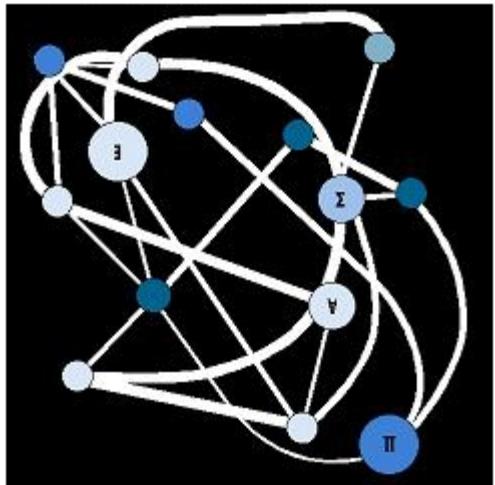


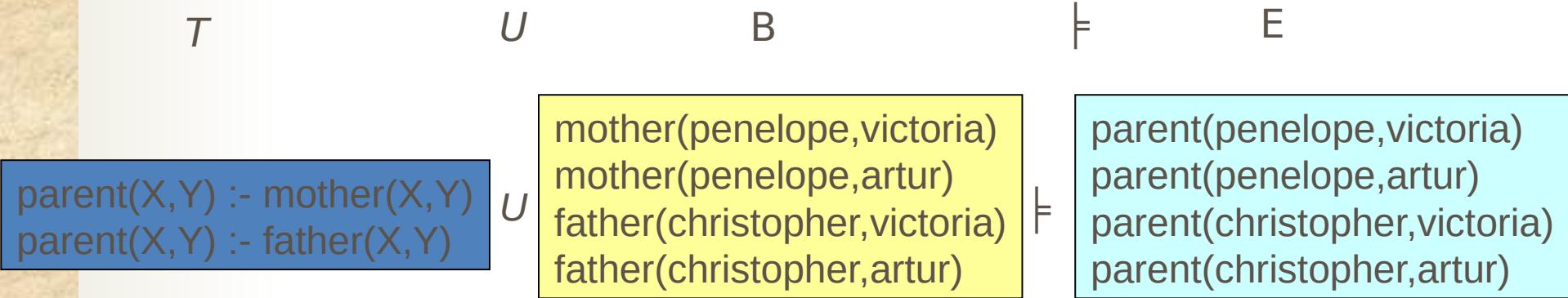
# Relational Machine Learning



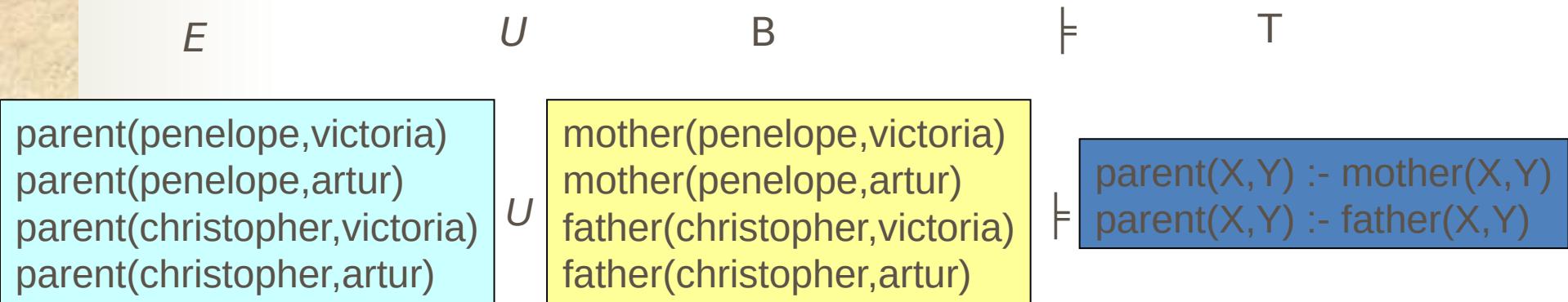
# (Multi) Relational Data Mining

- Inductive Logic Programming (ILP)
- Probabilistic Reasoning – PR
- ILP + PR = SRL
- Statistical Relational Learning

# Deductive Reasoning



# Inductive Reasoning





## TRAINS GOING EAST

- 1.
- 2.
- 3.
- 4.
- 5.

## TRAINS GOING WEST

- 1.
- 2.
- 3.
- 4.
- 5.

# Inductive Logic Programming: example



short(car\_12).

closed(car\_12).

long(car\_11).

long(car\_13).

short(car\_14).

open\_car(car\_11).

open\_car(car\_13).

open\_car(car\_14).

shape(car\_11,rectangle).

shape(car\_12,rectangle).

shape(car\_13,rectangle).

shape(car\_14,rectangle).

load(car\_11,rectangle,3).

load(car\_12,triangle,1).

load(car\_13,hexagon,1).

load(car\_14,circle,1).

wheels(car\_11,2).

wheels(car\_12,2).

wheels(car\_13,3).

wheels(car\_14,2).

has\_car(east1,car\_11).

has\_car(east1,car\_12).

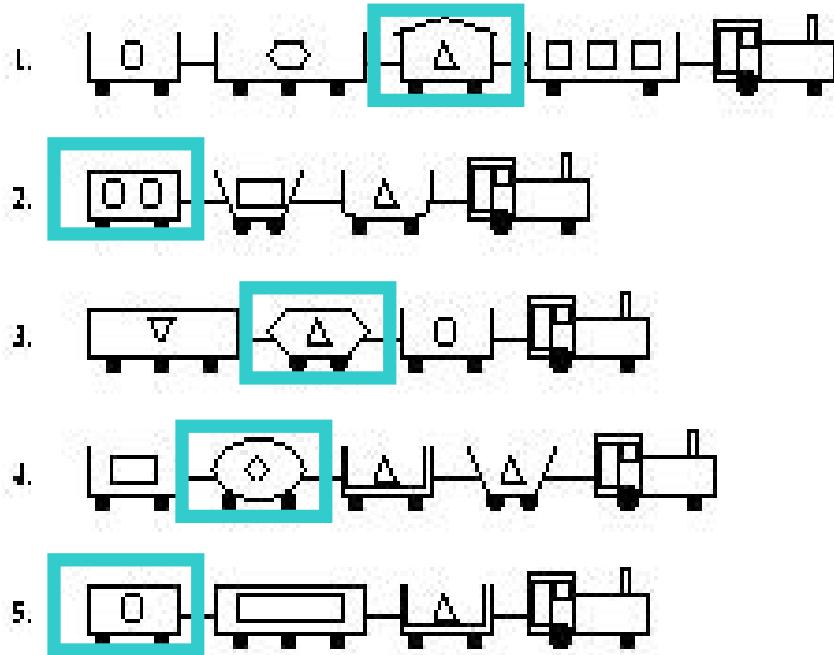
has\_car(east1,car\_13).

has\_car(east1,car\_14).

# Inductive Logic Programming: example

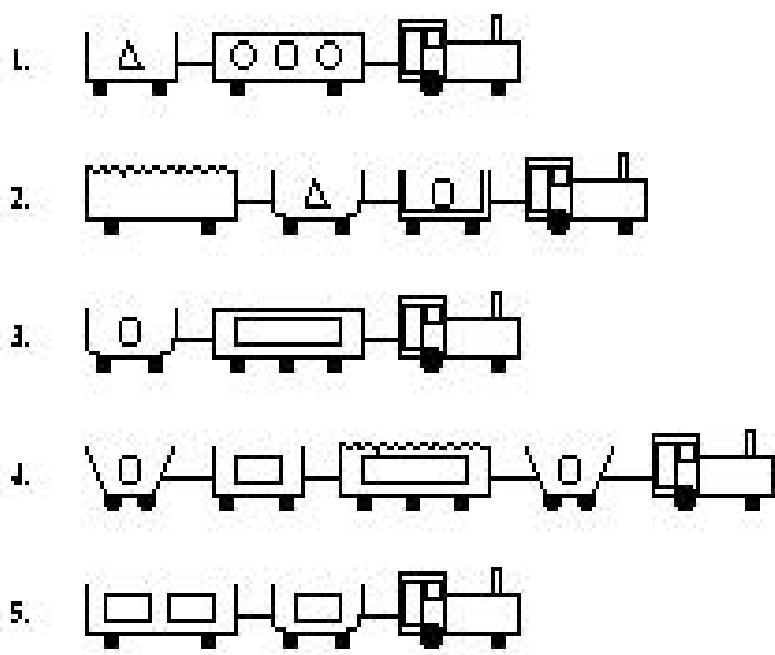
## TRAINS GOING EAST

### 1. TRAINS GOING EAST



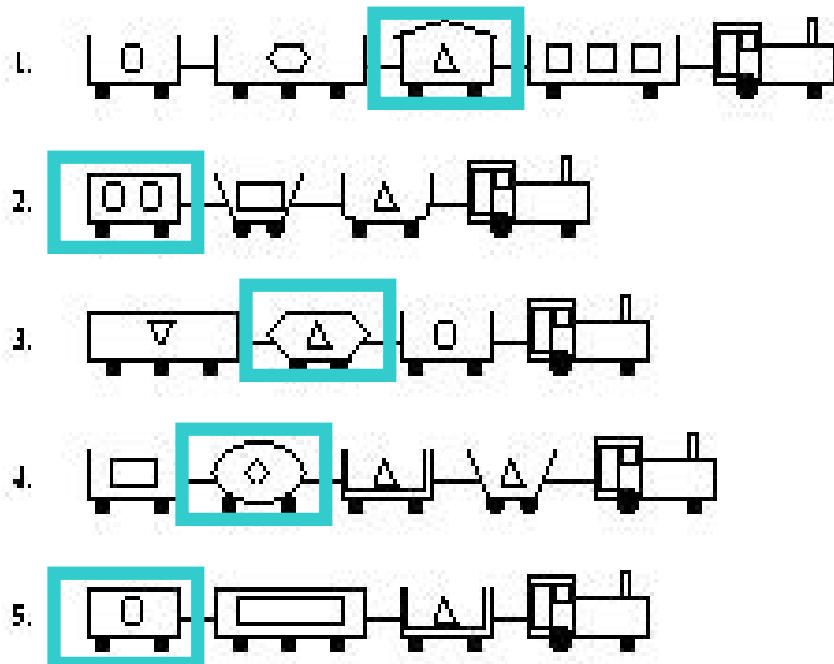
## TRAINS GOING WEST

### 2. TRAINS GOING WEST

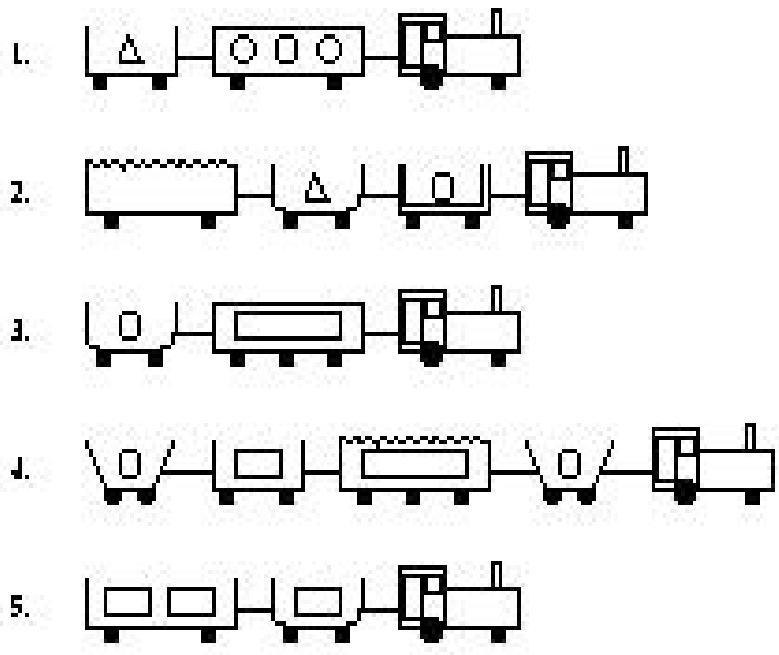


# Inductive Logic Programming: example

TRAIN GOING EAST



TRAIN GOING WEST



eastbound( $T$ ) IF has\_car( $T,C$ ) AND short( $C$ ) AND closed( $C$ )

# Another example: extracting knowledge from mammogram annotations

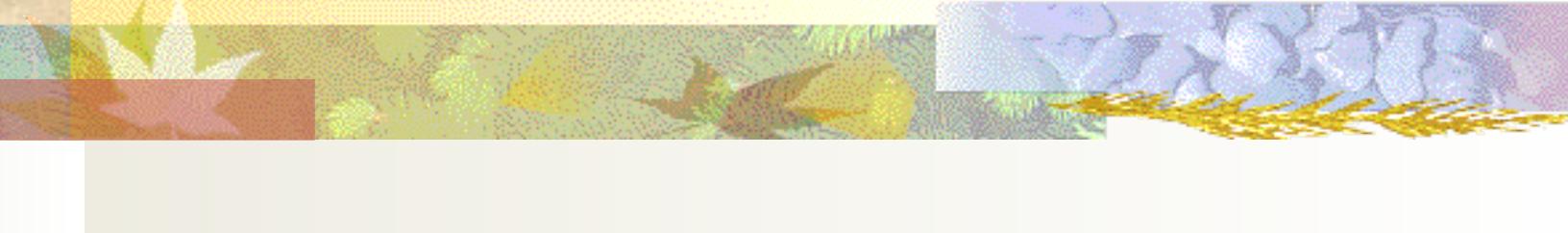
```
is_malignant(A) if  
  'BIRADS category'(A,b5), 'MassPAO'(A,present),  
  'Age'(A,age6570),  
  previous_finding(A,B), 'MassesShape'(B,none),  
  'Calc_Punctate'(B,notPresent),  
  previous_finding(A,C), 'BIRADS_category'(C,b3).
```

The learned rule above says:

A is classified as BI-RADS 5 AND had a mass present in a patient who:  
was between the ages of 65 and 70  
had two prior mammograms (B, C)  
AND prior mammogram (B):  
had no mass shape described  
had no punctate calcifications  
AND prior mammogram (C) was classified as BI-RADS 3

# Inductive Logic Programming

- More formally:
- Given:
  - A set of examples **e** (observations, cases, instances) labelled as positive or negative (class **c**)
  - A language
  - Possibly, a set of constraints
- Find:
  - A hypothesis **h**, such that  $\mathbf{h}(\mathbf{e}_i) = \mathbf{c}_i$
  - For most examples



# Inductive Logic Programming

- Advantages:
  - Utilization of a language that is easy to interpret
  - More concise classifiers
  - More powerful representation: relations
- Disadvantages:
  - Very large search space
  - Non-probabilistic classification

# Properties

- Prior satisfiability

$$B \wedge E^- \not\models \square$$

(H is not a consequence of B and E-)

- Posterior sufficiency

$$B \wedge H \models E^+$$

(H allows to explain E+ relative to B)

- Posterior satisfiability

$$B \wedge H \wedge E^- \not\models \square$$

(B and H are consistent with E-)

- Prior necessity

$$B \not\models E^+$$

(some e+ must be false relative to the model found for B)

# ILP: A Common Approach

- Use a greedy covering algorithm.
  - Repeat while some positive examples remain uncovered (not entailed):
    - Find a *good clause* (one that covers as many positive examples as possible but no/few negatives).
    - Add that clause to the current theory, and remove the positive examples that it covers.
  - ILP algorithms use this approach but vary in their method for finding a *good clause*.

# Some ILP Systems

- PROGOL, ALEPH (top-down): **saturates** first **uncovered** positive example, and then performs **top-down admissible** search of the **lattice** above this saturated example.
- GOLEM (**bottom-up**), FOIL (top-down), LINUS/DINUS.
- Tilde, Claudien, IndLog, ...

# ILP Saturation

- Consists of building a *bottom clause* (seed)
- Incorporates background knowledge to an atomic formula
- Example: (gene that codes for a protein responsible for metabolism)

**metabolism(A) :-**

**essential(A,'Non-Essential'), motif(A,'PS00510'), chromosome(A,'14'),**  
    **interaction(A,B,C,E),**  
    **essential(B,'Non-Essential'), motif(B,'PS00188'), chromosome(B,'2'),**  
    **interaction(A,F,D,G),**  
    **intertype(C,'Genetic'), intertype(D,?),**  
    **interaction(B,A,C,E),**  
    **interaction(B,H,C,I),**  
    **interaction(F,A,D,G),**  
**interaction(H,B,C,I), interaction(H,\_,\_,\_).**

# ILP: Aleph

- Procedure to extract theories from examples
- Complete (branch-and-bound) search for best clause in the ***whole*** space
- Search subject to several user control settings
  - Max clause length
  - Max chaining length
  - Minacc
  - Max nodes
  - Search strategy, etc.

# ILP: Aleph

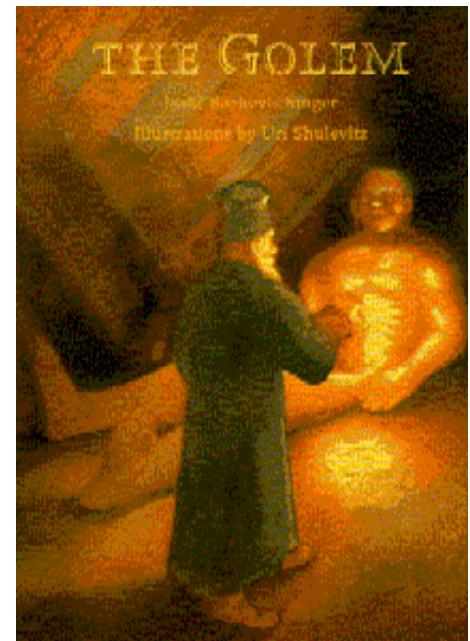
- Aleph
  - Desenvolvido na Universidade de Oxford por Ashwin Srinivasan

<http://www.comlab.ox.ac.uk/oucl/research/areas/machlearn/Aleph/>

# ILP: Aleph

Then the Rabbi said,  
*“Golem, you have not been completely formed, but I am about to finish you now... You will do as I will tell you.”*

Saying these words, Rabbi Leib finished engraving the letter **Aleph**. Immediately the golem began to rise.



# Aleph: algorithm

- Initial State:
  - Examples or observations
  - Descriptions: background knowledge (BK)
- Final State: hypothesis or theory or model
- Transitions: intermediate hypotheses

# Aleph: algorithm

- Select example
- Build most-specific-clause (**bottom clause**)
- Search. Find a clause more general than the bottom clause
- Remove redundant. The clause with the best score is added to the current theory, and all examples made redundant are removed. This step is sometimes called the "**cover removal**" step. Note here that the best clause may make clauses other than the examples redundant
- Return to first step

# Aleph: Knowledge Representation

**Input Files: Prolog Syntax**

**dtp.b:** BK

**dtp.f:** pos examples

**dtp.n:** neg examples

# Representation: BK

```
chromosome('G234064','1').  
chromosome('G234065','1').  
chromosome('G234070','1').  
chromosome('G234073','1').  
chromosome('G234074','1').  
chromosome('G234076','1').  
chromosome('G234084','2').  
chromosome('G234085','2').  
chromosome('G234089','2').
```

# Representation: BK

```
interaction('G234062','G235011','Physical',?).  
interaction('G234064','G234126','Genetic-  
Physical','0.9141').  
interaction('G234064','G235065','Genetic-  
Physical','0.7515').  
interaction('G234064','G235571','Physical','0.9691').  
interaction('G234065','G234073','Physical','0.7492').  
interaction('G234065','G235042','Physical',' -0.4659').
```

# Representation: Examples

```
metabolism('G239098').  
metabolism('G234980').  
metabolism('G235245').  
metabolism('G234108').  
metabolism('G238387').  
metabolism('G240504').  
metabolism('G236733').
```

# Example of clause learned

*metabolism(A) :-*

*chromosome(A,'15'),  
    interaction(A,B,\_,\_),  
    complex(B,'Transcription  
complexes/Transcriptosome').*

**A** and **B** are variables that represent genes

# Aleph: algorithm

- Example: Michalski´s trains

# Aleph: algorithm

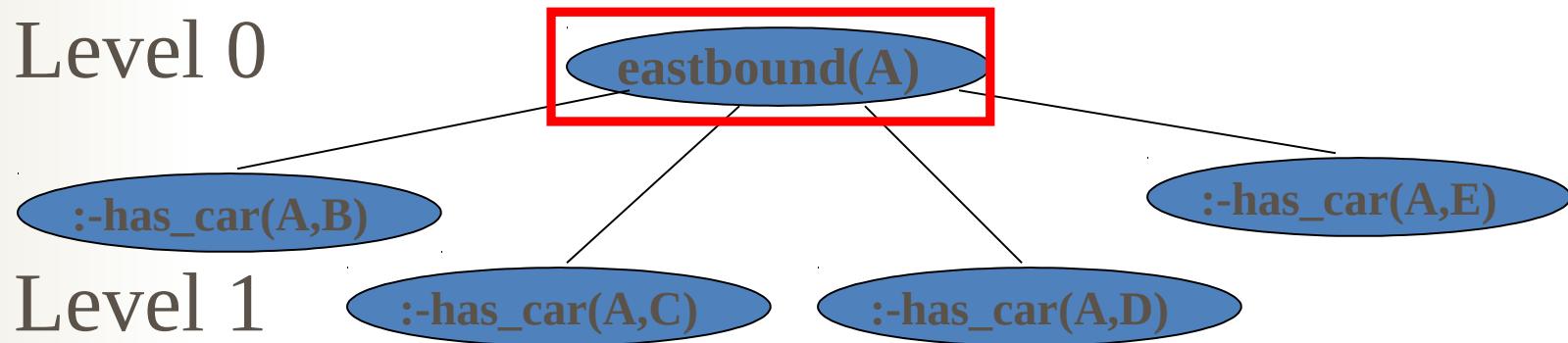
- Saturation (saturated / bottom clause):

eastbound(A) :-

    has\_car(A,B), has\_car(A,C), has\_car(A,D), has\_car(A,E),  
    short(B), short(D), closed(D), long(C),  
    long(E), open\_car(B), open\_car(C), open\_car(E),  
    shape(B,rectangle), shape(C,rectangle), shape(D,rectangle),  
    shape(E,rectangle),  
    wheels(B,2), wheels(C,3), wheels(D,2), wheels(E,2),  
    load(B,circle,1), load(C,hexagon,1), load(D,triangle,1),  
    load(E,rectangle,3).

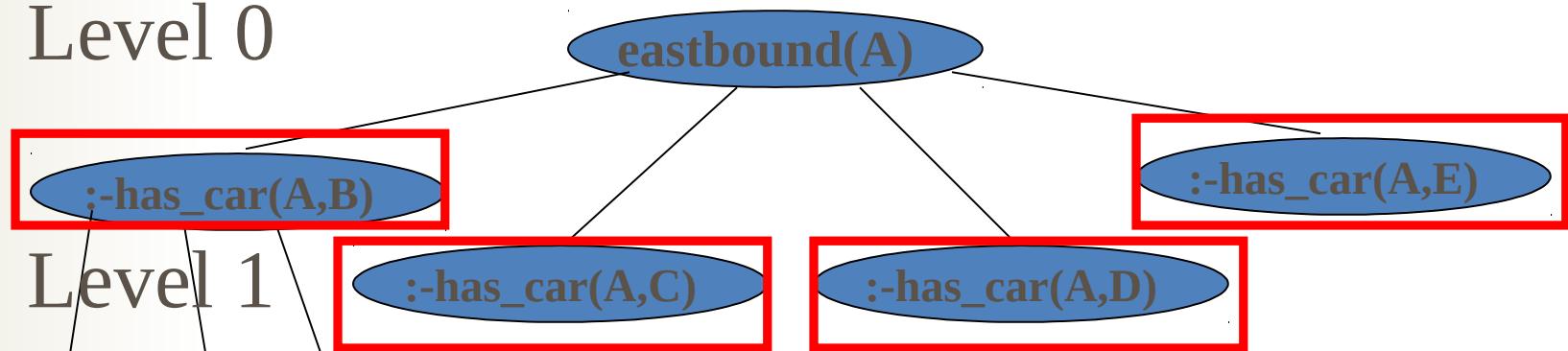
# Aleph: Search

Level 0

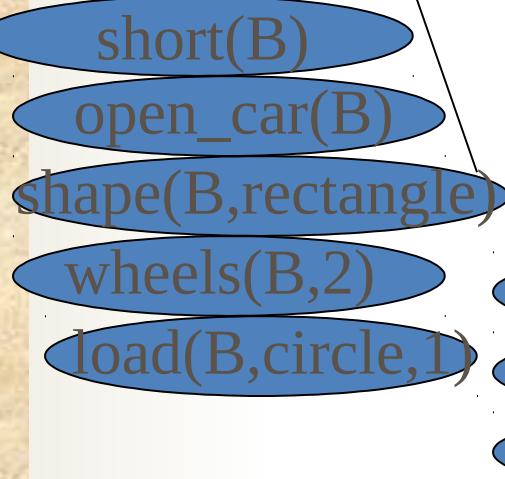


# Aleph: Search

Level 0



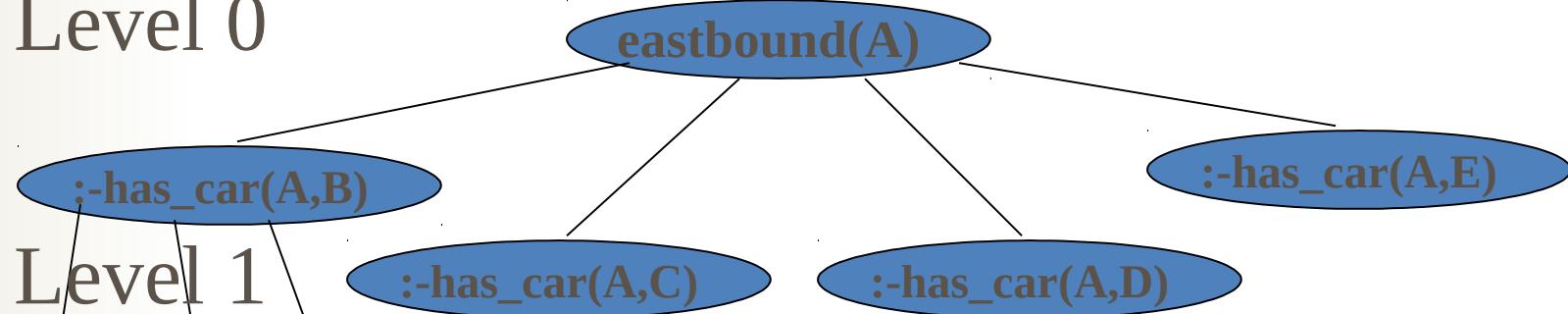
Level 1



Level 2

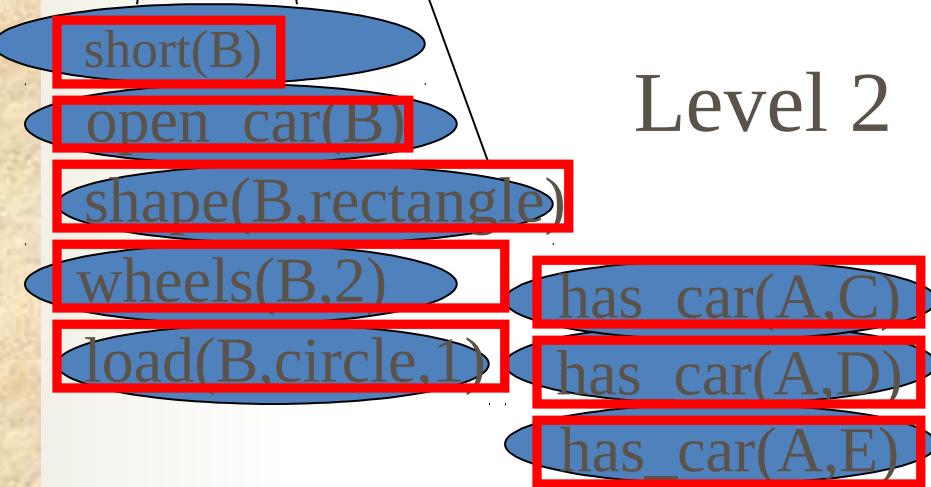
# Aleph: Search

Level 0



Level 1

Level 2



# Aleph: algorithm

- Search: most general clause

**eastbound(A) :-**

has\_car(A,B), has\_car(A,C), has\_car(A,D), has\_car(A,E),  
short(B), short(D), closed(D), long(C),  
long(E), open\_car(B), open\_car(C), open\_car(E),  
shape(B,rectangle), shape(C,rectangle), shape(D,rectangle),  
shape(E,rectangle),  
wheels(B,2), wheels(C,3), wheels(D,2), wheels(E,2),  
load(B,circle,1), load(C,hexagon,1), load(D,triangle,1),  
load(E,rectangle,3).

# Aleph: algorithm

- Search: add possible descendants (candidate literals of level 1)

eastbound(A) :-

```
has_car(A,B), has_car(A,C), has_car(A,D), has_car(A,E),  
short(B), short(D), closed(D), long(C),  
long(E), open_car(B), open_car(C), open_car(E),  
shape(B,rectangle), shape(C,rectangle), shape(D,rectangle),  
shape(E,rectangle),  
wheels(B,2), wheels(C,3), wheels(D,2), wheels(E,2),  
load(B,circle,1), load(C,hexagon,1), load(D,triangle,1),  
load(E,rectangle,3).
```

# Aleph: algorithm

- Search: add possible descendants of level 2

eastbound(A) :-

has\_car(A,B), has\_car(A,C), has\_car(A,D), has\_car(A,E),  
short(B), short(D), closed(D), long(C),  
long(E), open\_car(B), open\_car(C), open\_car(E),  
shape(B,rectangle), shape(C,rectangle), shape(D,rectangle),  
shape(E,rectangle),  
wheels(B,2), wheels(C,3), wheels(D,2), wheels(E,2),  
load(B,circle,1), load(C,hexagon,1), load(D,triangle,1),  
load(E,rectangle,3).

# Aleph: algorithm

- Search: second descendant of level 1

**eastbound(A) :-**

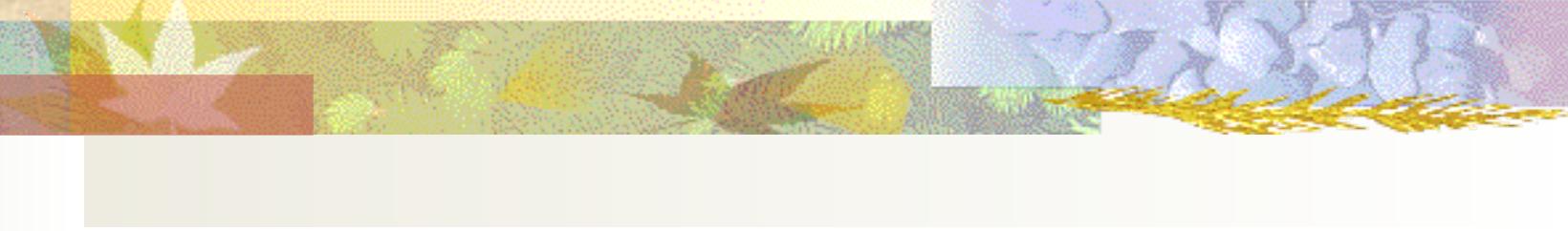
has\_car(A,B), **has\_car(A,C)**, has\_car(A,D), has\_car(A,E),  
short(B), short(D), closed(D), long(C),  
long(E), open\_car(B), open\_car(C), open\_car(E),  
shape(B,rectangle), shape(C,rectangle), shape(D,rectangle),  
shape(E,rectangle),  
wheels(B,2), wheels(C,3), wheels(D,2), wheels(E,2),  
load(B,circle,1), load(C,hexagon,1), load(D,triangle,1),  
load(E,rectangle,3).

# Aleph: algorithm

- Search: descendants of second descendant...

**eastbound(A) :-**

has\_car(A,B), has\_car(A,C), has\_car(A,D), has\_car(A,E),  
short(B), short(D), closed(D), long(C),  
long(E), open\_car(B), open\_car(C), open\_car(E),  
shape(B,rectangle), shape(C,rectangle), shape(D,rectangle),  
shape(E,rectangle),  
wheels(B,2), wheels(C,3), wheels(D,2), wheels(E,2),  
load(B,circle,1), load(C,hexagon,1), load(D,triangle,1),  
load(E,rectangle,3).



# Aleph: example of run

☷ aleph\_trains

# Aleph: how to run?

- You need to have a Prolog system
  - Yap: <http://yap.sourceforge.net> OU
  - SWI: <http://www.swi-prolog.org>
- Aleph:  
<http://www.comlab.ox.ac.uk/oucl/research/areas/machlearn/Aleph/>
- Files: .b, .f, .n
- To make things easier: everything in the same directory!

# Aleph: Basic Commands

- `read_all`
- `reduce`
- `induce`

# Aleph: Parameters

```
:- set(clauselength,5).  
:- set(depth, 200).  
:- set(i,3).  
:- set(noise,0).  
:- set(minacc,0.7).  
:- set(nodes,1000000).  
:- set(m,20).  
:- set(evalfn,mestimate).  
:- set(test_pos,'/u/dutra/Protein/prot_test_set.f').  
:- set(test_neg,'/u/dutra/Protein/prot_test_set.n').  
:- set(optimise_clauses,true).  
  
:- set(record,true).  
:- set(recordfile,'prot_train_set.out').  
:- set(samplesize,0).
```

$$\text{Strength estimate} = (\text{support} + m * \text{prior}) / (\text{coverage} + m)$$

$M \rightarrow 0$ , strength  $\rightarrow$  precision

Support = True positives

Coverage = True positives + false negatives

# Aleph: Modes and Types

```
:  
:- modeh(1,eastbound(+train)).  
:- modeb(1,short(+car)).  
:- modeb(1,closed(+car)).  
:- modeb(1,long(+car)).  
:- modeb(1,open_car(+car)).  
:- modeb(1,double(+car)).  
:- modeb(1,jagged(+car)).  
:- modeb(1,shape(+car,#shape)).  
:- modeb(1,load(+car,#shape,#int)).  
:- modeb(1,wheels(+car,#int)).  
:- modeb(*,has_car(+train,-car)).
```

```
:  
:- determination(eastbound/1,short/1).  
:- determination(eastbound/1,closed/1).  
:- determination(eastbound/1,long/1).  
:- determination(eastbound/1,open_car/1).  
:- determination(eastbound/1,double/1).  
:- determination(eastbound/1,jagged/1).  
:- determination(eastbound/1,shape/2).  
:- determination(eastbound/1,wheels/2).  
:- determination(eastbound/1,has_car/2).  
:- determination(eastbound/1,load/3).
```

# Aleph: Modes and Types

```
:  
:- modeh(1,metabolism(+gene)).  
  
:- modeb(1,essential(+gene,#essential)).  
:- modeb(1,class(+gene,#class)).  
:- modeb(1,complex(+gene,#complex)).  
:- modeb(1,phenotype(+gene,#phenotype)).  
:- modeb(1,motif(+gene,#motif)).  
:- modeb(1,chromosome(+gene,#chromosome)).  
:- modeb(*,gte(+number,#number)).  
:- modeb(*,interaction(+gene,-gene,-intertype,-number)).  
:- modeb(1,intertype(+intertype,#intertype)).
```

# Example: drug discovery using Aleph refinement operators

- Given:
  - Molecules active and inactive for dtp
  - Their description in terms of coordinates and bonds
- Find small structures that model active molecules

# Examples: drug discovery

- Examples of dtp groups:  
**hydrophobic**(m752,  
    hyphob([a2, a3, a5, a8, a7, a4, a2],  
    2.16452, -0.833917, 3.6379)).  
**hacc**(m9706,  
    hacc(a10, -6.2969, -1.3684, -0.4631)).

# Example: drug discovery

## ■ Utilisation of refinement operator

refine(false,Clause):-

```
member(Point1, [hydrophobic(M,P1), hdonor(M,P1),halogen(M,P1),hacc(M,P1)]),  
member(Point2,[hydrophobic(M,P2),hdonor(M,P2),halogen(M,P2),hacc(M,P2)]),  
Clause = (active(M) :- Point1, Point2, dist(M,P1,P2,D1,E)).
```

refine(Clause1,Clause2):-

```
Clause1 = (active(M) :- Point1,Point2, dist(M,P1,P2,D1,E)), member(Point3,  
[hydrophobic(M,P3),hdonor(M,P3),halogen(M,P3),hacc(M,P3)]),  
Clause2 = (active(M) :- Point1, Point2, dist(M,P1,P2,D1,E),  
Point3, dist(M,P1,P3,D2,E), dist(M,P2,P3,D3,E)).
```

## ■ Reduce search space!!!