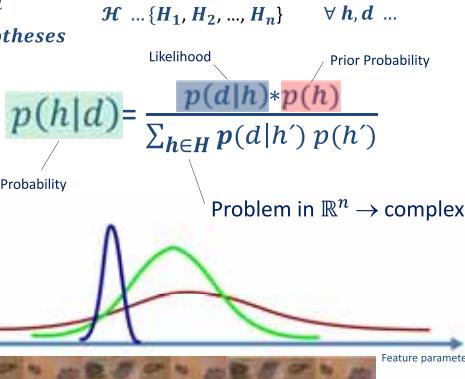


01 Decision Making under uncertainty

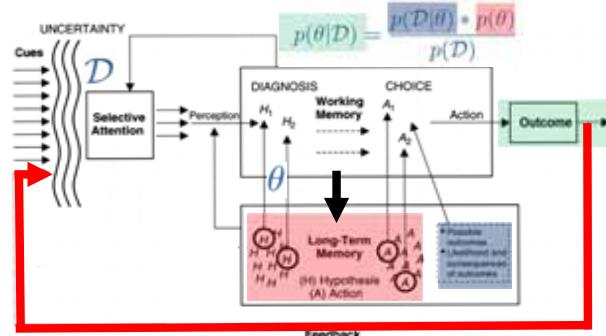
Laplace, P.-S. 1781. Mémoire sur les probabilités. *Mémoires de l'Académie Royale des sciences de Paris*, 1778, 227-332.



$d \dots \text{data}$
 $h \dots \text{hypotheses}$



Connection to Cognitive Science: Decision Making



Predicting Pragmatic Reasoning in Language Games

You are talking to your colleague and want to refer to the middle object – which wording would you prefer: circle or blue?



Frank, M. C. & Goodman, N. D. 2012. Predicting pragmatic reasoning in language games. *Science*, 336, (6084), 998-998, doi:10.1126/science.1218633.

Recursive reasoning: a case for probabilistic programming

```
var literalListener = function(property){
  Infer(function(){
    var object = refPrior(context)
    condition(object[property])
    return object
  })
}

var speaker = function(object) {
  Infer(function(){
    var property = propPrior()
    condition(
      object ==
        property
    )
  })
}

var listener = function(property) {
  Infer(function(){
    var object = refPrior(context)
    condition(utterance ==
      sample(speaker(object)))
    return object
  })
}
```



Goodman, N. D. & Frank, M. C. 2016. Pragmatic language interpretation as probabilistic inference. *Trends in Cognitive Sciences*, 20, (11), 818-829.

What are Probabilistic Graphical Models?

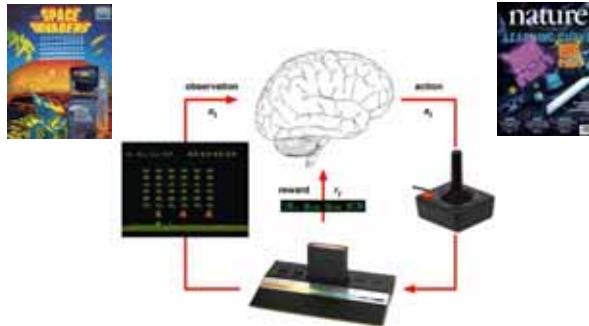
- PGM can be seen as a combination between
- **Graph Theory + Probability Theory + Machine Learning**
- One of the most exciting advancements in AI in the last decades – with enormous future potential
- Compact representation for exponentially-large probability distributions
- Example Question:
“Is there a path connecting two proteins?”
- $\text{Path } (X, Y) := \text{edge } (X, Y)$
- $\text{Path } (X, Y) := \text{edge } (X, Y), \text{path}(Z, Y)$
- This can NOT be expressed in first-order logic
- Would need a Turing-complete fully-fledged language

2) Some basics of Markov Processes in Machine Learning

Please remember:

- Markov processes are ...
- random processes in which the future, given the present, is independent of the past!
- one of the most important classes of random processes!

TU Learning to play an Atari Game



Mnih, V., Kavukcuoglu, K., Silver, D., Rusu, A. A., Veness, J., Bellemare, M. G., Graves, A., Riedmiller, M., Fidjeland, A. K., Ostrovski, G., Petersen, S., Beattie, C., Sadik, A., Antonoglou, I., King, H., Kumaran, D., Wierstra, D., Legg, S. & Hassabis, D. 2015. Human-level control through deep reinforcement learning. *Nature*, 518, (7540), 529-533, doi:10.1038/nature14236

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TU Example Video Atari Game



TU Goal: Select actions to maximize total future reward

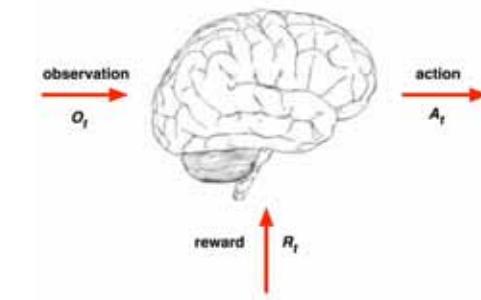


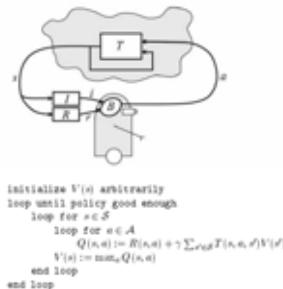
Image credit to David Silver, UCL

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TU Standard RL-Agent Model goes back to Cybernetics 1950



```
Initialize V(x) arbitrarily
loop until policy good enough
  loop for s in S
    loop for a in A
      Q(s,a) := R(s,a) + γ ∑ s' P(s,a,s')V(s')
      V(s) := max_a Q(s,a)
    end loop
  end loop
end loop
```

Kaelbling, L. P., Littman, M. L. & Moore, A. W. 1996. Reinforcement learning: A survey. *Journal of Artificial Intelligence Research*, 4, 237-285.

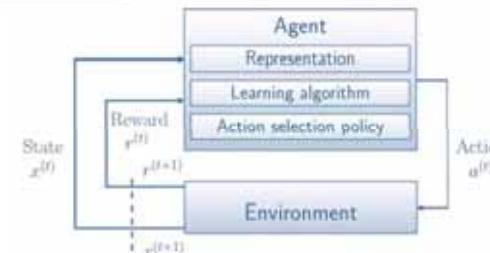
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TU RL-Agent seeks to maximize rewards

Intelligent behavior arises from the actions of an individual seeking to **maximize its received reward** signals in a **complex and changing world**



Sutton, R. S. & Barto, A. G. 1998. Reinforcement learning: An introduction, Cambridge MIT press

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TU RL – Types of Feedback (crucial!!)

- Supervised: Learner told best a
- Exhaustive: Learner shown every possible x
- One-shot: Current x independent of past a



Littman, M. L. 2015. Reinforcement learning improves behaviour from evaluative feedback. *Nature*, 521, (7553), 445-451.

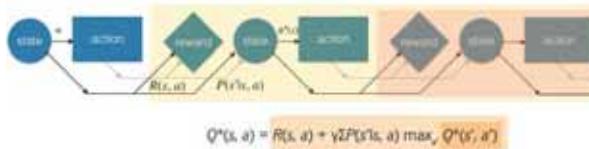
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TU Problem Formulation in a MDP

- Markov decision processes specify setting and tasks
- Planning methods use knowledge of P and R to compute a good policy π
- Markov decision process model captures both sequential feedback and the more specific one-shot feedback (when $P(s'|s, a)$ is independent of both s and a)



Littman, M. L. 2015. Reinforcement learning improves behaviour from evaluative feedback. *Nature*, 521, (7553), 445-451.

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TU Agent observes environmental state at each step t

- 1) Observes
- 2) Executes
- 3) Receives Reward
- Executes action A_t :
- $O_t = sa_t = se_t$
- Agent state = environment state = information state
- Markov decision process (MDP)

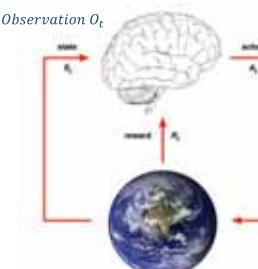


Image credit to David Silver, UCL

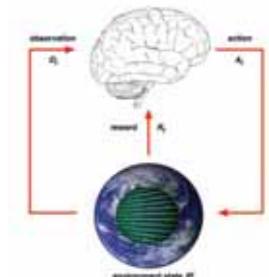
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TU Environmental State is the current representation

- i.e. whatever data the environment uses to pick the next observation/reward
- The environment state is not usually visible to the agent
- Even if S is visible, it may contain irrelevant information
- A State S_t is Markov iff:

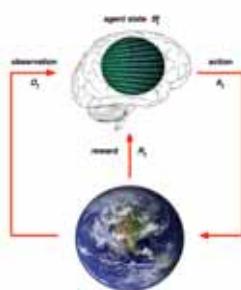


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- i.e. whatever information the agent uses to pick the next action
- it is the information used by reinforcement learning algorithms
- It can be any function of history:
- $S = f(H)$



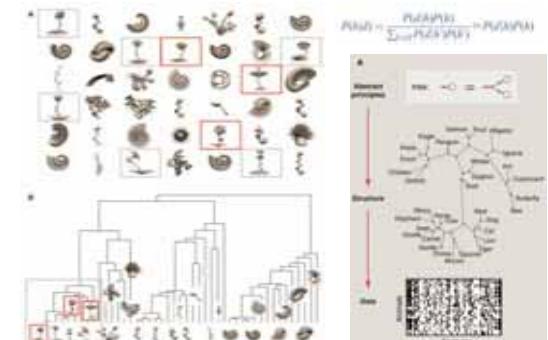
$$H_t = O_1, R_1, A_1, \dots, A_{t-1}, O_t, R_t$$

- RL agent components:
 - Policy: agent's behaviour function
 - Value function: how good is each state and/or action
 - Model: agent's representation of the environment
- Policy as the agent's behaviour
 - is a map from state to action, e.g.
 - Deterministic policy: $a = (s)$
 - Stochastic policy: $(a|s) = P[At = aj | St = s]$
- Value function is prediction of future reward:

$$v_\pi(s) = \mathbb{E}_\pi [R_{t+1} + \gamma R_{t+2} + \gamma^2 R_{t+3} + \dots | S_t = s]$$

- Partial observability: when agent only indirectly observes environment (robot which is not aware of its current location; good example: Poker play: only public cards are observable for the agent):
- Formally this is a Partially Observable Markov Decision Process (POMDP):
 - Agent must construct its own state representation S , for example:
 - Complete history: $S_t^a = H_t$
 - Beliefs of environment state: $S_t^a = (\mathbb{P}[S_t^a = s^1], \dots, \mathbb{P}[S_t^a = s^d])$
 - Recurrent neural network: $S_t^a = \sigma(S_{t-1}^a W_s + O_t W_o)$

3) Some basics of Concept Learning



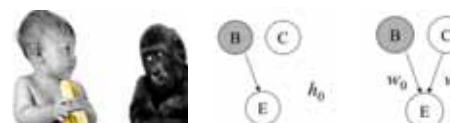
- which is highly relevant for ML research, concerns the factors that determine the subjective difficulty of concepts:
- Why are some concepts psychologically extremely simple and easy to learn,
- while others seem to be extremely difficult, complex, or even incoherent?
- These questions have been studied since the 1960s but are still unanswered ...

Feldman, J. 2000. Minimization of Boolean complexity in human concept learning. *Nature*, 407, (6804), 630-633, doi:10.1038/35036586.

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▪ Cognition as probabilistic inference

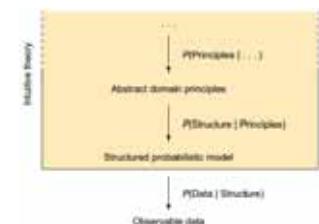
- Visual perception, language acquisition, motor learning, associative learning, memory, attention, categorization, reasoning, causal inference, decision making, theory of mind
- Learning concepts from examples
- Learning causation from correlation
- Learning and applying intuitive theories (balancing complexity vs. fit)

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- Similarity
- Representativeness and evidential support
- Causal judgement
- Coincidences and causal discovery
- Diagnostic inference
- Predicting the future

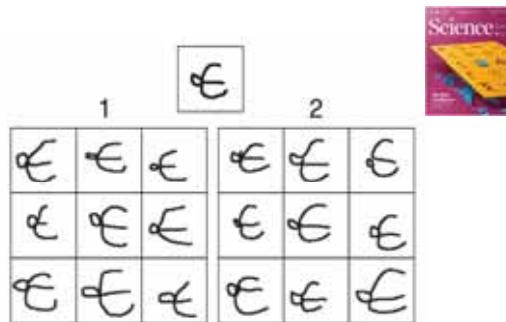


Tenenbaum, J. B., Griffiths, T. L. & Kemp, C. 2006. Theory-based Bayesian models of inductive learning and reasoning. *Trends in cognitive sciences*, 10, (7), 309-318.

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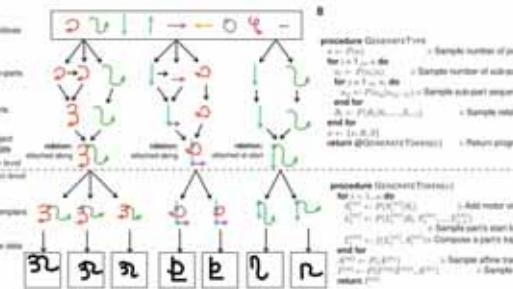
Lake, B. M., Salakhutdinov, R. & Tenenbaum, J. B. 2015. Human-level concept learning through probabilistic program induction. *Science*, 350, (6266), 1332-1338, doi:10.1126/science.aab3050.

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A Bayesian program learning (BPL) framework, capable of learning a large class of visual concepts from just a single example and generalizing in ways that are mostly indistinguishable from people



Lake, B. M., Salakhutdinov, R. & Tenenbaum, J. B. 2015. Human-level concept learning through probabilistic program induction. *Science*, 350, (6266), 1332-1338.

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4) Graphs=Networks

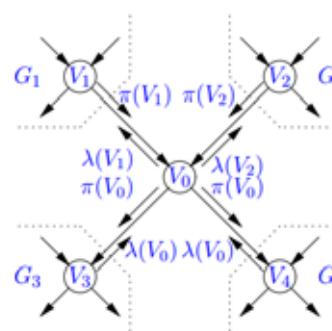


Image from <https://people.kth.se/~carlofi/teaching/FEL3250-2013/courseinfo.html>

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Pearl, J. 1988. Embracing causality in default reasoning. *Artificial Intelligence*, 35, (2), 259-271.

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Source: Based on the Nobel Prize in Chemistry 2013
DEVELOPMENT OF MULTICALE MODELS FOR COMPLEX QUANTUM SYSTEMS
Wolfgang Klemm, Martin Karplus, Michael Levitt
Prize share: 1/2
http://www.nobelprize.org/nobel_prizes/chemistry/laureates/2013/



http://news.harvard.edu/gazette/story/2013/10/nobel_prize_awarded_2013/

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We skip this interesting chapter for now ...

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Network challenges

NGC 5139 Omega Centauri by Edmund Halley in 1677, ESO, Atacama, Chile

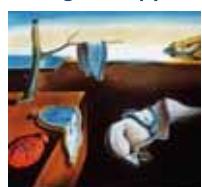
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Time

e.g. Entropy



Dali, S. (1931) The persistence of memory

Space

e.g. Topology

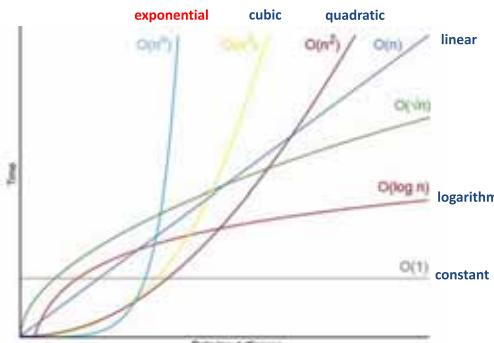


Bagula & Bourke (2012) Klein-Bottle

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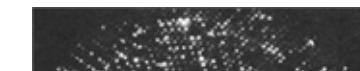


P versus NP and the Computational Complexity Zoo, please have a look at
<https://www.youtube.com/watch?v=YX40hbAHx3s>

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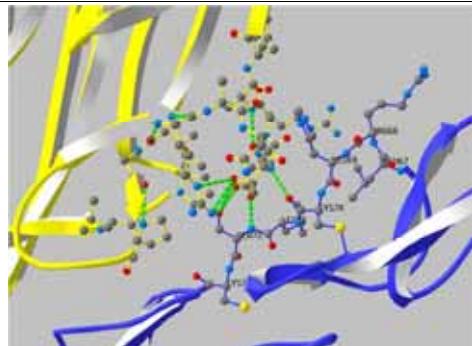
ATOM	1	N	GLY	A	1	44,942	51,014	101,284	0.01	27,10
ATOM	2	C8	GLY	A	1	45,440	50,120	100,389	0.01	26,99
ATOM	3	C	GLY	A	1	46,694	49,448	101,309	0.01	26,80
ATOM	4	O	GLY	A	1	46,895	50,222	102,381	0.01	26,91
ATOM	5	H	BER	A	2	47,283	49,518	100,951	1.00	26,26
ATOM	6	C4	BER	A	2	48,277	47,666	101,761	1.00	26,17
ATOM	7	C	BER	A	2	49,252	47,700	100,845	1.00	24,21
ATOM	8	O	BER	A	2	49,400	47,155	100,490	1.00	27,79
ATOM	9	C8	BER	A	2	47,459	49,091	100,500	1.00	26,31
ATOM	10	O6	BER	A	2	46,276	44,156	102,404	1.00	27,99
ATOM	11	N	BIS	A	3	50,147	46,186	101,370	1.00	23,90
ATOM	12	C4	BIS	A	3	51,129	45,389	100,659	1.00	21,44
ATOM	13	C	BIS	A	3	50,953	43,905	100,849	1.00	20,32
ATOM	14	O	BIS	A	3	50,539	43,595	101,956	1.00	22,00
ATOM	15	C8	BIS	A	3	52,558	45,674	100,990	1.00	19,69
ATOM	16	C	BIS	A	3	52,1940	45,000	100,400	1.00	23,84
ATOM	17	N93	BIS	A	3	53,177	47,170	101,423	1.00	20,87
ATOM	18	C93	BIS	A	3	53,956	48,175	101,433	1.00	21,69
ATOM	19	CE3	BIS	A	3	53,676	48,730	99,476	1.00	20,87

Wiltgen, M., & Holzinger, A. (2005) Visualization in Bioinformatics: Protein Structures with Physicochemical and Biological Annotations. In: Central European Multimedia and Virtual Reality Conference. Prague, Czech Technical University (CTU), 69-74

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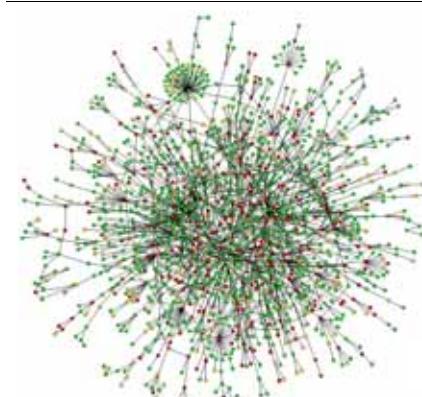


Wiltgen, M., Holzinger, A., & Tilz, G. P. (2007) Interactive Analysis and Visualization of Macromolecular Interfaces Between Proteins. In: *Lecture Notes in Computer Science (LNCS 4799)*. Berlin, Heidelberg, New York, Springer, 199-212.

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Nodes = proteins
Links = physical interactions (bindings)
Red Nodes = lethal
Green Nodes = non-lethal
Orange = slow growth
Yellow = not known

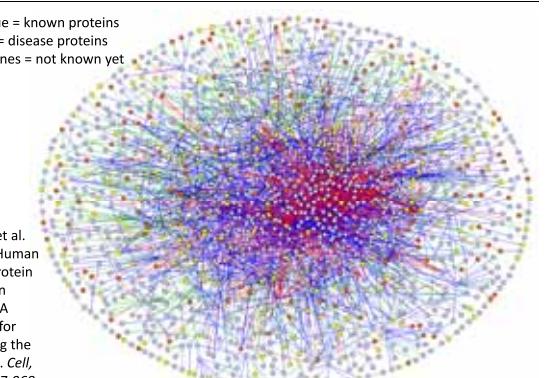
Jeong, H., Mason, S. P., Barabasi, A. L. & Oltvai, Z. N. (2001) Lethality and centrality in protein networks. *Nature*, 411, 6833, 41-42.

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Light blue = known proteins
Orange = disease proteins
Yellow ones = not known yet

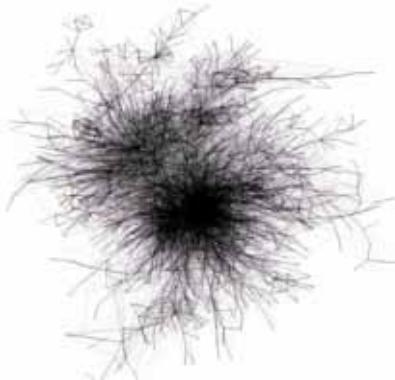


Stelzl, U. et al. (2005) A Human Protein-Protein Interaction Network: A Resource for Annotating the Proteome. *Cell*, 122, 6, 957-968.

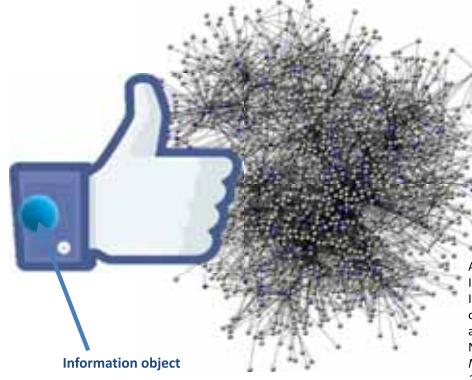
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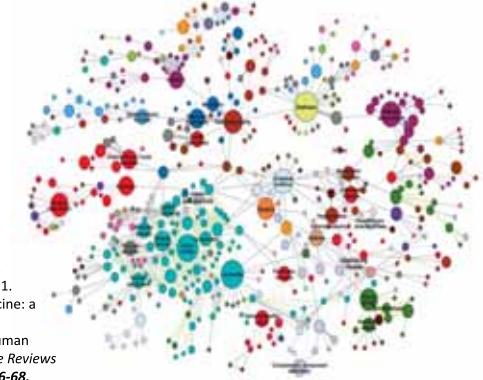
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Hurst, M. (2007). Data Mining: Text Mining, Visualization and Social Media. Online available: http://datamining.typepad.com/data_mining/2007/01/the_blogosphere.html, last access: 2011-09-24



Aral, S. (2011) Identifying Social Influence: A Comment on Opinion Leadership and Social Contagion in New Product Diffusion. *Marketing Science*, 30, 2, 217-223.



Barabási, A. L., Gulbahce, N. & Loscalzo, J. 2011. Network medicine: a network-based approach to human disease. *Nature Reviews Genetics*, 12, 56-68.

05 Bayesian Networks "Bayes' Nets"

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

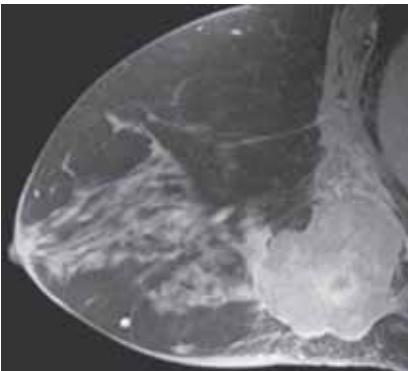
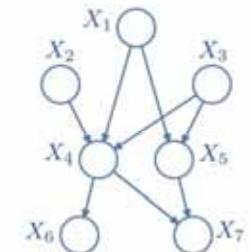
$$p(x_1, \dots, x_n) = \prod_{i=1}^n p(x_i | Pa(x_i))$$

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

BN inherently model the uncertainty in the data. 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.

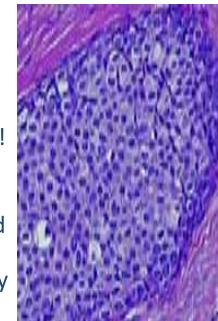
Pearl, J. (1988) *Probabilistic reasoning in intelligent systems: networks of plausible inference*. San Francisco, Morgan Kaufmann.

$$p(X_1, \dots, X_7) = \\ p(X_1)p(X_2)p(X_3)p(X_4|X_1, X_2, X_3) \cdot \\ p(X_5|X_1, X_3)p(X_6|X_4)p(X_7|X_4, X_5)$$

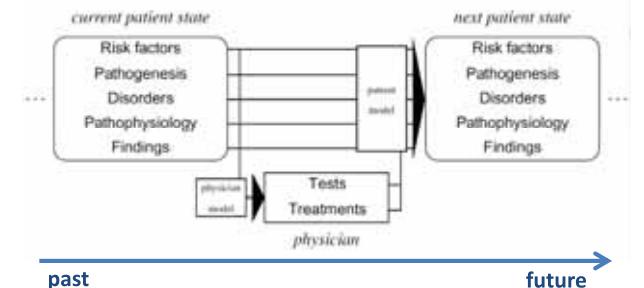


Overmoyer, B. A., Lee, J. M. & Lerwill, M. F. (2011) Case 17-2011 A 49-Year-Old Woman with a Mass in the Breast and Overlying Skin Changes. *New England Journal of Medicine*, 364, 23, 2246-2254.

- = the prediction of the future course of a disease conditional on the patient's history and a projected treatment strategy
- Danger: probable Information !
- Therefore valid prognostic models can be of great benefit for clinical decision making and of great value to the patient, e.g., for notification and quality of-life decisions



Knaus, W. A., Wagner, D. P. & Lynn, J. (1991) Short-term mortality predictions for critically ill hospitalized adults: science and ethics. *Science*, 254, 5030, 389.



van Gerven, M. A. J., Taal, B. G. & Lucas, P. J. F. (2008) Dynamic Bayesian networks as prognostic models for clinical patient management. *Journal of Biomedical Informatics*, 41, 4, 515-529.

TU Example: Breast cancer - Probability Table

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Category	Node description	State description
Diagnosis	Breast cancer	Present, absent.
Clinical history	Habit of drinking alcoholic beverages and smoking	Yes, no
	Taking female hormones	Yes, no
	Have gone through menopause	Yes, no
	Have ever been pregnant	Yes, no
	Family member has breast cancer	Yes, no
Physical findings	Nipple discharge	Yes, no
	Skin thickening	Yes, no
	Breast pain	Yes, no
	Have a lump	Yes, no
Mammographic findings	Architectural distortion:	Present, absent.
	Mass	Score from one to three, score from four to five, absent
	Microcalcification cluster	Score from one to three, score from four to five, absent
	Asymmetry	Present, absent.

Wang, X. H., et al. (1999) Computer-assisted diagnosis of breast cancer using a data-driven Bayesian belief network. *International Journal of Medical Informatics*, 54, 2, 115-126.

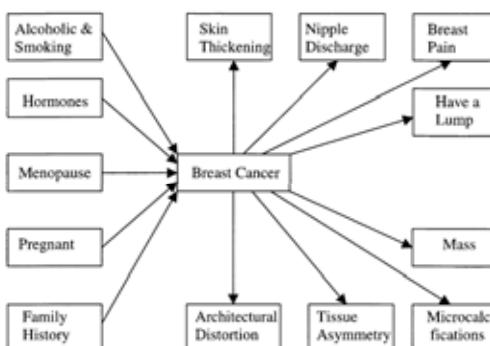
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TU Breast cancer – big picture – state of 1999

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Wang, X. H., et al. (1999) Computer-assisted diagnosis of breast cancer using a data-driven Bayesian belief network. *International Journal of Medical Informatics*, 54, 2, 115-126.

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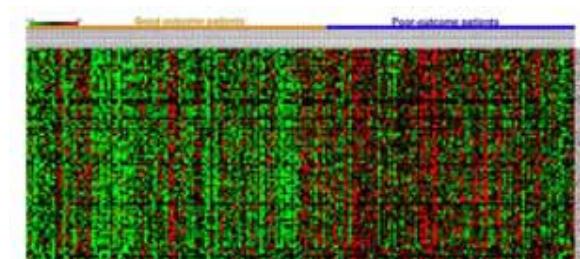
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TU 10 years later: Integration of microarray data

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- Integrating microarray data from multiple studies to increase sample size;
- approach to the development of more robust prognostic tests



Xu, L., Tan, A., Winslow, R. & Geman, D. (2008) Merging microarray data from separate breast cancer studies provides a robust prognostic test. *BMC Bioinformatics*, 9, 1, 125-139.

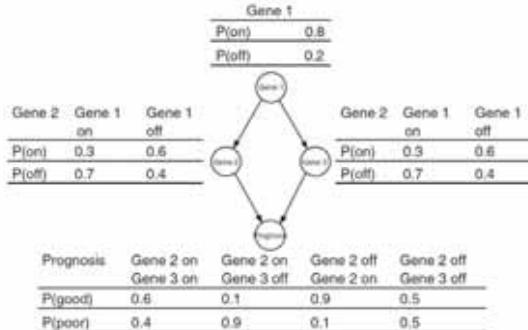
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TU Example: BN with four binary variables

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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.

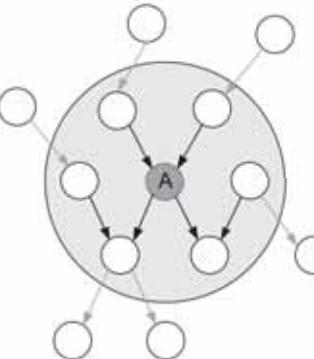
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TU Concept Markov-Blanket

HCI-KDD



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.

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TU Dependency Structure -> first step (1/2)

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- First the structure is learned using a search strategy.
- Since the number of possible structures increases super exponentially with the number of variables,
- the well-known greedy search algorithm K2 can be used in combination with the Bayesian Dirichlet (BD) scoring metric:

$$p(S|D) \propto p(S) \prod_{i=1}^n \prod_{j=1}^{q_i} \left[\frac{\Gamma(N'_{ij})}{\Gamma(N'_{ij} + N_{ij})} \prod_{k=1}^{r_i} \frac{\Gamma(N'_{ijk} + N_{ijk})}{\Gamma(N'_{ijk})} \right]$$

N_{ijk} ... number of cases in the data set D
having variable i in state k associated with the j -th instantiation of its parents in current structure S .
 n is the total number of variables.

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TU Dependency Structure – first step (2/2)

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- Next, N_{ij} is calculated by summing over all states of a variable:
- $N_{ij} = \sum_{k=1}^{r_i} N_{ijk} \cdot N'_{ijk}$ and N'_{ijk} have similar meanings but refer to prior knowledge for the parameters.
- When no knowledge is available they are estimated using $N_{ijk} = N / (r_i q_i)$ with N the equivalent sample size,
- r_i the number of states of variable i and
- q_i the number of instantiations of the parents of variable i .
- $\Gamma(\cdot)$ corresponds to the gamma distribution.
- Finally $p(S)$ is the prior probability of the structure.
- $p(S)$ is calculated by:
- $p(S) = \prod_{i=1}^n \prod_{j=1}^{p_i} p(l_i \rightarrow x_i) \prod_{m_i=1}^{o_i} p(m_i x_i)$ with p_i the number of parents of variable x_i and o_i all the variables that are not a parent of x_i .
- Next, $p(a \rightarrow b)$ is the probability that there is an edge from a to b while $p(ab)$ is the inverse, i.e. the probability that there is no edge from a to b

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TU Parameter learning -> second step

HCI-KDD

- Estimating the parameters of the local probability models corresponding with the dependency structure.
- CPTs are used to model these local probability models.
- For each variable and instantiation of its parents there exists a CPT that consists of a set of parameters.
- Each set of parameters was given a uniform Dirichlet prior:

$$p(\theta_{ij}|S) = Dir(\theta_{ij}|N'_{ij1}, \dots, N'_{ijk}, \dots, N'_{ijr_i})$$

Note: With θ_{ij} a parameter set where i refers to the variable and j to the j -th instantiation of the parents in the current structure. θ_{ij} contains a probability for every value of the variable x_i given the current instantiation of the parents. Dir corresponds to the Dirichlet distribution with $(N'_{ij1}, \dots, N'_{ijr_i})$ as parameters of this Dirichlet distribution. Parameter learning then consists of updating these Dirichlet priors with data. This is straightforward because the multinomial distribution that is used to model the data, and the Dirichlet distribution that models the prior, are conjugate distributions. This results in a Dirichlet posterior over the parameter set:

$$p(\theta_{ij}|D, S) = Dir(\theta_{ij}|N'_{ij1} + N_{ij1}, \dots, N'_{ijk} + N_{ijk}, \dots, N'_{ijr_i} + N_{ijr_i})$$

with N_{ijk} defined as before.

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TU Predicting the prognosis of breast cancer (integrated a.)

HCI-KDD



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, 184-190.

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- For certain cases it is tractable if:
 - Just one variable is unobserved
 - We have singly connected graphs (no undirected loops -> belief propagation)
 - Assigning probability to fully observed set of variables
- Possibility: Monte Carlo Methods (generate many samples according to the Bayes Net distribution and then count the results)
- Otherwise: approximate solutions, NOTE:
Sometimes it is better to have an approximate solution to a complex problem – than a perfect solution to a simplified problem

Often it is better to have a good solution within time – than an perfect solution (much) later ...

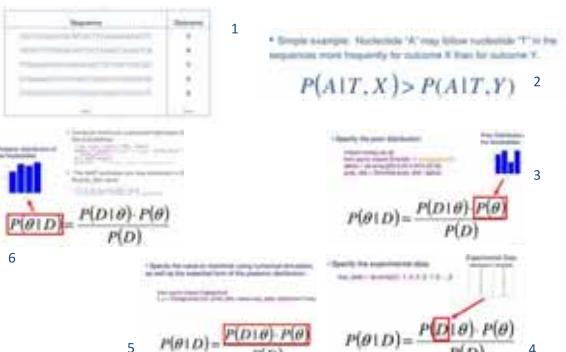


- C → Probabilistic-C
- Scala → Figaro
- Scheme → Church
- Excel → Tabular
- Prolog → ProbLog
- Javascript → webPP
- → Venture
- Python → PyMC



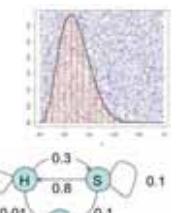
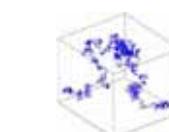
PyMC
Pythonic Markov chain Monte Carlo

Probabilistic Program	Graphical Model
Variables	Variable nodes
Functions/operators	Factor nodes/edges
Fixed size loops/arrays	Plates
If statements	Gates (Minka & Winn)
Variable sized loops, Complex indexing, jagged arrays, mutation, recursion, objects/ properties...	No common equivalent



07 Markov Chain Monte Carlo (MCMC)

**Monte Carlo Method (MC)
Monte Carlo Sampling
Markov Chains (MC)
MCMC
Metropolis-Hastings**



- often we want to calculate characteristics of a **high-dimensional** probability distribution ... $p(\mathcal{D}|\theta)$

$$p(h|d) \propto p(\mathcal{D}|\theta) * p(h)$$

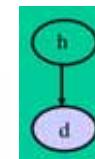
Posterior integration problem: (almost) all statistical inference can be deduced from the posterior distribution by calculating the appropriate sums, which involves an integration:

$$J = \int f(\theta) * p(\theta|\mathcal{D}) d\theta$$

- Statistical physics:** computing the partition function – this is evaluating the posterior probability of a hypothesis and this requires summing over all hypotheses ... remember:

$$\mathcal{H} = \{H_1, H_2, \dots, H_n\} \quad \forall(h, d)$$

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

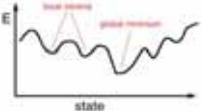


- Class of algorithms that rely on **repeated random sampling**
- Basic idea: using **randomness** to solve problems with high uncertainty (Laplace, 1781)
- For solving **multidimensional integrals** which would otherwise intractable
- For simulation of systems with **many dof**
- e.g. fluids, gases, particle collectives, **cellular structures** - see our last tutorial on Tumor growth simulation!

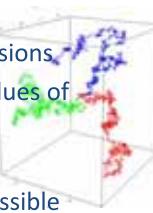
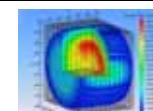
- for solving problems of probabilistic inference involved in developing computational models
- as a source of hypotheses about how the human mind might solve problems of inference
- For a function $f(x)$ and distribution $P(x)$, the expectation of f with respect to P is generally the average of f , when x is drawn from the probability distribution $P(x)$

$$\mathbb{E}_{p(x)}(f(x)) = \sum_X f(x)P(x)dx$$

- Solving intractable integrals
- Bayesian statistics: **normalizing** constants, expectations, marginalization
- Stochastic Optimization
- Generalization of simulated annealing
- Monte Carlo expectation maximization (EM)



- Physical simulation
- estimating neutron diffusion time
- Computing expected utilities and best responses toward Nash equilibria
- Computing volumes in high-dimensions
- Computing eigen-functions and values of operators (e.g. Schrödinger)
- Statistical physics
- Counting many things as fast as possible



- Expectation of a function $f(x, y)$ with respect to a random variable x is denoted by $\mathbb{E}_x [f(x, y)]$
- In situations where there is no ambiguity as to which variable is being averaged over, this will be simplified by omitting the suffix, for instance $\mathbb{E}x$.
- If the distribution of x is conditioned on another variable z , then the corresponding conditional expectation will be written $\mathbb{E}_x[f(x)|z]$
- Similarly, the variance is denoted $var[f(x)]$, and for vector variables the covariance is written $cov[x, y]$

$$\underset{x}{\operatorname{argmax}} f(x)$$

Normalization: $p(x|y) = \frac{p(y|x) * p(x)}{\int_X p(y|x) * p(x) dx}$

Marginalization: $p(x) = \int_Z p(x, z) dz$

Expectation: $\mathbb{E}_{p(x)}(f(x)) = \int_X f(x)p(x)dx$

TU Metropolis Hastings MCMC sampling

Barber, D. 2012. Bayesian reasoning and machine learning. Cambridge, Cambridge University Press, p. 500

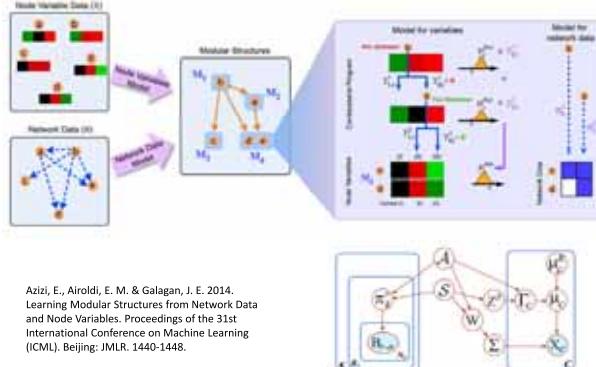
```

1: Choose a starting point  $x^1$ .
2: for  $i = 2$  to  $L$ , do
3:   Draw a candidate sample  $x^{i,\text{cand}}$  from the proposal  $\hat{q}(x^i|x^{i-1})$ .
4:   Let  $a = \frac{\hat{q}(x^{i-1}|x^{i,\text{cand}})}{\hat{q}(x^i|x^{i-1})}$ 
5:   if  $a \geq 1$  then  $x^i = x^{i,\text{cand}}$ 
6:   else
7:     draw a random value uniformly from the unit interval  $[0, 1]$ .
8:     if  $u < a$  then  $x^i = x^{i,\text{cand}}$ 
9:     else
10:       $x^i = x^{i-1}$ 
11:    end if
12:  end if
13: end for

```



TU Example



TU Finally a practical example

Algorithm 1 RJMCMC for sampling parameters

Inputs:
Node Variables Data X .
Network Data B .
For iterations $j = 1$ to J do
 Sample $\mathcal{A}^{(j+1)}$ given $\mathcal{A}^{(j)}$ using Alg 2 in (Azizi et al., 2014).
 Sample $\mathcal{S}^{(j+1)}$ given $\mathcal{S}^{(j)}$ using Alg 3 in (Azizi et al., 2014).
 For modules $k = 2$ to $R^{(j)}$ do
 Propose $w_k^{(j+1)} \sim \mathcal{N}(w_k^{(j)}, I)$. Accept with probability P_{acc} . Update $\Sigma^{(j+1)}$.
 For parents $r = 1$ to C do
 Propose $\mu_r^{(j+1)} \sim \mathcal{N}(\mu_r^{(j)}, I)$; accept with P_{acc} .
 Propose $\gamma_r^{(j+1)} \sim \mathcal{N}(\gamma_r^{(j)}, I)$; accept with P_{acc} .
 end for
 end for
 For condition $r = 1$ to C do
 Propose $\mu_{B(r+1)}^{(j+1)} \sim \mathcal{N}(\mu_{B(r)}^{(j)}, I)$; accept with P_{acc} .
 Propose $\gamma_{B(r+1)}^{(j+1)} \sim \mathcal{N}(\gamma_{B(r)}^{(j)}, I)$; accept with P_{acc} .
 end for
end for

Azizi, E., Airolldi, E. M. & Galagan, J. E. 2014. Learning Modular Structures from Network Data and Node Variables. Proceedings of the 31st International Conference on Machine Learning (ICML), Beijing: JMLR. 1440-1448.

08 Metropolis-Hastings Algorithm

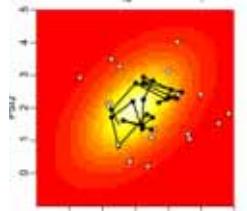
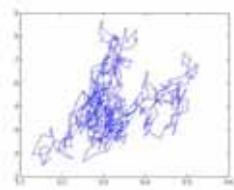


Image Source: Peter Mueller,
Anderson Cancer Center

TU Importance sampling

- Importance sampling is a technique to approximate averages with respect to an intractable distribution $p(x)$.
- The term ‘sampling’ is arguably a misnomer since the method does not attempt to draw samples from $p(x)$.
- Rather the method draws samples from a simpler importance distribution $q(x)$ and then reweights them
- such that averages with respect to $p(x)$ can be approximated using the samples from $q(x)$.

TU Gibbs Sampling

- The Gibbs Sampler is an interesting special case of MH:

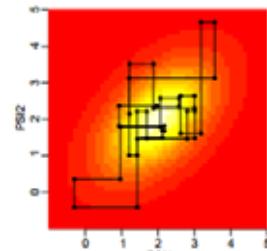
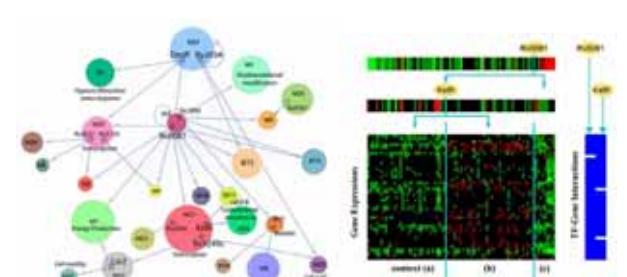
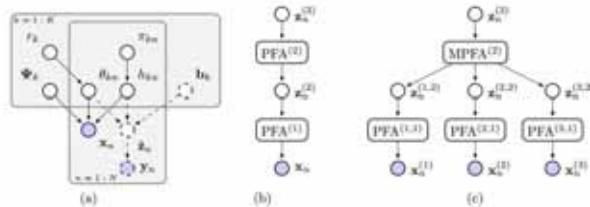


Image Source: Peter Mueller,
Anderson Cancer Center

TU Myobacterium tuberculosis Gene Regulatory Network



Azizi, E., Airolldi, E. M. & Galagan, J. E. 2014. Learning Modular Structures from Network Data and Node Variables. Proceedings of the 31st International Conference on Machine Learning (ICML), Beijing: JMLR. 1440-1448.



Henao, R., Lu, J. T., Lucas, J. E., Ferranti, J. & Carin, L. 2016. Electronic health record analysis via deep poisson factor models. Journal of Machine Learning Research JMLR, 17, 1-32.

TU Sample Questions

- What is the main difference between the ideas of Pierre Simon de Laplace and Lady Lovelace?
- What is medical action consisting most of the time?
- How does a human make a decision - as far as we know?
- What is the main idea of a probabilistic programming language?
- Why did Judea Pearl receive the Turing Award (Noble Prize in Computer Science)?
- What fields are coming together in PGM?
- What are the challenges in network structures?
- Give a classification of Graphical Models!
- What are plates and nested plates?
- Provide corresponding examples of metabolic networks!

TU Basics and Background reading



Bishop, C. M. 2007. Pattern Recognition and Machine Learning, Heidelberg, Springer. Chapter 8 on graphical models openly available: <http://research.microsoft.com/en-us/um/people/cmbishop/prml/>

Murphy, K. P. 2012. Machine learning: a probabilistic perspective, MIT press. Chapter 26 (pp. 907) – Graphical model structure learning

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



Thank you!

Questions

- What is a factored graph?
- Describe the protein structure prediction problem! Why is it hard?
- Why are protein-protein interactions so important?
- Describe the problem of graph-isomorphism!
- How does a Bayes Net work?
- Why is predicting important in clinical medicine?
- What is a Markov-Blanket?
- Which two tasks do we have in Graphical Model Learning?
- Why would we need probabilistic programming languages?
- Describe the main idea of MCMC!
- What is the main problem in marginalization?
- What is the benefit of the MH Algorithm?

TU Some more specialist literature



Rubinstein, R. Y. & Kroese, D. P. 2013. The cross-entropy method: a unified approach to combinatorial optimization, Monte-Carlo simulation and machine learning, Springer



Cameron Davidson-Pilon 2015. Bayesian methods for hackers: probabilistic programming and Bayesian inference, Addison-Wesley Professional.



Rubinstein, R. Y. & Kroese, D. P. 2013. Simulation and the Monte-Carlo Method, Wiley

TU My friend has glasses: can you show me my friend?



Stiller, A., Goodman, N. & Frank, M. C. Ad-hoc scalar implicature in adults and children. CogSci, 2011.

- Remember: GM are a marriage between probability theory and graph theory and provide a tool for dealing with our two grand challenges in the biomedical domain:

Uncertainty and complexity

- The learning task is two-fold:
 - Learning unknown probabilities
 - Learning unknown structures

Jordan, M. I. 1998. Learning in graphical models, Springer

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- Test if a distribution is decomposable with regard to a given graph.
 - This is the most direct approach. It is not bound to a graphical representation,
 - It can be carried out w.r.t. other representations of the set of subspaces to be used to compute the (candidate) decomposition of a given distribution.
- Find a suitable graph by measuring the strength of dependences.
 - This is a heuristic, but often highly successful approach, which is based on the frequently valid assumption that in a conditional independence graph an attribute is more strongly dependent on adjacent attributes than on attributes that are not directly connected to them.
- Find an independence map by conditional independence tests.
 - This approach exploits the theorems that connect conditional independence graphs and graphs that represent decompositions.
 - It has the advantage that a single conditional independence test, if it fails, can exclude several candidate graphs. Beware, because wrong test results can thus have severe consequences.

Borgelt, C., Steinbrecher, M. & Kruse, R. R. 2009. Graphical models: representations for learning, reasoning and data mining, John Wiley & Sons.

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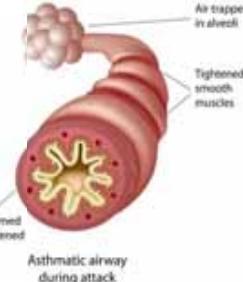
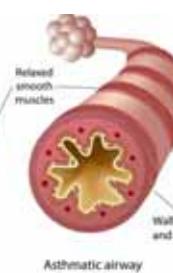
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Who of you is
NON-Smoker ?



Who of you is
Smoker ?

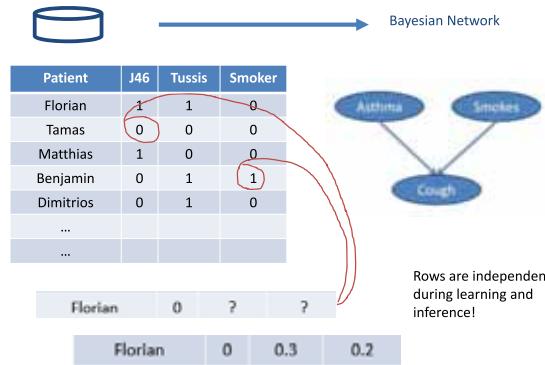


Beasley, R. 1998. Worldwide variation in prevalence of symptoms of asthma, allergic rhinoconjunctivitis, and atopic eczema: ISAAC. The Lancet, 351, (9111), 1225-1232,
doi:[http://dx.doi.org/10.1016/S0140-6736\(97\)07302-9](http://dx.doi.org/10.1016/S0140-6736(97)07302-9).

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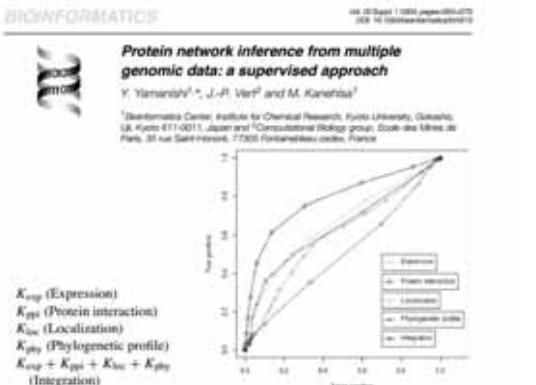
- Asthma can be hereditary
- Friends may have similar smoking habits
- Augmenting graphical model with relations between the entities – Markov Logic



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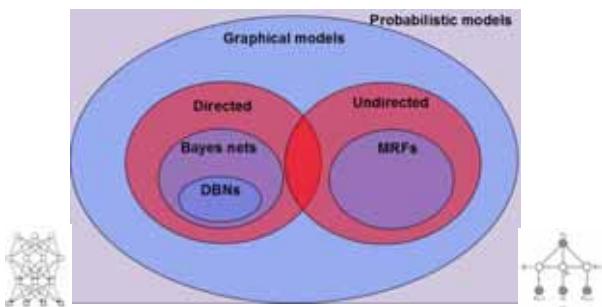


$$\mathcal{D} \equiv \{X_1^{(i)}, X_2^{(i)}, \dots, X_m^{(i)}\}_{i=1}^N$$

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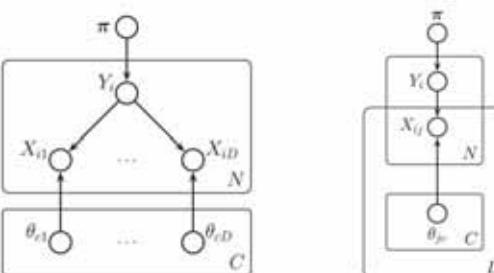


Murphy, K. P. 2012. Machine learning: a probabilistic perspective, Cambridge (MA), MIT press.

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π ... multinomial parameter vector, Stationary distribution of Markov chain

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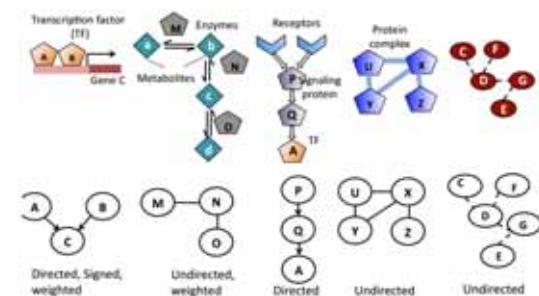


Image credit to Anna Goldenberg, Toronto

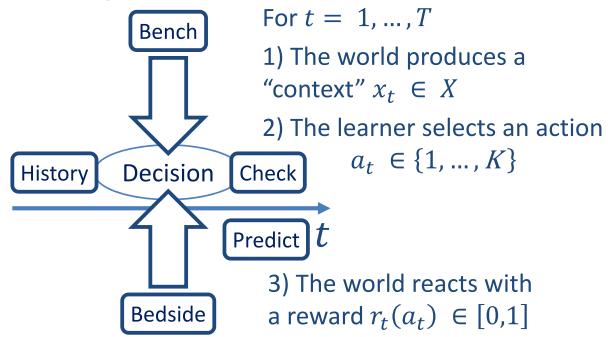
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TU Decision Making: Learn good policy for selecting actions

Goal: Learn an **optimal policy** for selecting best actions within a given context



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TU GM are amongst the most important ML developments

- Key Idea: Conditional independence assumptions are very useful – however: Naïve Bayes is extreme!
- X is *conditionally independent* of Y , given Z , if the $P(X)$ governing X is independent of value Y , given value of Z :
 $(\forall i, j, k)P(X = x_i | Y = y_j, Z = z_k) = P(X = x_i | Z = z_k)$
can be abbr. with $P(X|Y, Z) = P(X|Z)$
- Graphical models express sets of conditional independence assumptions via graph structure
- The graph structure plus associated parameters define joint probability distribution over the set of variables

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TU Remember

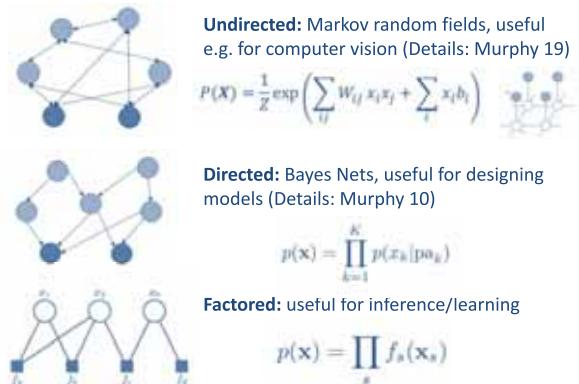
- Medicine is an extremely complex application domain – dealing most of the time with uncertainties -> **probable information**!
- When we have big data but little knowledge automatic ML can help to gain insight:
- **Structure learning and prediction in large-scale biomedical networks with probabilistic graphical models**
- If we have little data and deal with NP-hard problems we still need the human-in-the-loop

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TU Three types of Probabilistic Graphical Models



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TU From structure to function prediction



Baldi, P. & Pollastri, G. 2003. The principled design of large-scale recursive neural network architectures—dag-rnns and the protein structure prediction problem. *The Journal of Machine Learning Research*, 4, 575-602.

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TU Protein Network Inference

- Hypothesis: most biological functions involve the interactions between many proteins, and the complexity of living systems arises as a result of such interactions.
- In this context, the problem of inferring a global protein network for a given organism,
- - using all (genomic) data of the organism,
- is one of the main challenges in computational biology

Yamanishi, Y., Vert, J.-P. & Kanehisa, M. 2004. Protein network inference from multiple genomic data: a supervised approach. *Bioinformatics*, 20, (suppl 1), i363-i370.

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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