Cancer classification based on miRNA profiles using ASP

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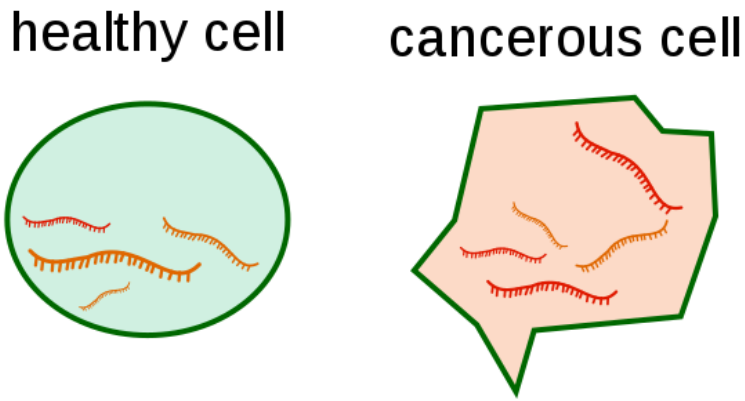
Selective cell targeting

- **Problem:** Discrimination of tumor from healthy tissues



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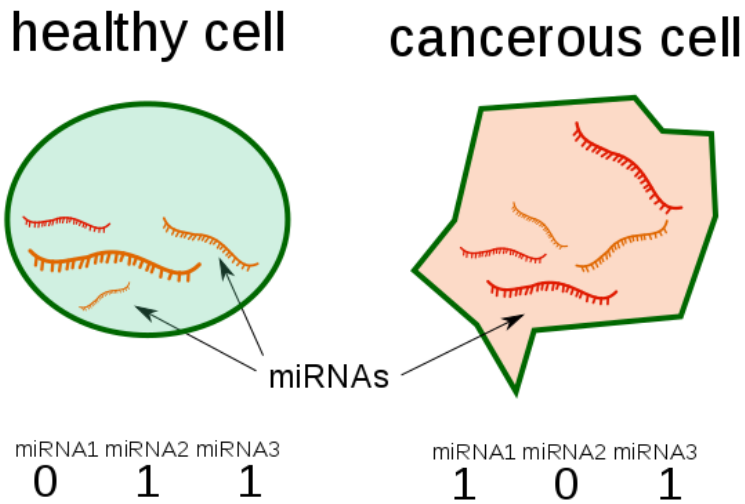


- **Idea:** Cells differ in miRNA profiles

In vitro classification

Constraints from biology

- less than 10 inputs in total
- no more than 6 inputs attached to the AND gate
- no more than 3 inputs atttached to any OR gate
- no NOT gates attached to an OR gate
- no more than 2 OR gates
- no more than 4 NOT gates

Input: Data

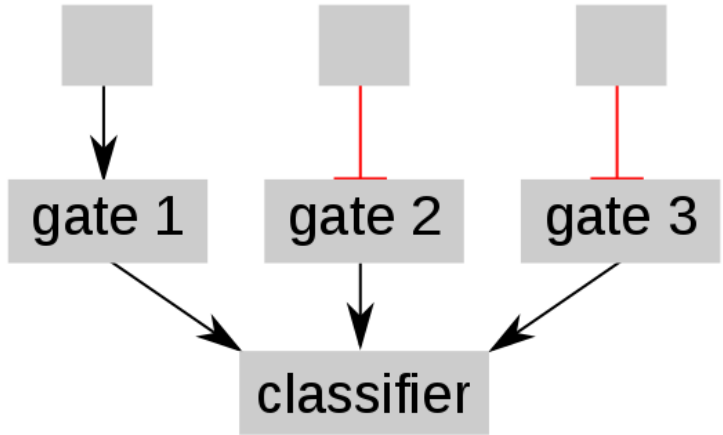
		cancer?	**miRNAs**		
	ID	Annots	g1	g2	g3
tissues	1	0	1	1	0
	2	0	0	0	1
	3	1	0	1	0

```
tissue(1,healthy). tissue(2,healthy). tissue(3,cancer).

data(1,g1,high). data(1,g2,high). data(1,g3,low).
data(2,g1,low).  data(2,g2,low).  data(2,g3,high).
data(3,g1,low).  data(3,g2,high). data(3,g3,low).

is_miRNA(Y) :- data(X,Y,Z).
```

Input: Classifier structure




```
is_gate_type(1..2).

upper_bound_pos_inputs(1, 1).
upper_bound_neg_inputs(1, 0).
lower_bound_pos_inputs(1, 0).
lower_bound_neg_inputs(1, 0).
upper_bound_gate_type(1, 1).

upper_bound_total_inputs(2).
```

bounds for gate type 1

Decision 1: Number of gates

```
1 {number_of_gates(1..2)} 1.

is_integer(1..2).
is_gate_id(GateID) :- number_of_gates(X),is_integer(GateID),
                      GateID<=X.
```

Decision 2: Gate types

```
1 {gate_type(GateID, X) : is_gate_type(X)} 1 :- is_gate_id(GateID).
```

Decision 3: Inputs for each gate

positive inputs:

```
X{gate_input(GateID,positive,MiRNA):feasible_pos_miRNA(MiRNA)}Y
   :-is_gate_id(GateID),gate_type(GateID,GateType),
     lower_bound_pos_inputs(GateType,X),
     upper_bound_pos_inputs(GateType,Y).
```

negative inputs:

```
X{gate_input(GateID,negative,MiRNA):feasible_neg_miRNA(MiRNA)}Y
   :-is_gate_id(GateID),gate_type(GateID,GateType),
     lower_bound_neg_inputs(GateType,X),
     upper_bound_neg_inputs(GateType,Y).
```