

# Graphical Models

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# Graphical models: Graphical representations of *conditional independence*

Helps with...

- Understanding
- Combining expert knowledge and data
- Making inference faster
- Learning cause and effect

# Overview

- **Basic concepts (probability and conditional independence)**
- **Dependency networks → undirected graphs**
- **Directed acyclic graphs (“Bayes nets”)**
- **Learning cause and effect from observational data**
  - **Application: HIV vaccine design**

# Probability

$p(X=x|Y=y)$  has at least two meanings:

- Bayesian: The belief of an individual that variable  $X$  takes on value  $x$ , given that  $Y=y$
- Frequentist: The long run fraction that  $X=x$  when  $Y=y$

Doesn't matter for this talk!

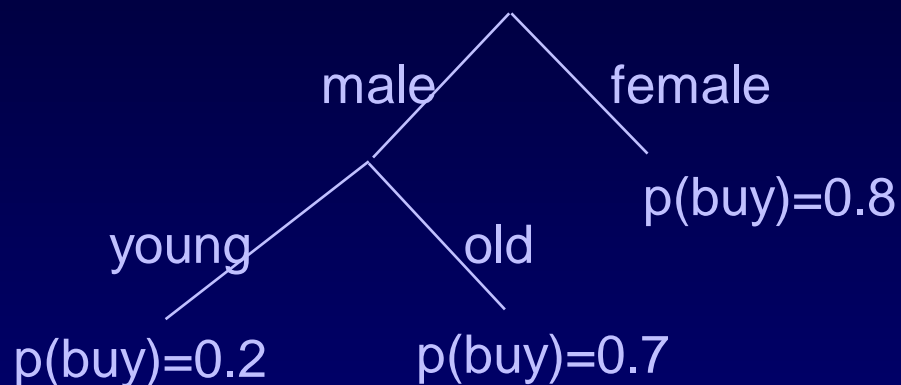
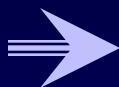
# Conditional independence

## Equivalent statements for variables X, Y, and Z:

- Y and Z are conditionally independent given X
- $Y \perp Z \mid X$
- $p(y|x,z) = p(y|x)$
- X is just as good a predictor of Y as X and Z
- $p(z|x,y) = p(z|x)$
- X is just as good a predictor of Z as X and Y

# Conditional independence

buy	age	sex	month born
y	old	male	jan
y	old	female	mar
n	young	male	nov
n	young	female	july
n	young	female	august
...	...	...	...



$$p(\text{buy} \mid \text{sex, age, month born}) = p(\text{buy} \mid \text{sex, age})$$
$$\text{buy} \perp \text{month born} \mid \text{sex, age}$$

# Identifying conditional independence

- From personal belief (Bayesian)
- From data (Bayesian or frequentist)
  - Cross validation (example later)
  - Bayesian methods
  - Penalized likelihood
  - Others?

# Overview

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  - Application: HIV vaccine design

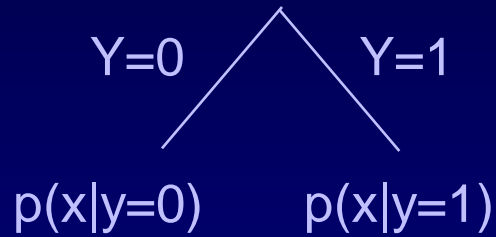


# Application: Data exploration

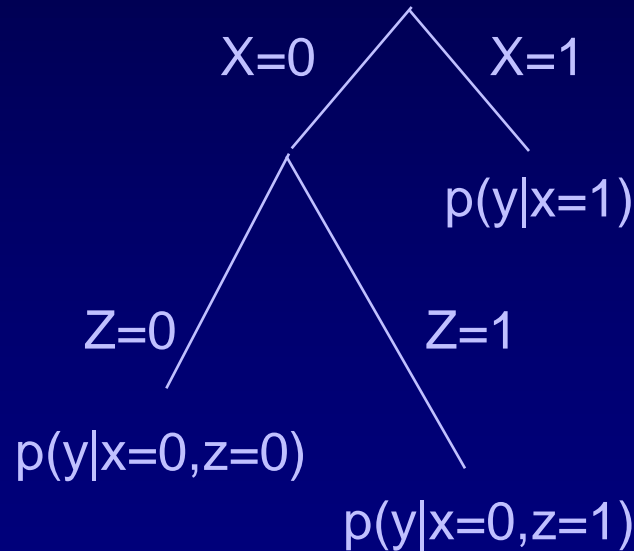
- Suppose you have thousands of variables and you're not sure about the interactions among those variables
- Build a classification/regression model for each variable, using the rest of the variables as inputs

# Example with three variables X, Y, and Z

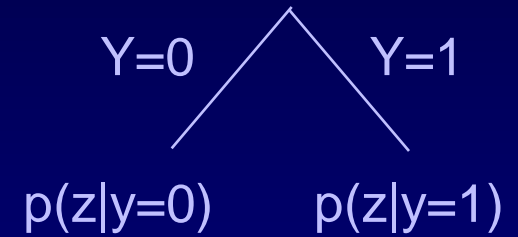
Target: X  
Inputs: Y,Z



Target: Y  
Inputs: X,Z

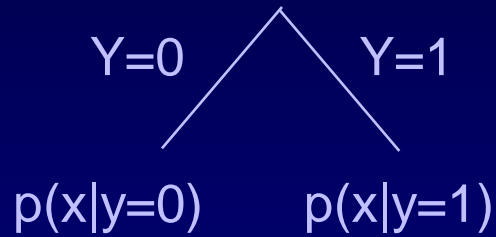


Target: Z  
Inputs: X,Y

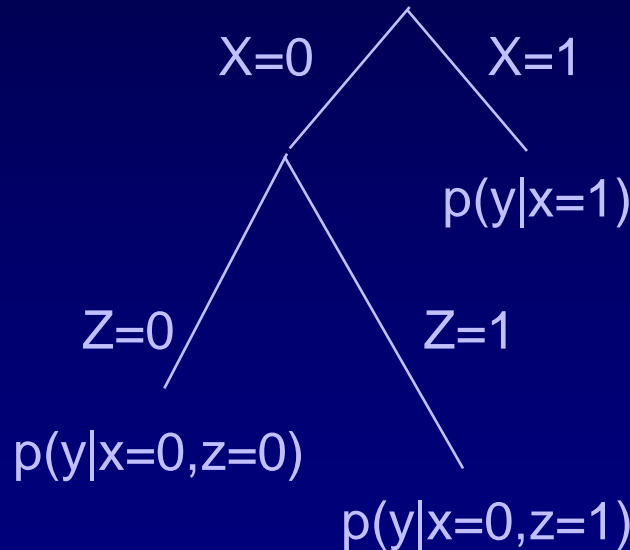


# Summarize the trees with a single graph

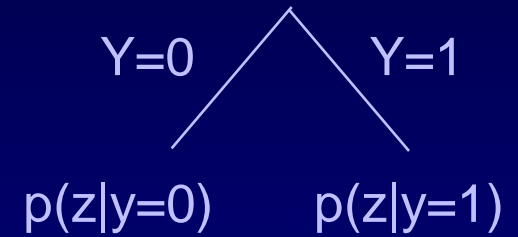
Target: X  
Inputs: Y,Z



Target: Y  
Inputs: X,Z



Target: Z  
Inputs: X,Y



# Dependency Network

- Build a classification/regression model for every variable given the other variables as inputs
- Construct a graph where
  - Nodes correspond to variables
  - There is an arc from X to Y if X helps to predict Y
- The graph along with the individual classification/regression model is a “dependency network”

(Heckerman, Chickering, Meek, Rounthwaite, Cadie 2000)

# Example: TV viewing

Nielsen data: 2/6/95-2/19/95

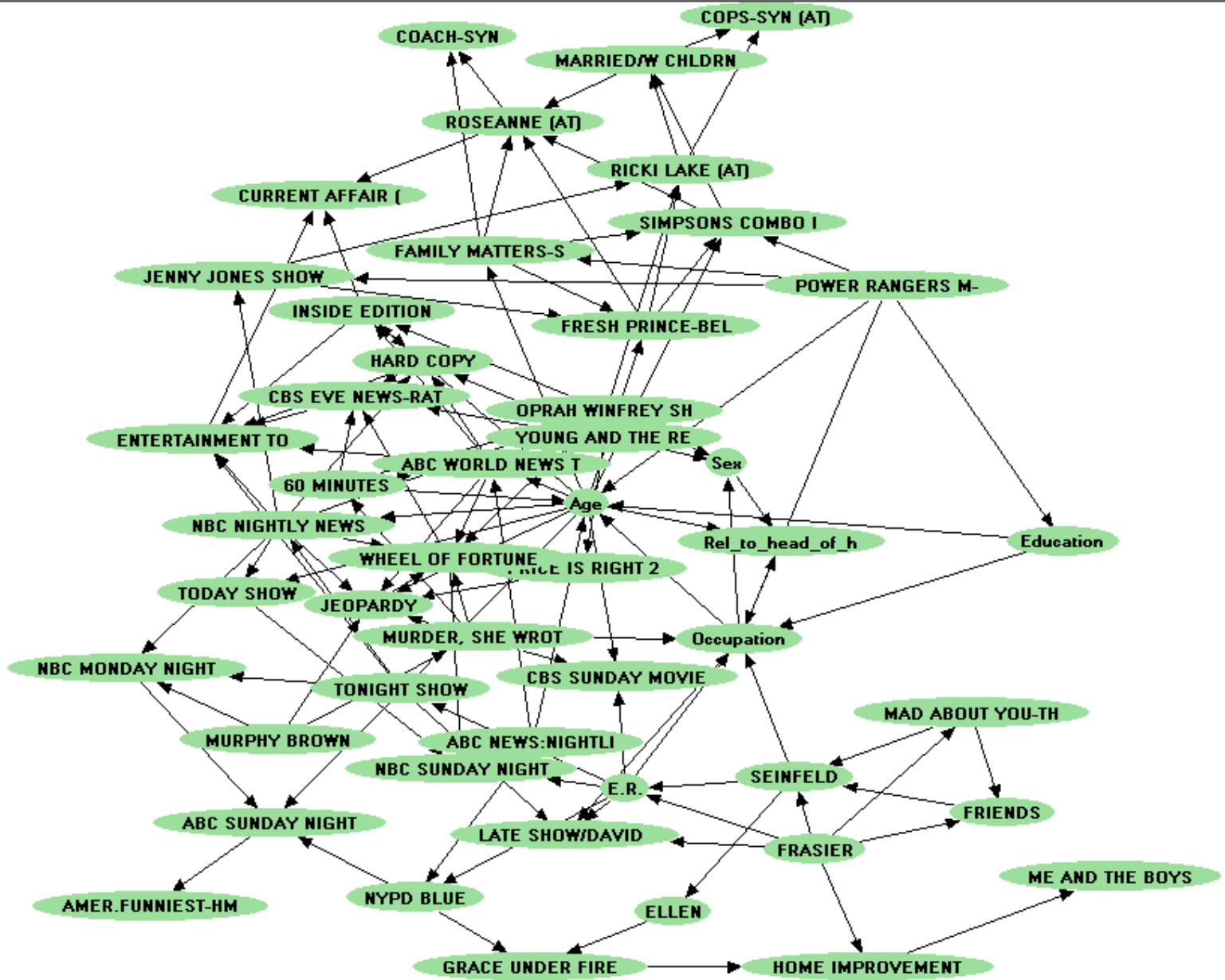
	Age	Show1	Show2	Show3	
viewer 1	73	y	n	n	
viewer 2	16	n	y	y	...
viewer 3	35	n	n	n	
			etc.		

~400 shows, ~3000 viewers

**Goal: exploratory data analysis (acausal)**



All links



Strongest links

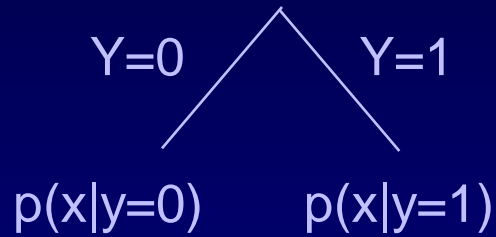
Select a node to highlight its dependencies

## **A bit of history**

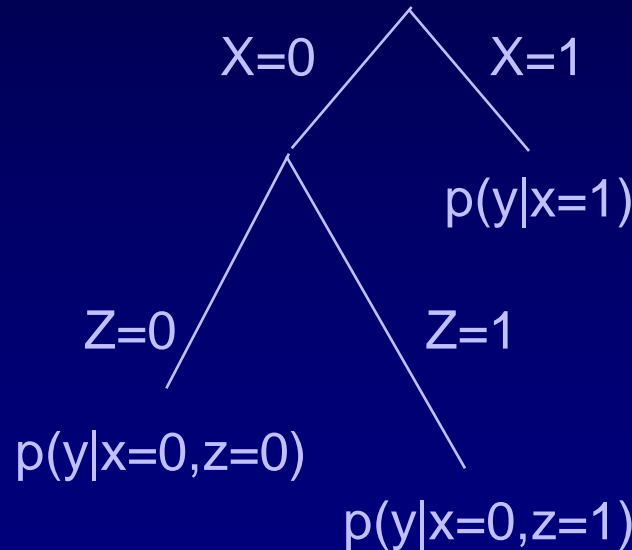
- **Julian Besag (and others) invented dependency networks (under another name) in the mid 1970s**
- **But they didn't like them, because they could be inconsistent**

# A consistent dependency network

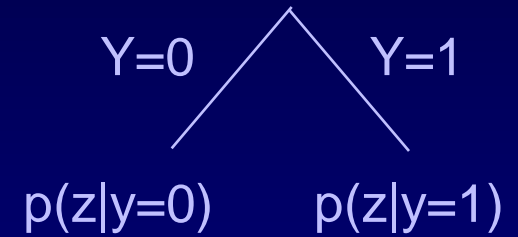
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Inputs: Y,Z



Target: Y  
Inputs: X,Z



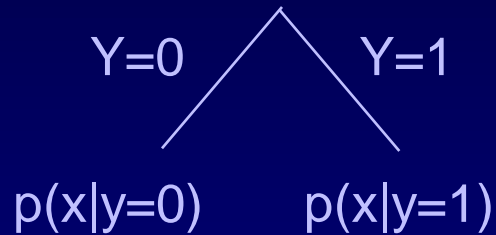
Target: Z  
Inputs: X,Y



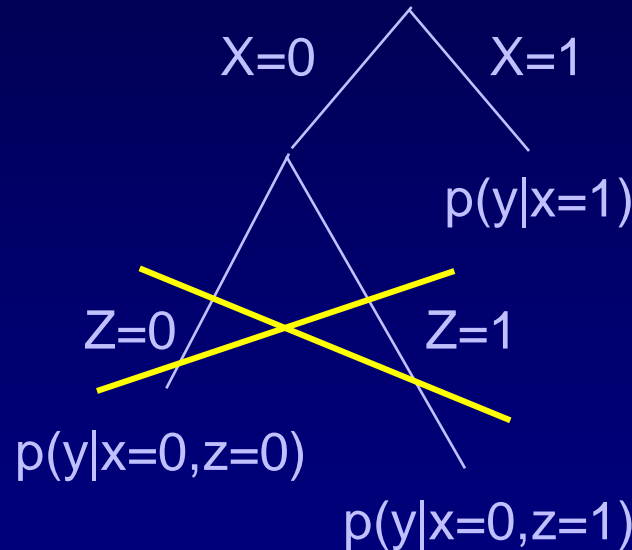


# An inconsistent dependency network

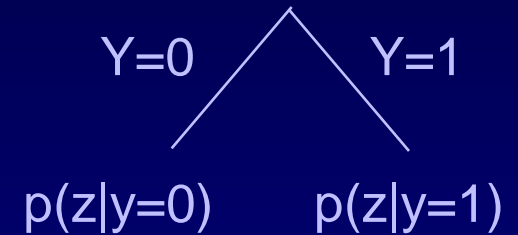
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Target: Y  
Inputs: X,Z



Target: Z  
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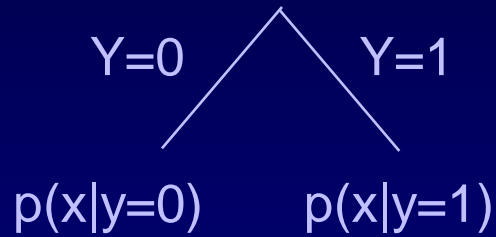


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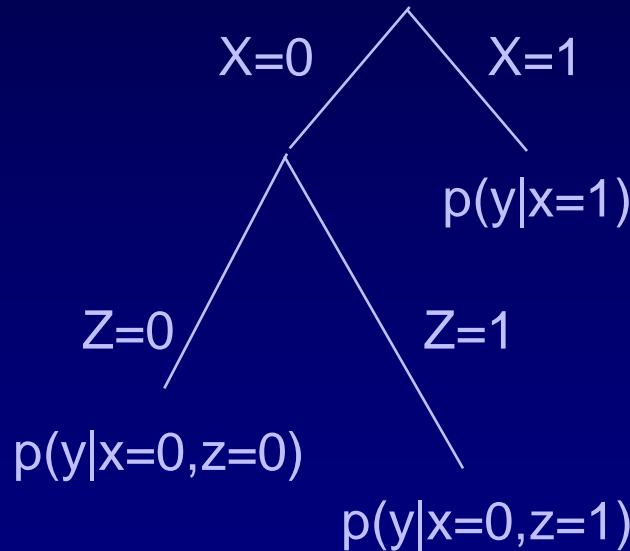
- Julian Besag (and others) invented dependency networks (under the name “Markov graphs”) in the mid 1970s
- But they didn’t like them, because they could be inconsistent
- **So they used a property of consistent dependency networks to develop a new characterization of them**

# Conditional independence

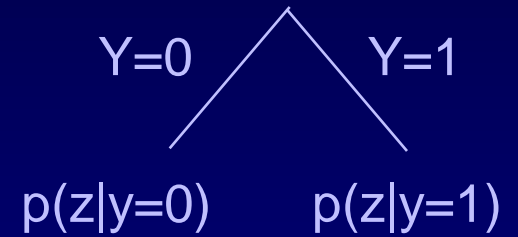
Target: X  
Inputs: Y,Z



Target: Y  
Inputs: X,Z



Target: Z  
Inputs: X,Y



$$X \perp Z | Y$$



# Conditional independence in a consistent dependency network


Each variable is independent of all other variables given its immediate neighbors

# Hammersley-Clifford Theorem (Besag 1974)

- Given a set of variables which has a positive joint distribution
- Where each variable is independent of all other variables given its immediate neighbors in some graph  $G$
- It follows that

$$p(\mathbf{x}) = \prod_{i=1}^N f_i(\mathbf{c}_i)$$

“clique potentials”



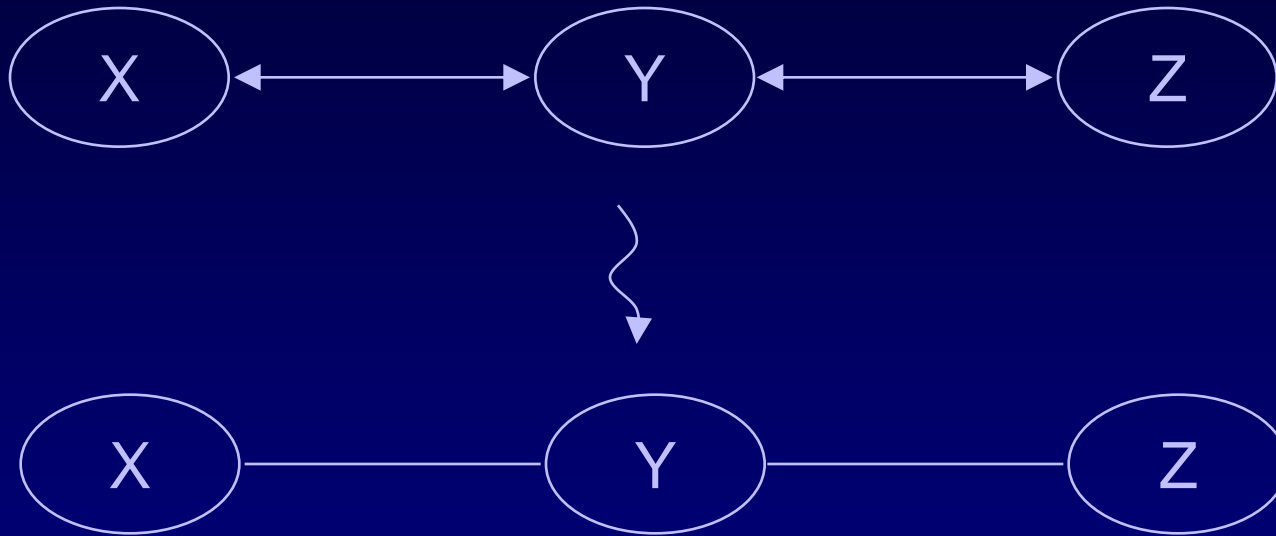
where  $\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_n$  are the maximal cliques in the graph  $G$ .

# Example



$$p(x, y, z) = f_1(x, y) f_2(y, z)$$

# Consistent dependency networks: Directed arcs not needed



$$p(x, y, z) = f_1(x, y) f_2(y, z)$$

# A bit of history

- Julian Besag (and others) invented dependency networks (under the name “Markov graphs”) in the mid 1970s
- But they didn’t like them, because they could be inconsistent
- So they used a property of consistent dependency networks to develop a new characterization of them
- **“Markov Random Fields” aka “undirected graphs” were born**



# Inconsistent dependency networks aren't that bad

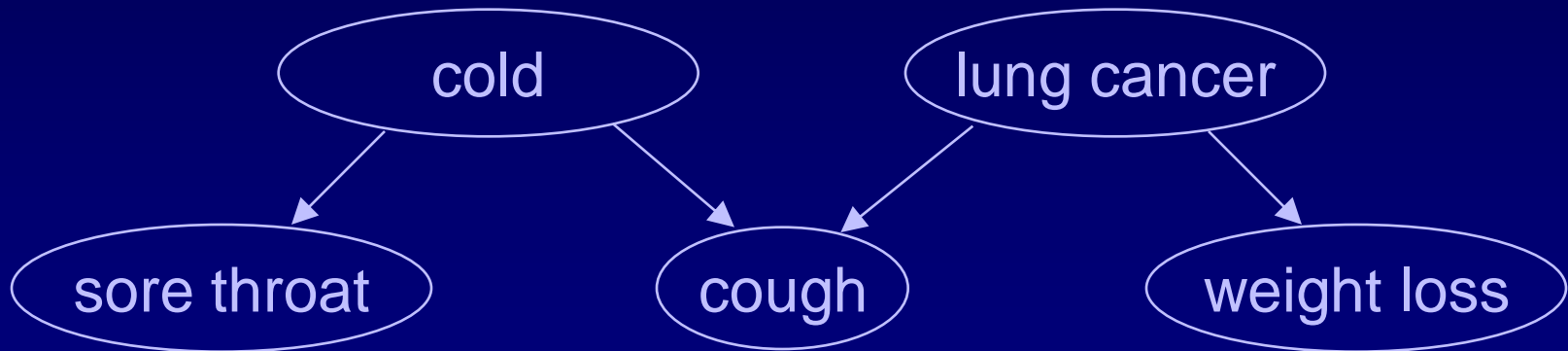
- They are *\*almost consistent\** because each classification/regression model is learned from the same data set (can be formalized)
- They are easy to learn from data (build separate classification/regression model for each variable)
- Conditional distributions (e.g., trees) are easier to understand than clique potentials

# Inconsistent dependency networks aren't that bad

- They are *\*almost consistent\** because each classification/regression model is learned from the same data set (can be formalized)
- They are easy to learn from data (build separate classification/regression model for each variable)
- Conditional distributions (e.g., trees) are easier to understand than clique potentials
- Over the last decade, has proven to be a very useful tool for data exploration

# Shortcomings of undirected graphs

- Lack a generative story (e.g., Lat Dir Alloc)
- Lack a causal story



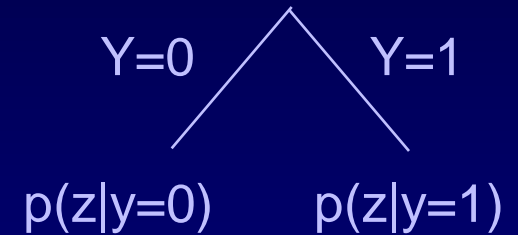
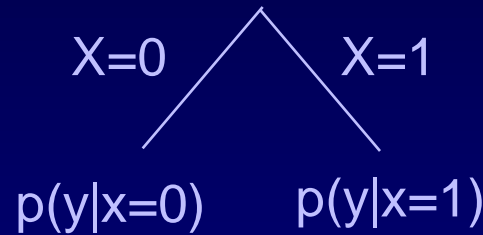
# Solution: Build trees in some order

1. Target: X  
Inputs: none

2. Target: Y  
Inputs: X

3. Target: Z  
Inputs: X, Y

■  
 $p(x)$



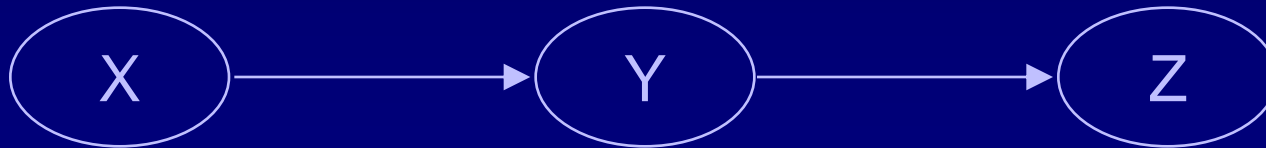
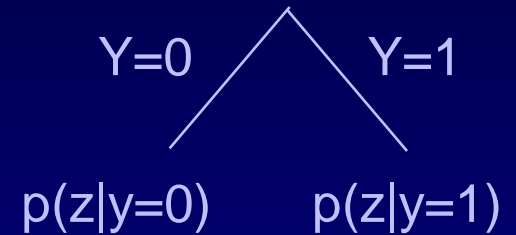
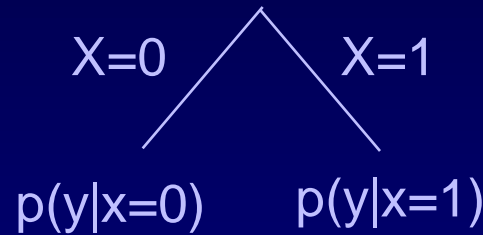
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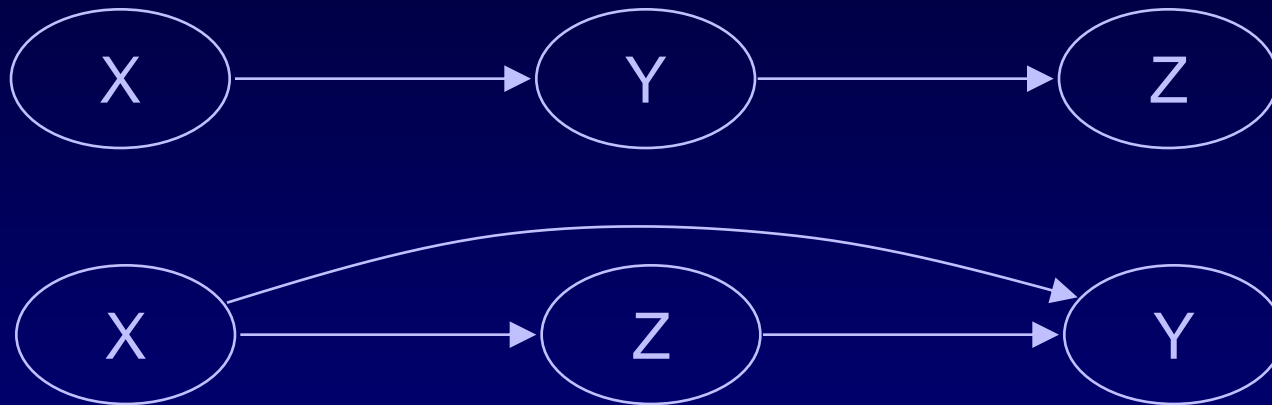
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3. Target: Z  
Inputs: X, Y

■  
 $p(x)$



# Some orders are better than others



- **Prior, often causal knowledge (Bayesian)**
- **Infer better orderings from data (Bayesian and frequentist)**
  - Try random orders
  - Monte-Carlo methods
  - Greedy search

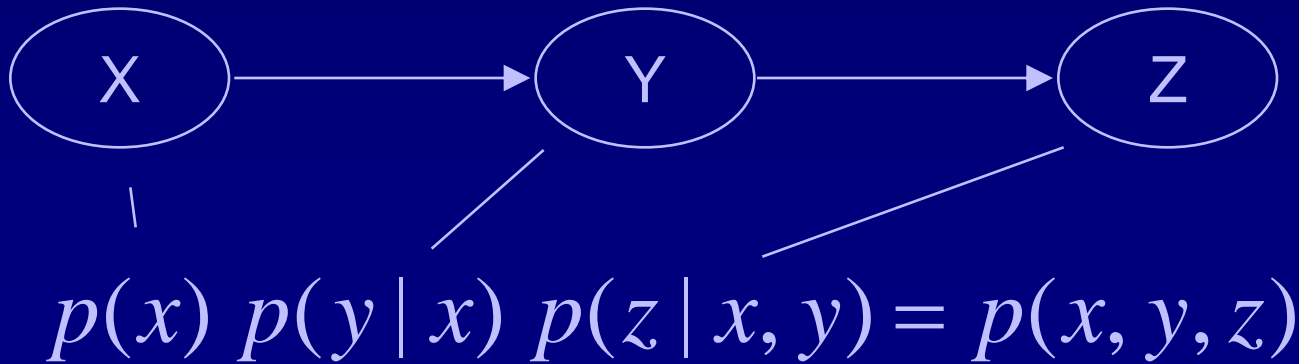
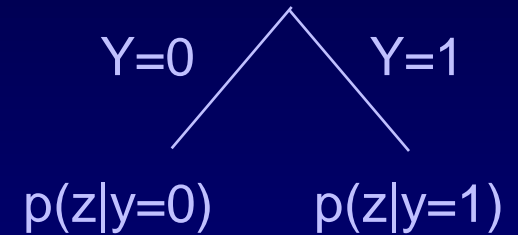
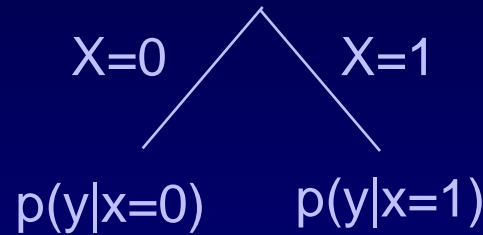
# Joint distribution is easy to obtain

1. Target: X  
Inputs: none

2. Target: Y  
Inputs: X

3. Target: Z  
Inputs: X, Y

■  
 $p(x)$



# Directed Acyclic Graphical (DAG) models

$$\begin{aligned} p(x_1, \dots, x_n) &= \prod_i p(x_i \mid x_1, \dots, x_{i-1}) \\ &= \prod_i p(x_i \mid \text{parents}(x_i)) \end{aligned}$$

**Many inventors: Wright 1921; Good 1961; Howard & Matheson 1976, Pearl 1982**

**Pearl developed them in the context of expert systems (where an individual provided the independencies and probabilities), hence the commonly used term “Bayesian Network”**



# Graphical models: Graphical representations of *conditional independence*

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- **Making inference faster**
- Learning cause and effect

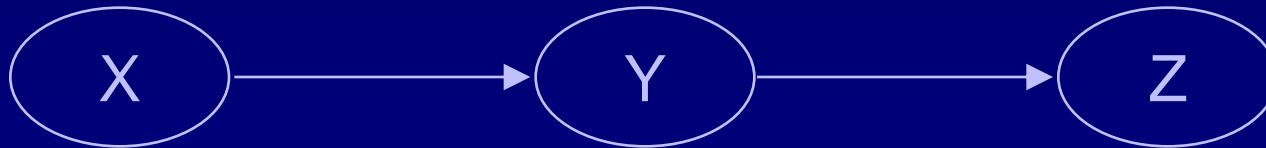
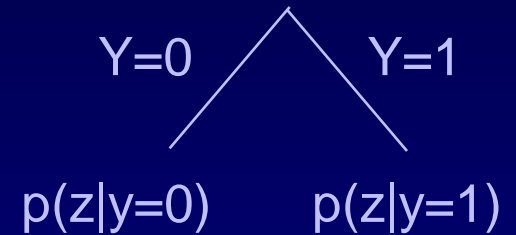
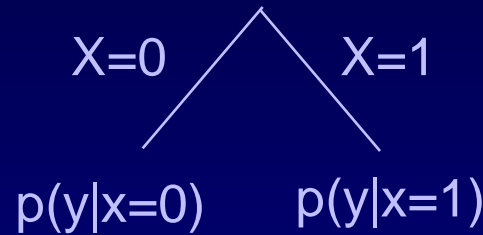
# Inference

1. Target: X  
Inputs: none

2. Target: Y  
Inputs: X

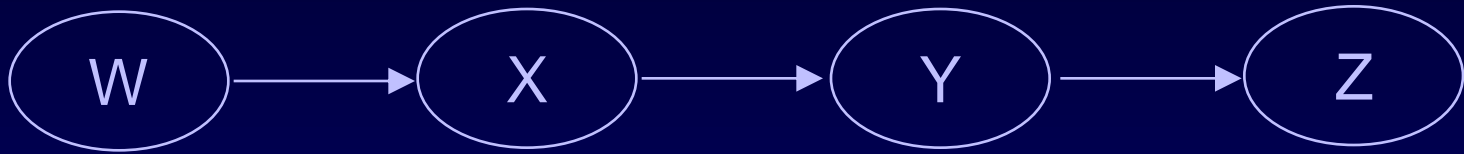
3. Target: Z  
Inputs: X, Y

■  
 $p(x)$



What is  $p(z|x=1)$ ?

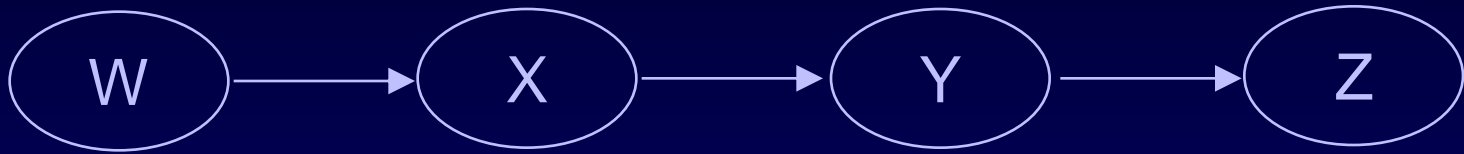
# Inference: Example



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

# Inference: Example

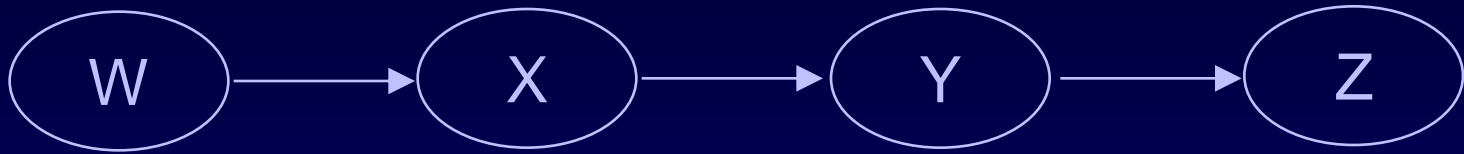
(“Elimination Algorithm”)



$$\begin{aligned} p(z) &= \sum_{w,x,y} p(w) p(x|w) p(y|x) p(z|y) \\ &= \sum_{w,x} p(w) p(x|w) \left( \sum_y p(y|x) p(z|y) \right) \end{aligned}$$

# Inference: Example

(“Elimination Algorithm”)



$$\begin{aligned} p(z) &= \sum_{w,x,y} p(w) p(x|w) p(y|x) p(z|y) \\ &= \sum_{w,x} p(w) p(x|w) \left( \sum_y p(y|x) p(z|y) \right) \\ &= \sum_w p(w) \left( \sum_x p(x|w) \left( \sum_y p(y|x) p(z|y) \right) \right) \end{aligned}$$

# Inference

- **Exact methods for inference that exploit conditional independence are well developed (e.g., Shachter, Lauritzen & Spiegelhalter, Dechter)**
- **Exact methods fail when there are many cycles in the graph**
  - MCMC (e.g., Geman and Geman 1984)
  - Loopy propagation (e.g., Murphy et al. 1999)
  - Variational methods (e.g., Jordan et al. 1999)

# Graphical models: Graphical representations of *conditional independence*

Helps with...

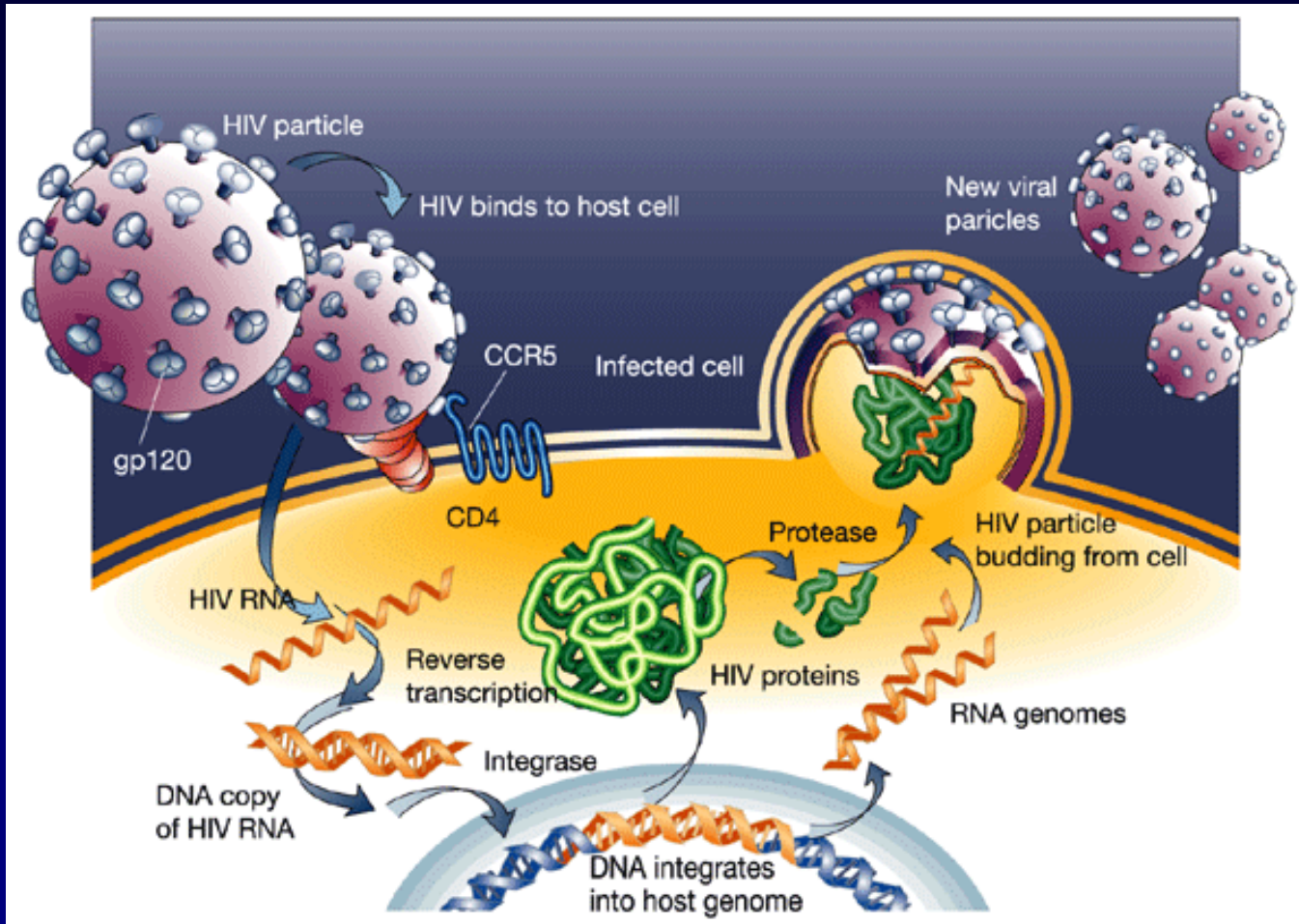
- Understanding
- Combining expert knowledge and data
- Making inference faster
- **Learning cause and effect**

# Learning cause and effect

- The standard way:  
Manipulate  $X$  and see if  $p(Y)$  changes
- A new way:  
**Observe**  $X$ ,  $Y$ , and other variables and infer that  $X$  causes  $Y$

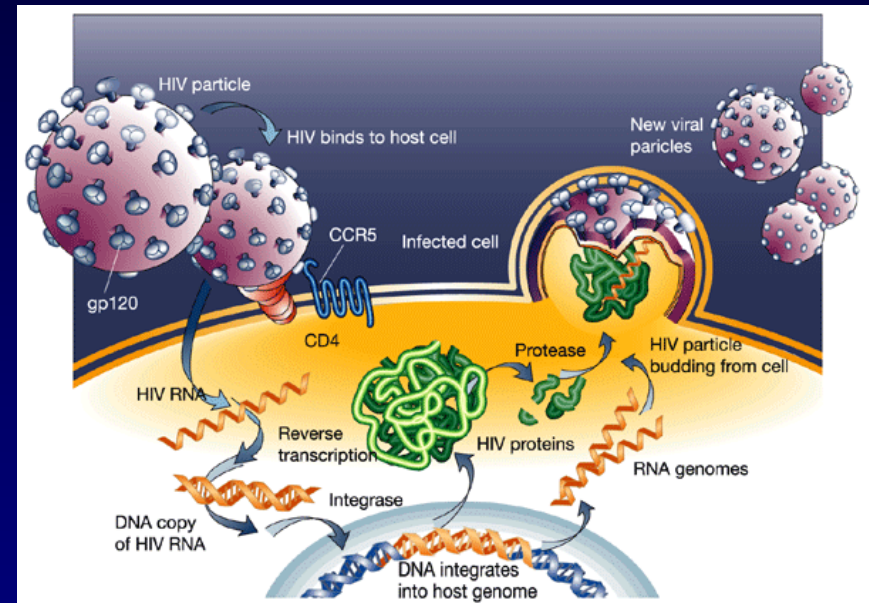


# HIV Life Cycle



# Two arms of Adaptive Immune Response

- **Humoral arm (antibodies):** Recognize, neutralize and respond to free floating virus particles
- **Cellular arm (killer T cells):** Identify and destroy already infected cells



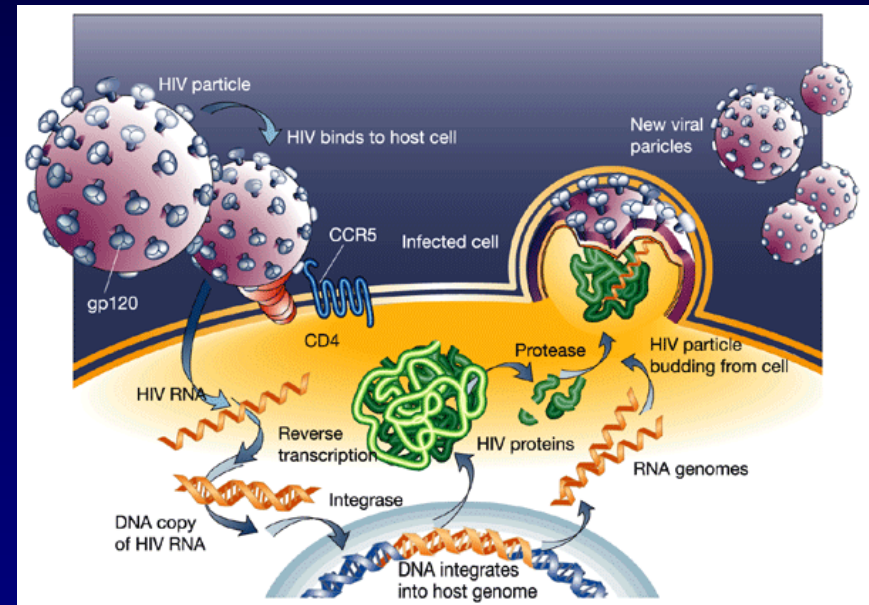
# Two arms of Adaptive Immune Response

- **Humoral arm (antibodies):** Have been trying for 20 years without success

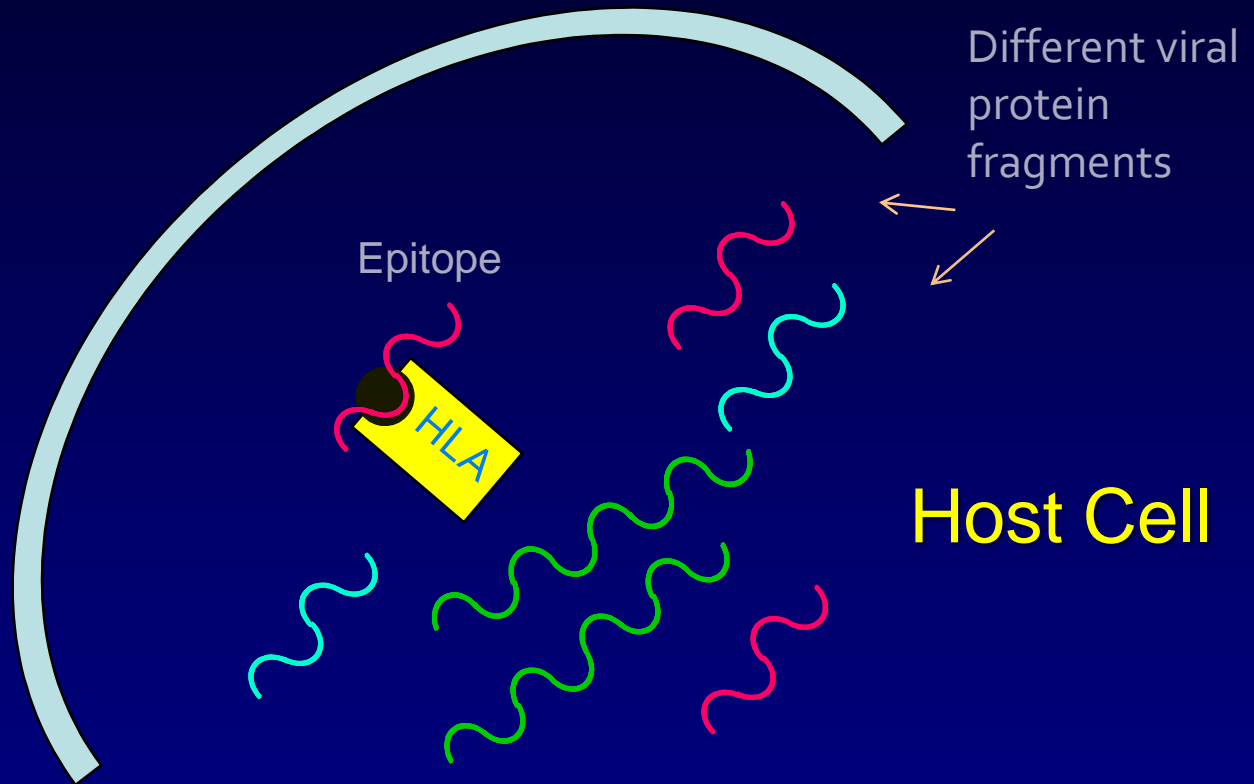
- **Cellular arm (killer T cells)**

Today's talk

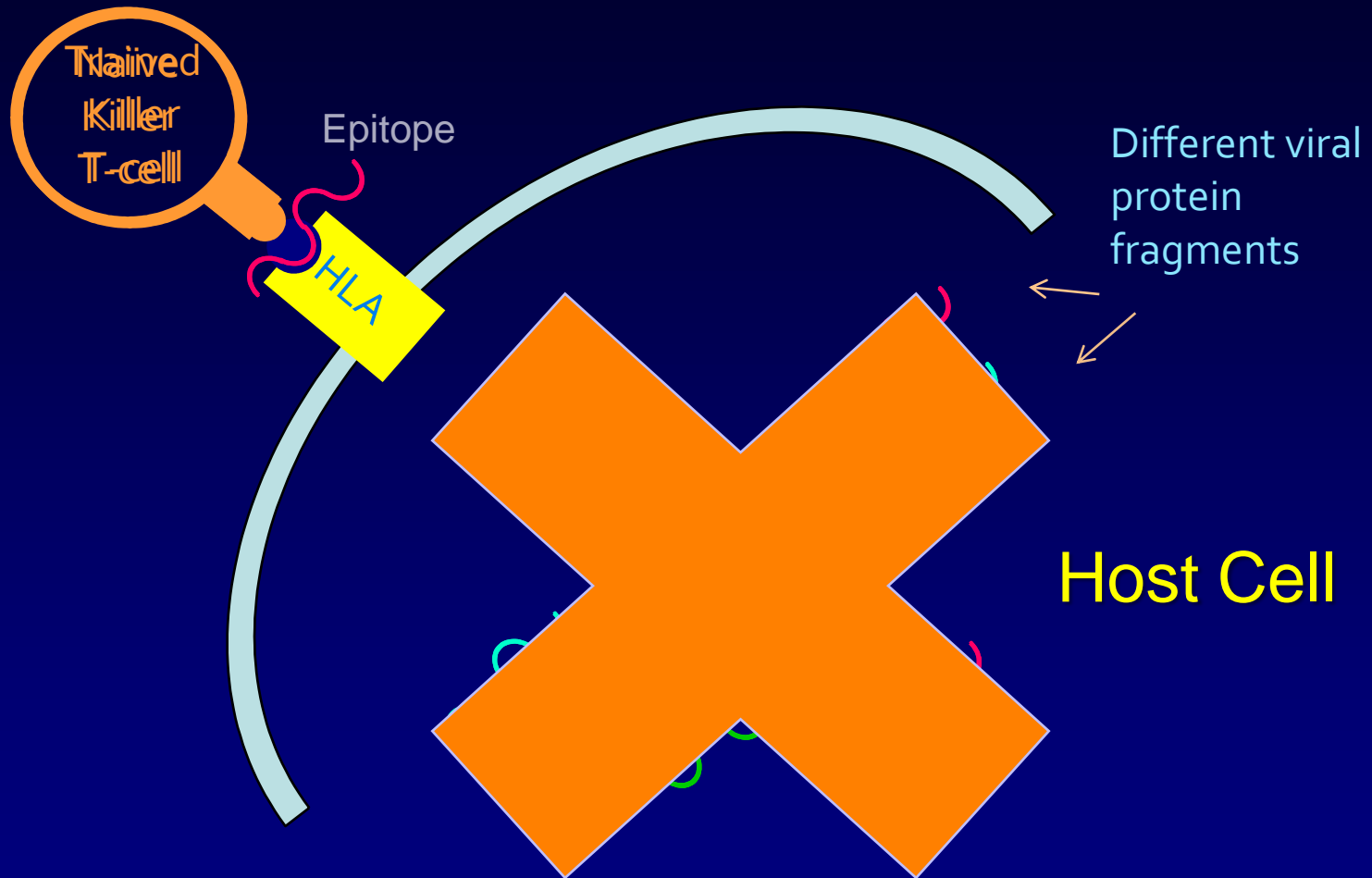
Vector vs. immunogen



# Cellular Arm Details

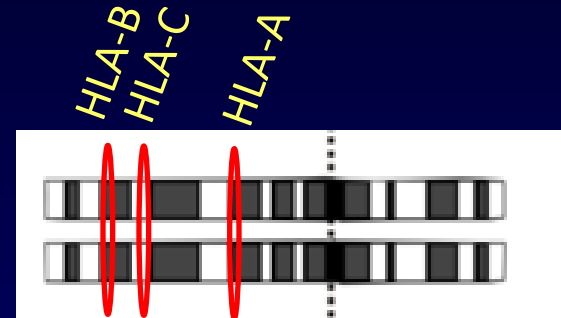
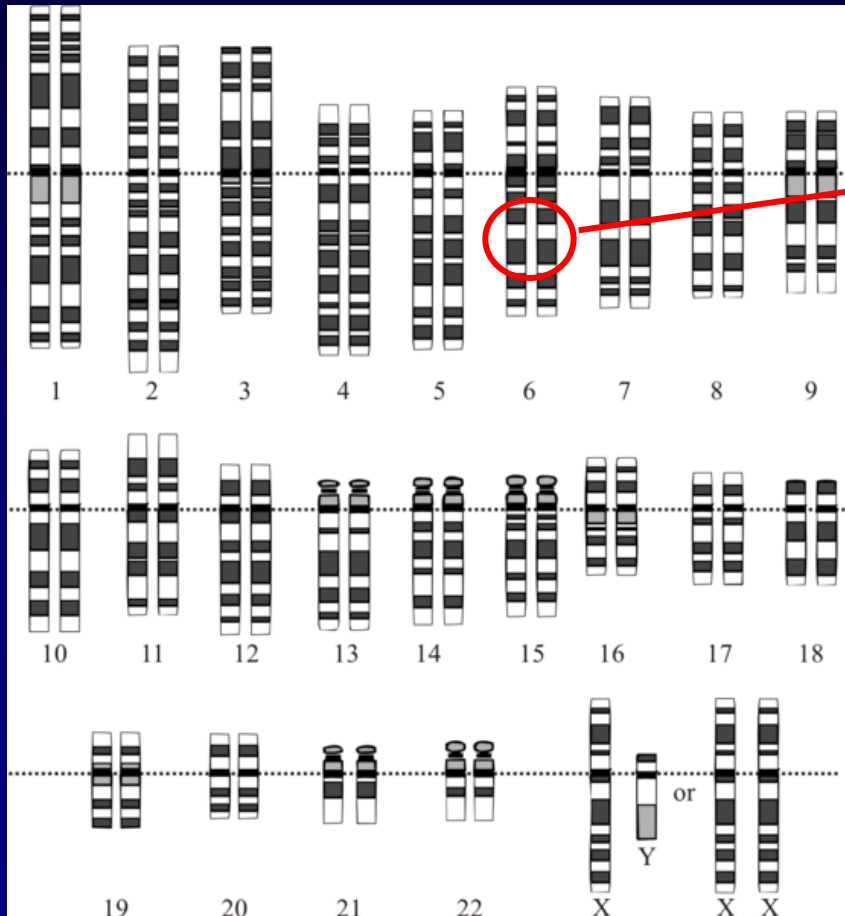


# Cellular Arm Details



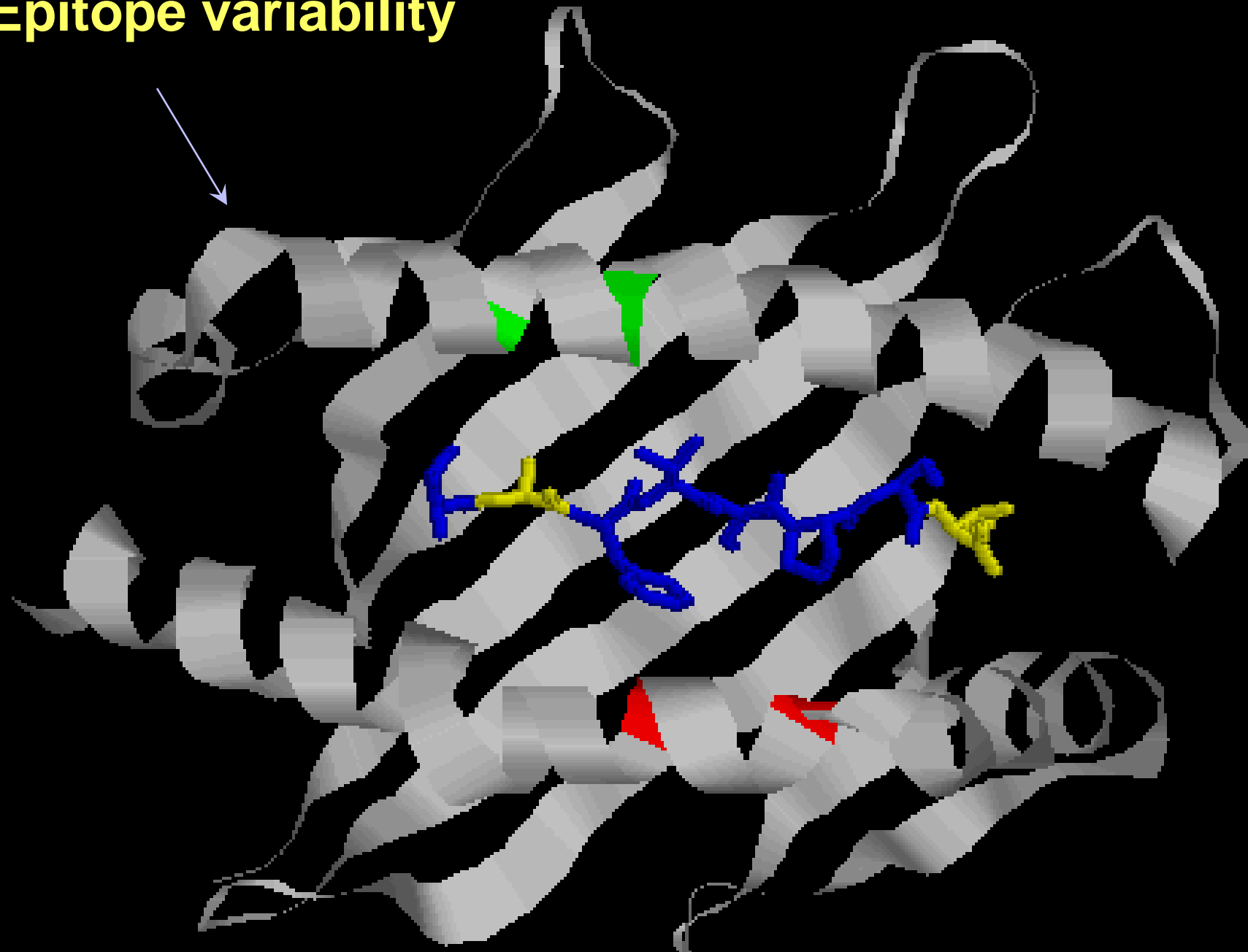


# HLA variability

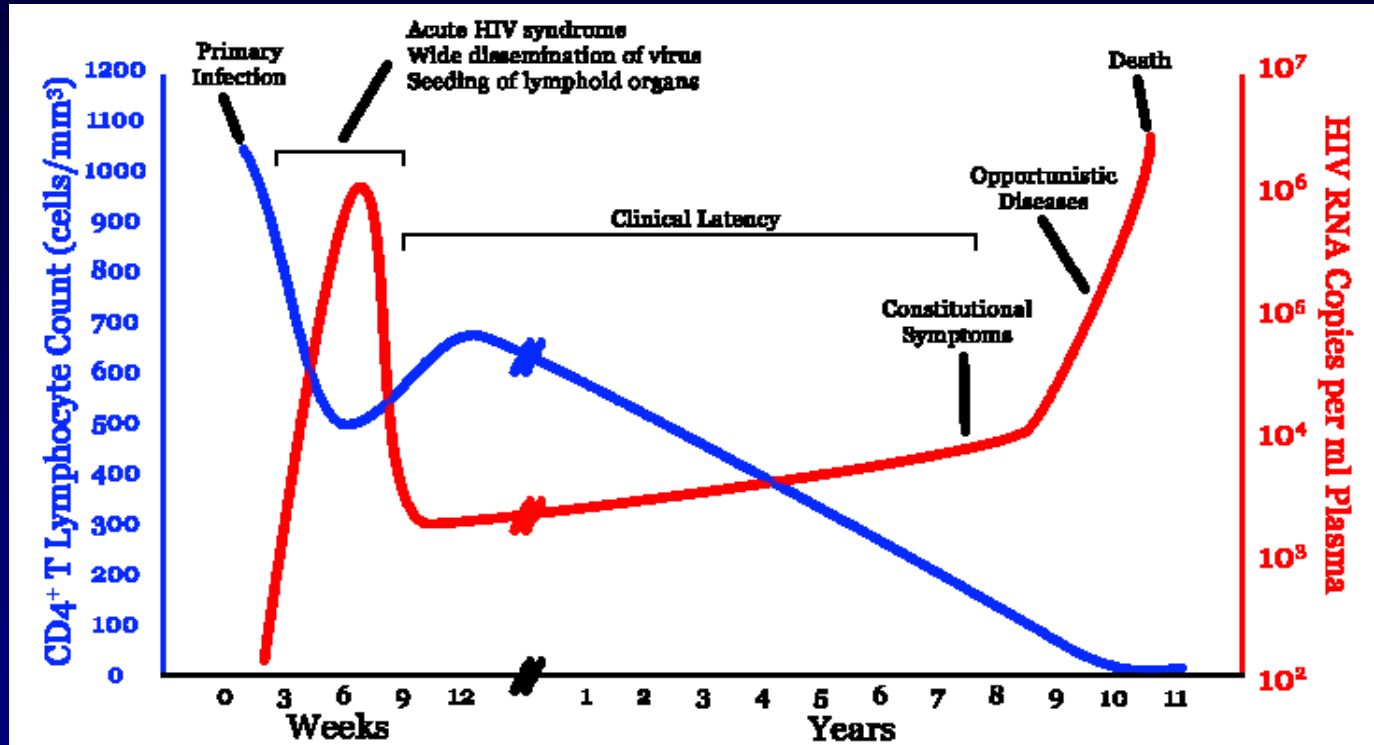


- Each person has up to 6 different HLA types: (2 'A', 2 'B', 2 'C')
- HLA region is most variable region of the genome

# Epitope variability

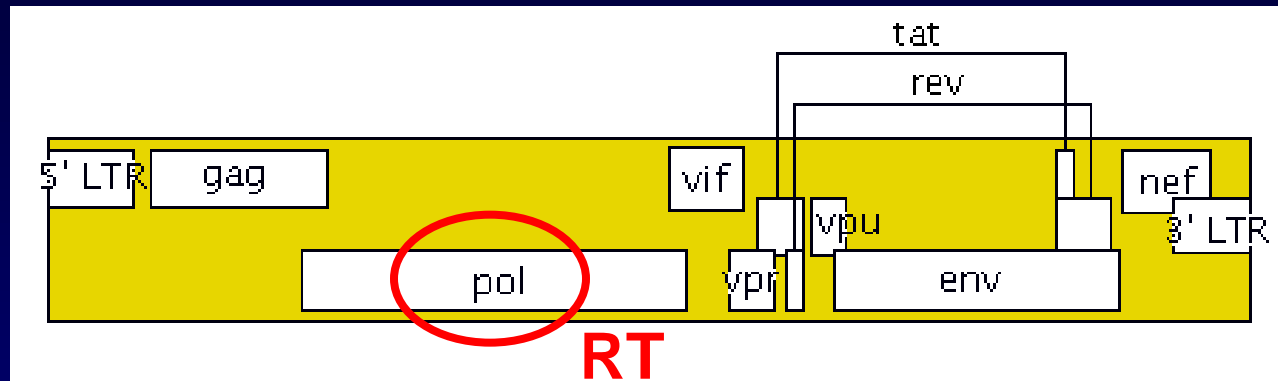


# HIV Disease Progression



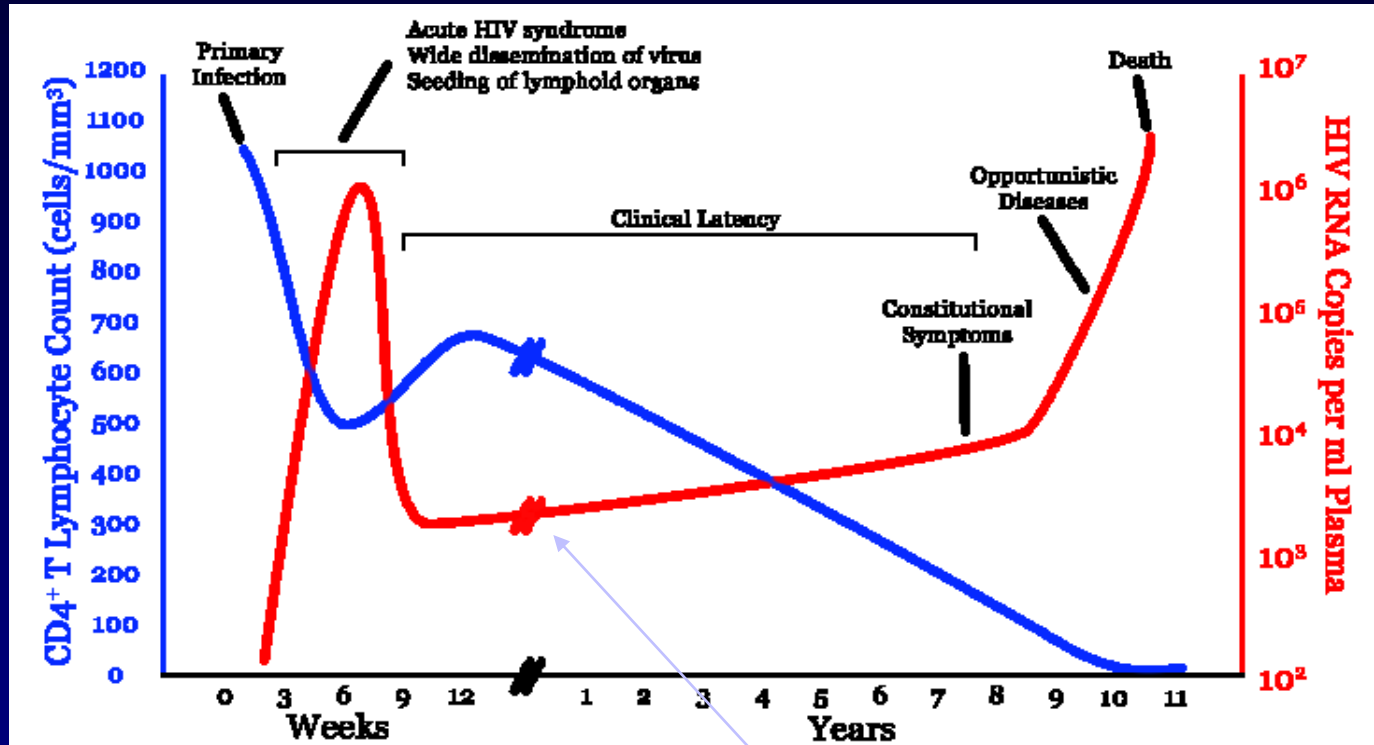


# Why do our immune systems fail to control HIV?



- HIV mutates a lot
- If our immune system attacks an epitope, HIV can mutate an AA within (or near) that epitope to avoid the attack

# HIV Disease Progression



Vaccine goal: keep viral load low

# Some HLA types control HIV better than others

- Protective HLAs: B\*57, B\*27
- Non-protective HLAs: B\*35

## Possible causal models

- Is there something intrinsic about protective HLAs that lead to better protection?

HLA → Viral control

- Is there something about the epitopes targeted that lead to better protection?

HLA → Epitope → Viral control

- Both of the above?

HLA → Epitope → Viral control

The diagram illustrates a causal model where HLA leads to Epitope, which in turn leads to Viral control. A curved arrow also points from HLA directly to Viral control, suggesting a direct effect of HLA on viral control.

# Learning causal models from data

(Pearl 1993; Spirtes, Glymour, Scheines, 1993)

- Key assumption: Lack of cause implies conditional independence (causal Markov assumption)

HLA  $\rightarrow$  Epitope  $\rightarrow$  Viral control

implies

HLA and Viral control are independent given Epitope

# Learning causal models from data

- Another example:

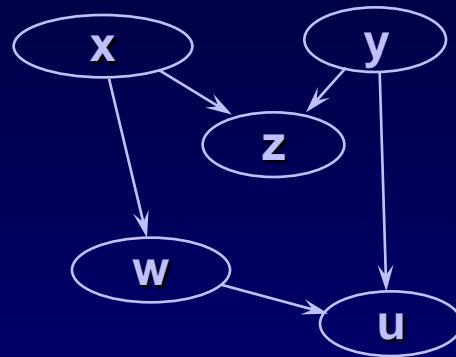
Epitope  $\leftarrow$  HLA  $\rightarrow$  Viral control

implies

Epitope and Viral control are independent given HLA

# Learning causal models from data

Causal Markov assumption:



When the causal graph is interpreted as a DAG model,

the conditional independencies implied by the DAG model hold true in the joint distribution of the variables.

# Learning causal models from data

## Causal Markov assumption:

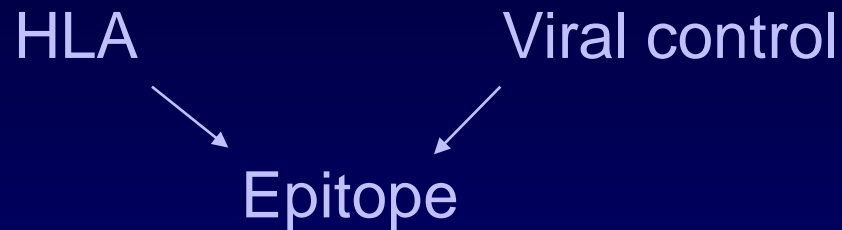


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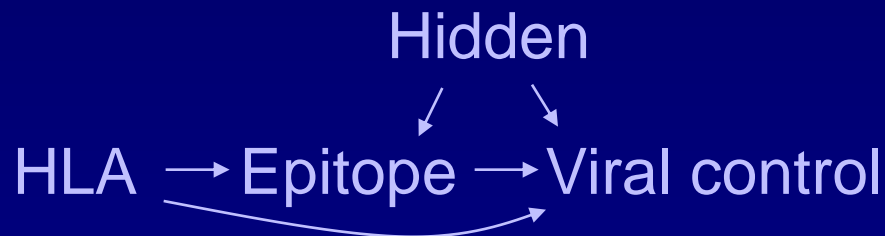
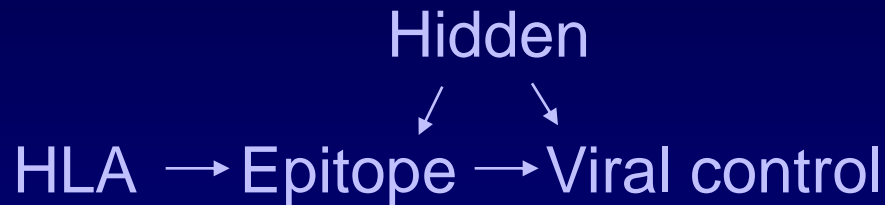
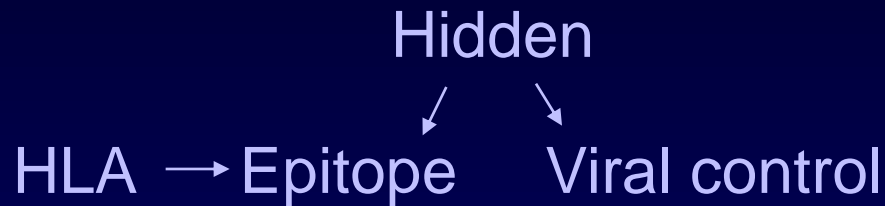


# Excluding causal models



Implies HLA and Viral control are independent

# Unable to distinguish these causal models



these models  
have the same  
conditional  
independencies  
among the  
observed  
variables

# Simplifying assumptions for our problem

- HLA is a root cause
- HLA causes Epitope

## Our possibilities

- Epitope and Viral control independent given HLA

Epitope  $\leftarrow$  HLA  $\rightarrow$  Viral control

- HLA and Viral control independent given Epitope

HLA  $\rightarrow$  Epitope  $\rightarrow$  Viral control

- No independence

HLA  $\rightarrow$  Epitope  $\rightarrow$  Viral control

A diagram illustrating the relationship between HLA, Epitope, and Viral control. It shows a linear sequence: HLA  $\rightarrow$  Epitope  $\rightarrow$  Viral control. Additionally, there is a curved arrow pointing from HLA directly to Viral control, indicating a direct relationship or influence.

# Details

## Other assumptions:

- Faithfulness (conditional independence doesn't happen by accident)
- Causal model is not cyclic (e.g., Epitope  $\leftrightarrow$  Viral control)
- It's not the case that one model applies to one HLA/epitope and another causal model applies to another HLA/epitope

# The Analysis

## Subjects:

- **Viremic controllers (n=148)**
  - At least 3 x VL < 2000 for at least 12 months
  - Blips if infrequent and non-consecutive
- **Chronic progressors (n=102)**
  - Untreated VL > 10,000

## Measuring Epitope:

- **IFN- $\gamma$  ELISpot assays**
- **Known list: Frahm et al., HIV Mol Imm, 2008; N=222**

## Predictive models:

- **Logistic regression (L1 prior; LASSO)**
- **Evaluate predictive ability with ROC curves**

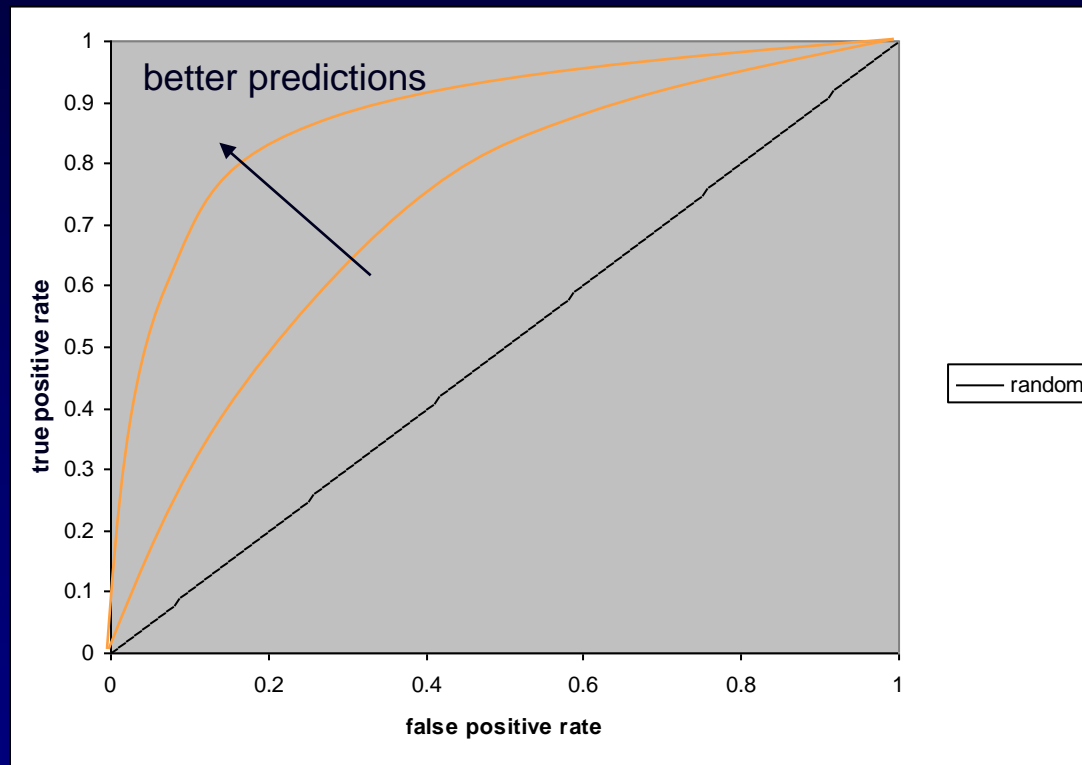
# Logistic regression

$$\log \frac{p(y | \mathbf{x})}{1 - p(y | \mathbf{x})} = w_0 + \sum_{i=1}^k w_i x_i$$

LASSO: MAP values for  $w$  are those that maximize

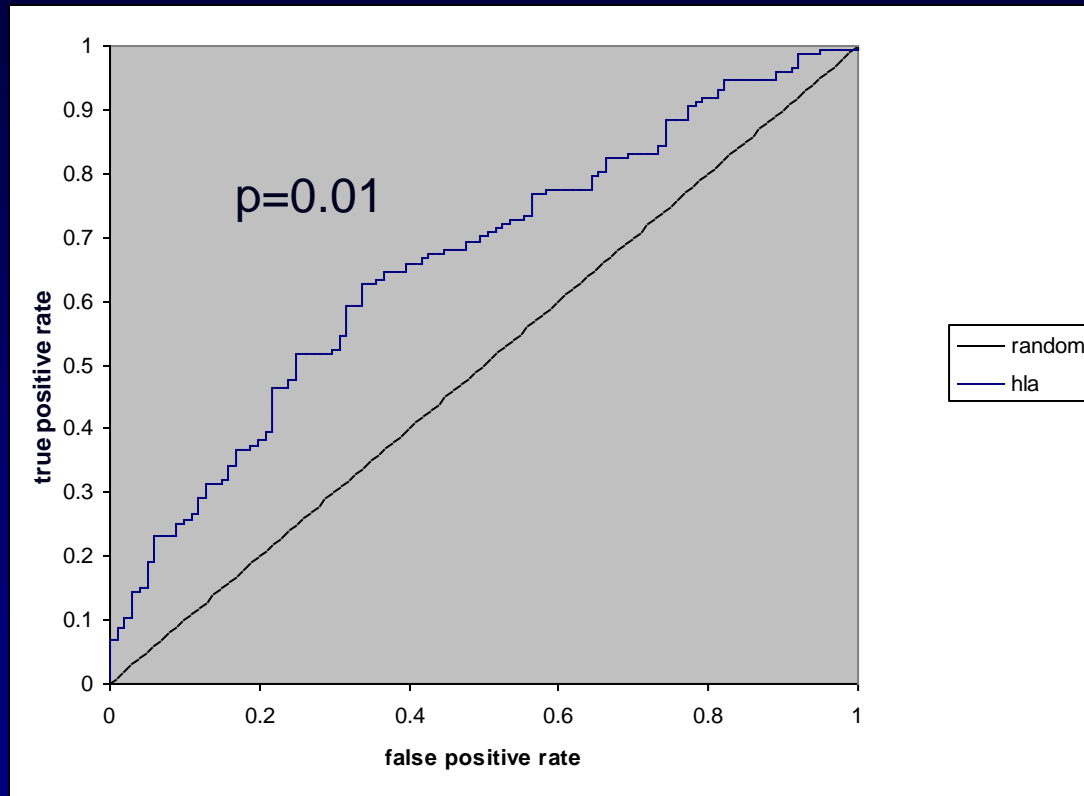
$$\log L - \alpha \sum_{i=1}^k |w_i|$$

# ROC curve: A measure of predictive accuracy

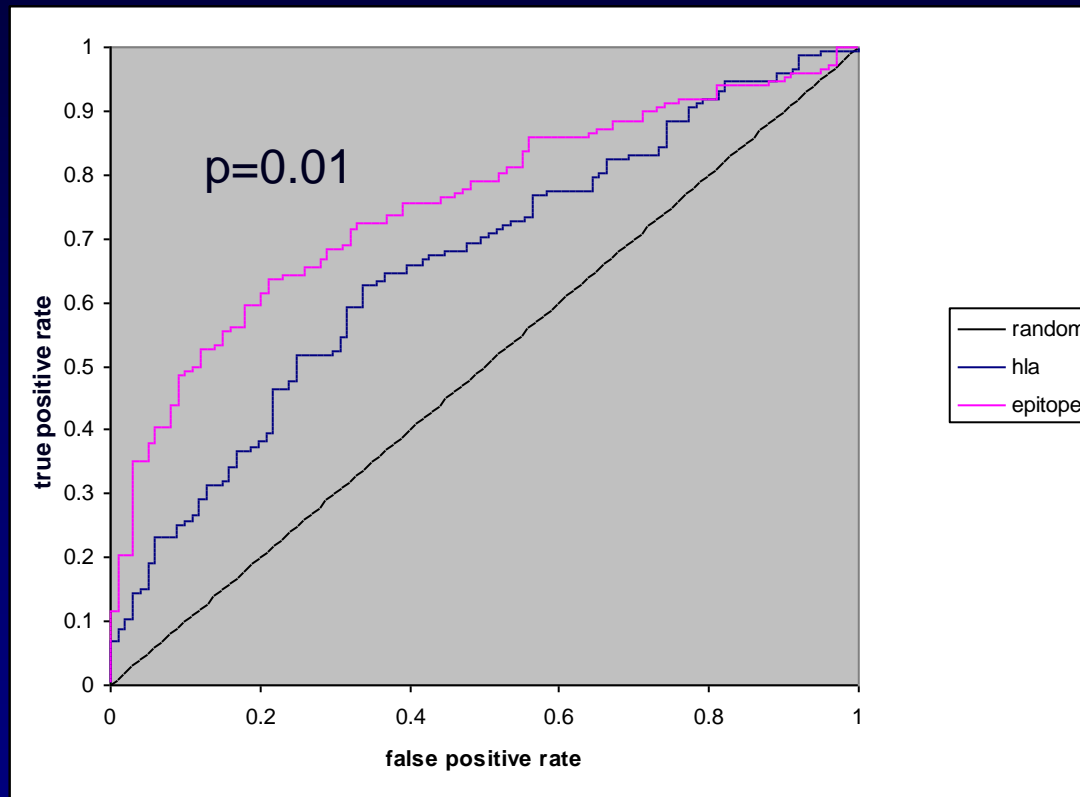




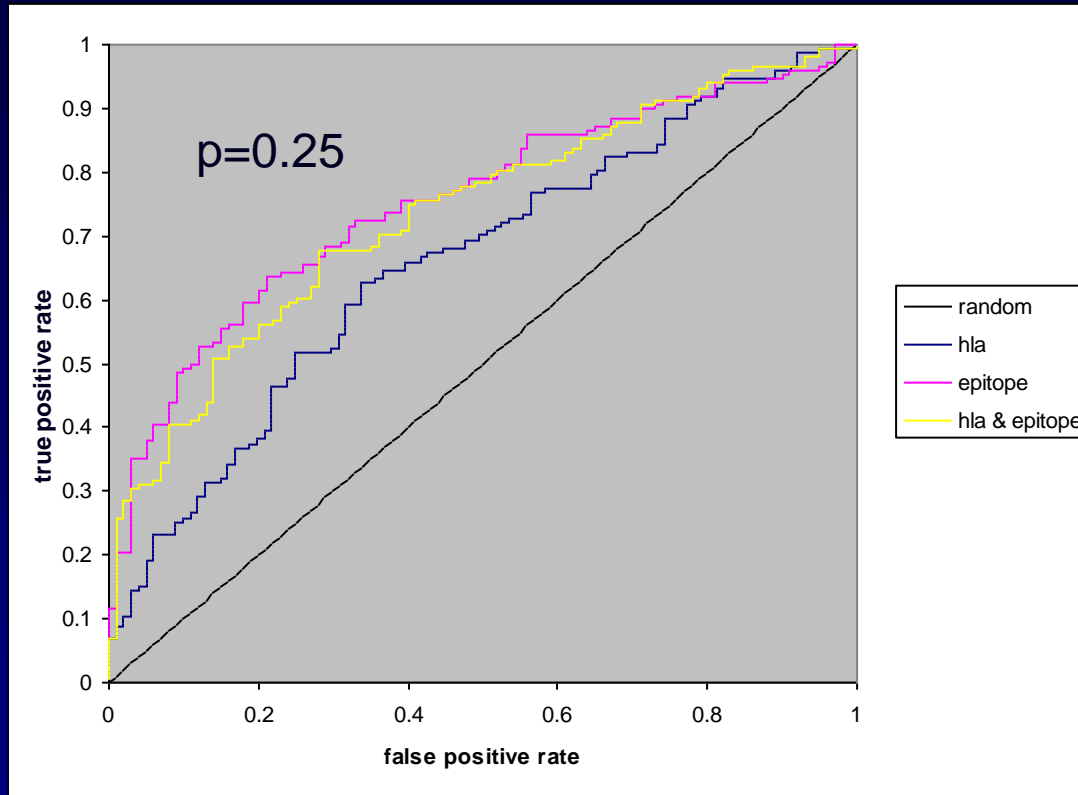
# HLA predicts viral control better than random



# Epitope responses predict viral control better than HLA



# HLA adds no additional information over epitope responses



# Inferring causal model from data

- Epitope and Viral control independent given HLA

Epitope  $\leftarrow$  HLA  $\rightarrow$  Viral control

- HLA and Viral control independent given Epitope

HLA  $\rightarrow$  Epitope  $\rightarrow$  Viral control

- No independence

HLA  $\rightarrow$  Epitope  $\rightarrow$  Viral control



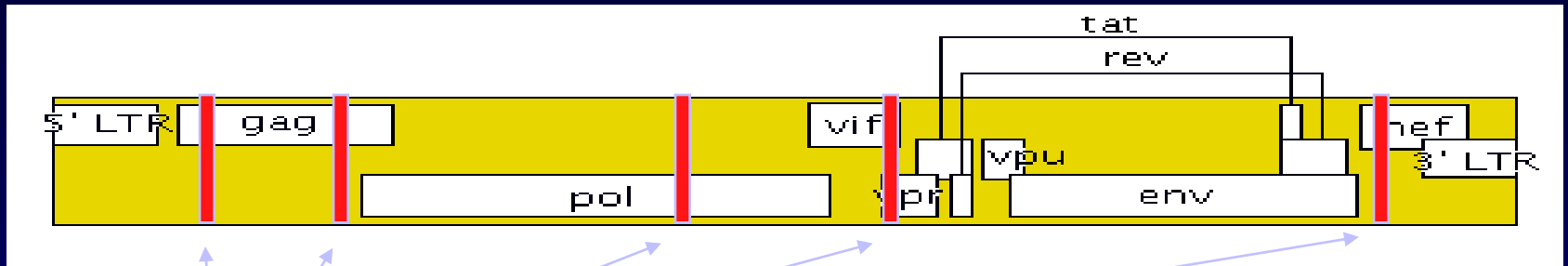
# Targeting of which epitopes leads to viral control / chronic progression?

Use logistic regression with forward selection to identify the epitope specific CD8+ T cell responses that correlate with HIV control (q-value  $< 0.2$ )

## Epitope specific CD8+ T cell responses associated with viral control--“good” epitopes

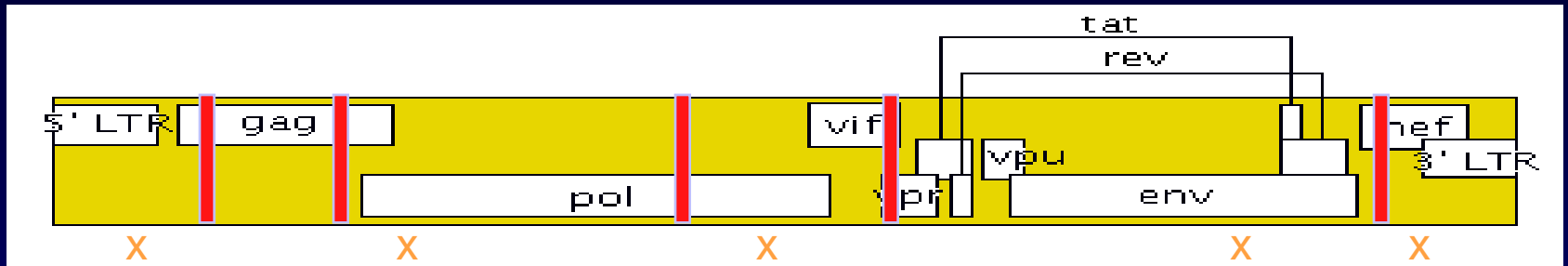
PEPTIDE	HLA	PROTEIN	P VALUE	Q VALUE	L1 WEIGHT
AW9	B*57	<i>Vpr</i>	1.2 $10^{-7}$	0	3.19
KK10	B*27	<i>p24</i>	<0.001	0.02	1.78
TW10	B*57	<i>p24</i>	0.001	0.02	0.87
HW9	B*57	<i>Nef</i>	0.002	0.08	1.11
DA9	B*14	<i>p24</i>	0.003	0.12	0.88
LV10	A*02	<i>Nef</i>	0.004	0.18	0.55

# Consequences for vaccine design



A few epitopes make HIV vulnerable

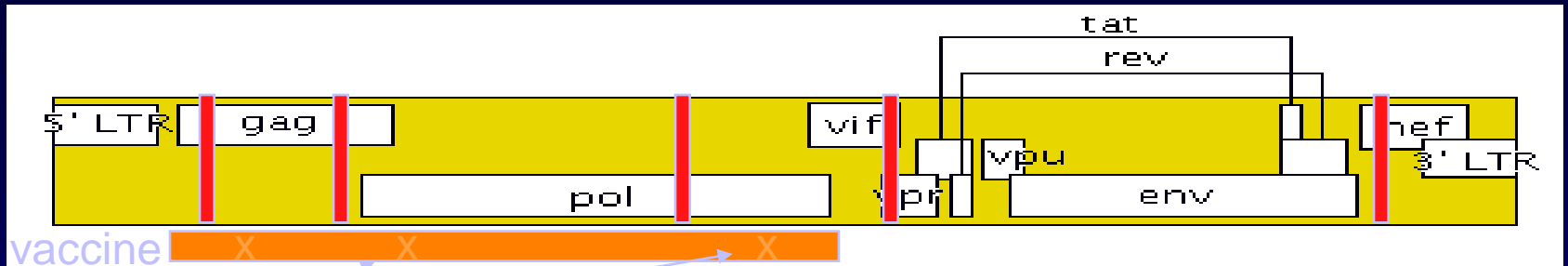
# Consequences for vaccine design



Left to its own devices, our immune system attacks at random epitopes (immunodominance)

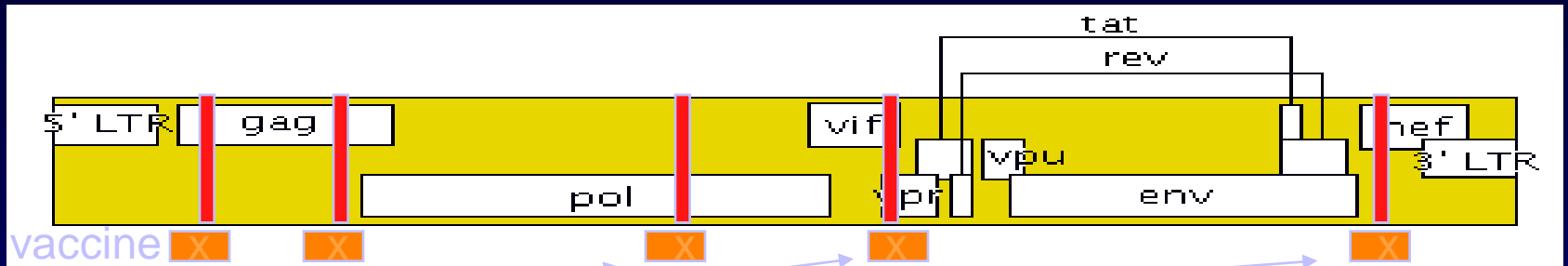


# Consequences for vaccine design



A "whole protein" vaccine does little to help the situation

# Consequences for vaccine design



A focused vaccine can show immune system where to attack

# Things I didn't have time to talk about

- Factor graphs, mixed graphs, etc.
- Relational learning: PRMs, Plates, PERs
- Bayesian methods for learning
- Variational methods
- Non-parametric distributions

# To learn more

Tutorial on my home page

Main conferences:

- Uncertainty in Artificial Intelligence (UAI)
- Neural information Processing Systems (NIPS)