Cancer classification based on miRNA profiles using ASP

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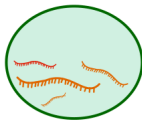
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Selective cell targeting

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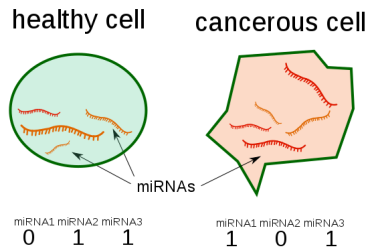

healthy cell   cancerous cell

Selective cell targeting

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

- **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
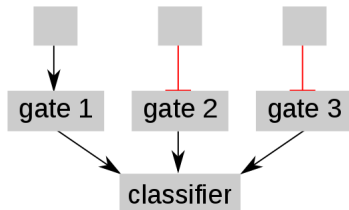- no more than 2 OR gates
- no more than 4 NOT gates

Input data

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

tissues { (rows 1, 2, 3)

```
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).
```

bounds for gate type 1