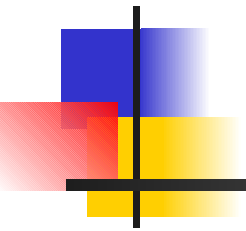
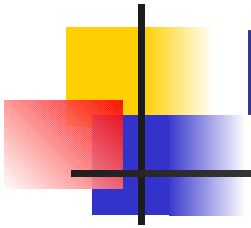


Length-driven communication mechanism for DNA computing

E. Csuhaj-Varjú

S. Verlan



Motivation

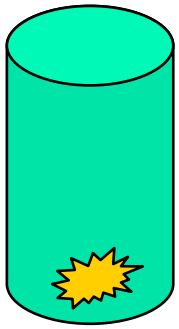
Separation by length (using gel electrophoresis) is a common operation performed in the lab.

Surprisingly, there are not many theoretical models using this operation.

We combine existing models with length separation which becomes the main ingredient of the model.

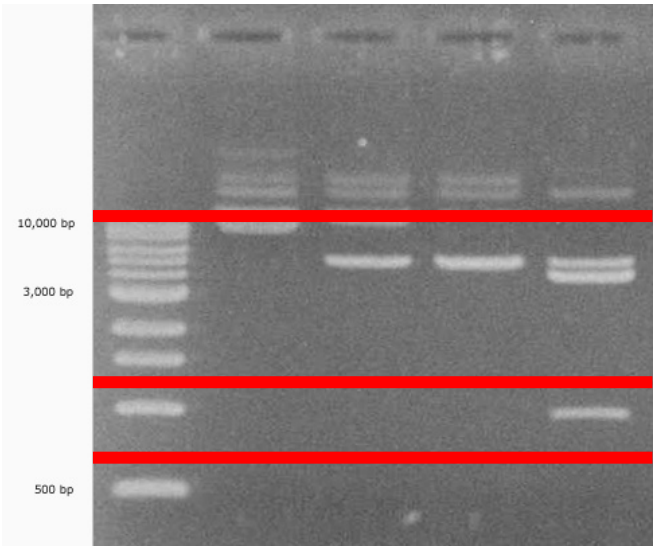
Ideas

test tube

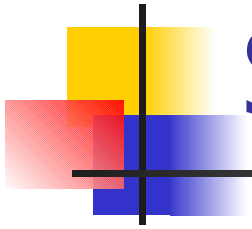


Reaction

Gel electrophoresis



Cut



Separation by length

Gel electrophoresis is not the only possibility to separate molecules by length:

Size Exclusion Chromatography

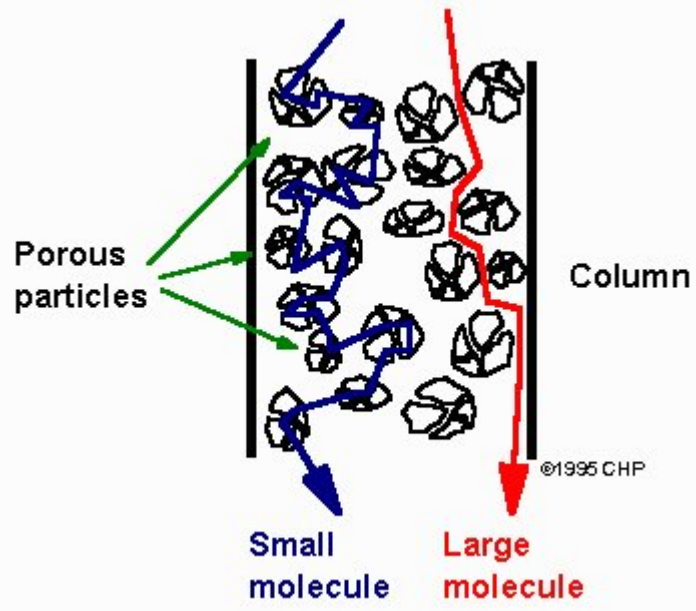
Size Exclusion Chromatography

A chemical method for separation of molecules by their length.

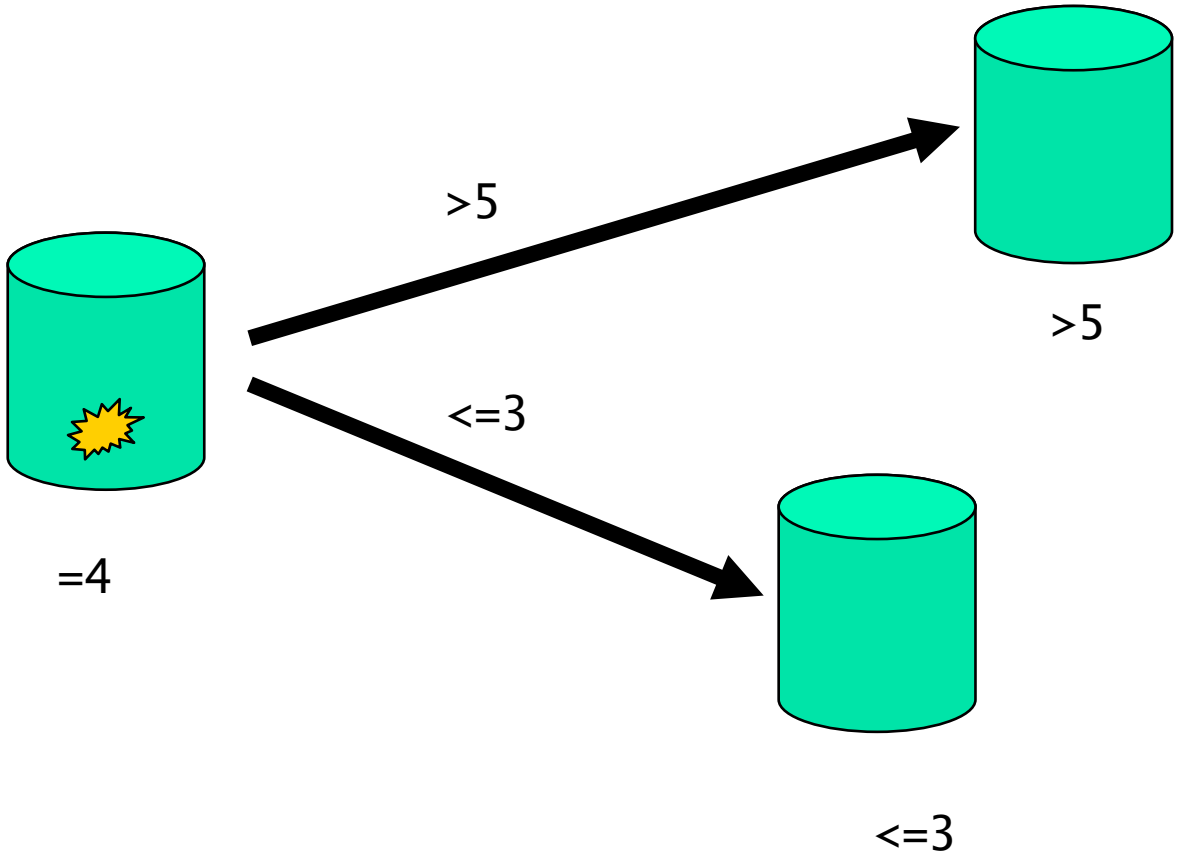
A widely used technique for the purification and analysis of synthetic and biological polymers.

Very fast and accurate.

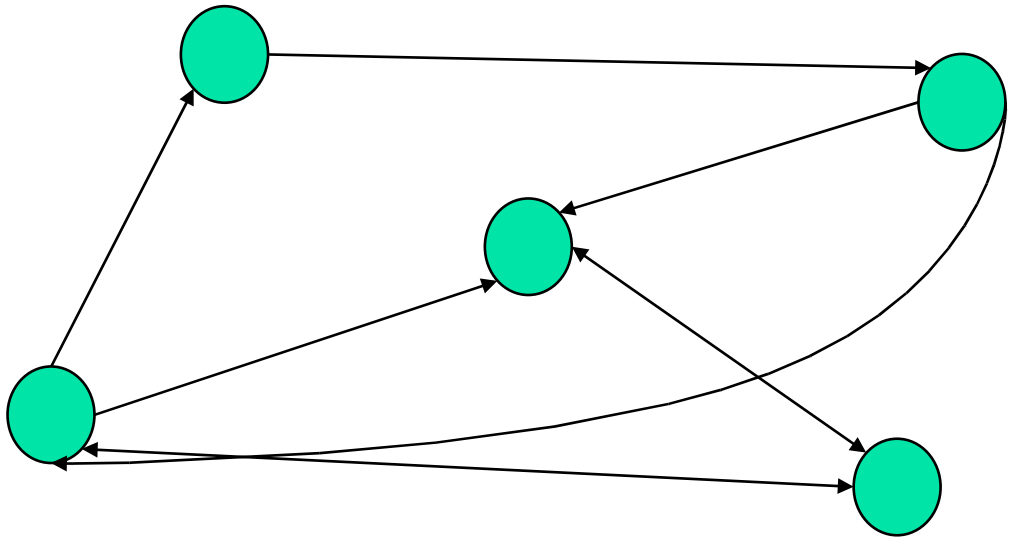
Automatic.



Combining actions



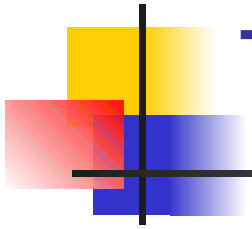
Generalizing



Graph

Operation(s) in nodes (test tubes) on (DNA) strings

Communication driven by length



The model

Directed graph.

Strings located in nodes.

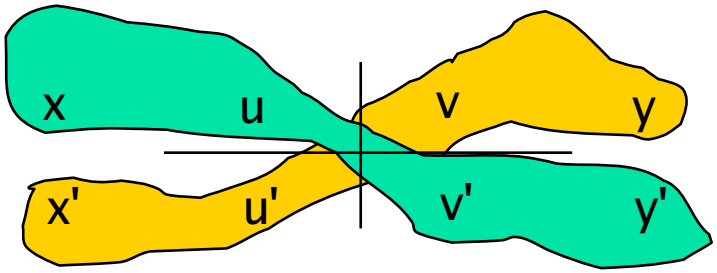
An operation (we chose *splicing*)

Numerical mappings (or predicates) associated to edges.

Result: contents of a tube (modulo a terminal filter).

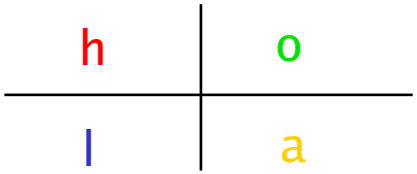
Splicing

(T. Head)



(xuvy,x'u'v'y') |- (xuv'y',x'u'vy)

Example



show blame

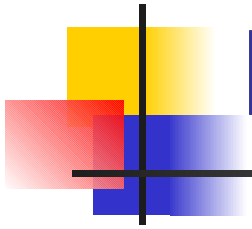
Example

h	o
l	a

show blame

sh	ow
bl	ame

$\vdash$ shame / blow



Mappings

<k

>k

<=k

>=k

max

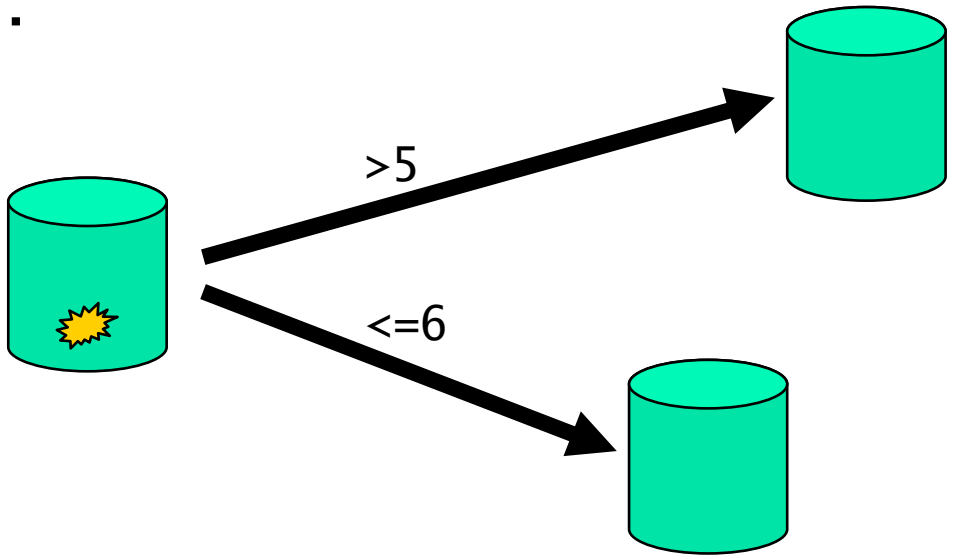
¬max

min

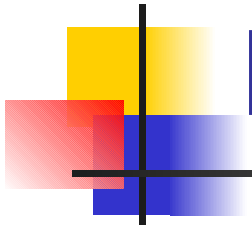
¬min

Non-contradictoriness

Mappings shall be non-contradictory, i.e. there shall not be a situation like this:



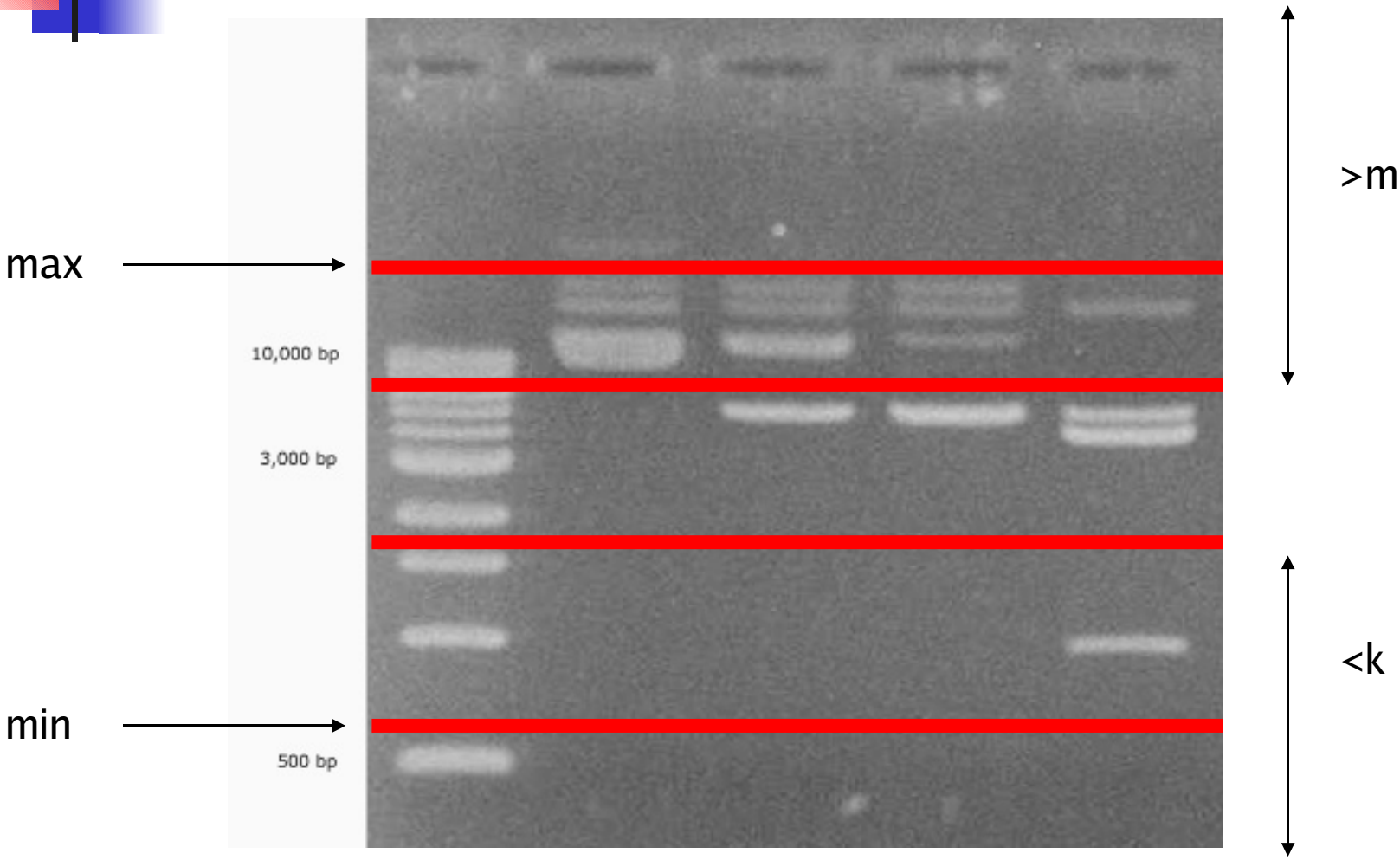
where to place =6 ?



Min and max

In particular, min and max mappings can be only coupled with ¬min and ¬max mappings.

Back to the gel



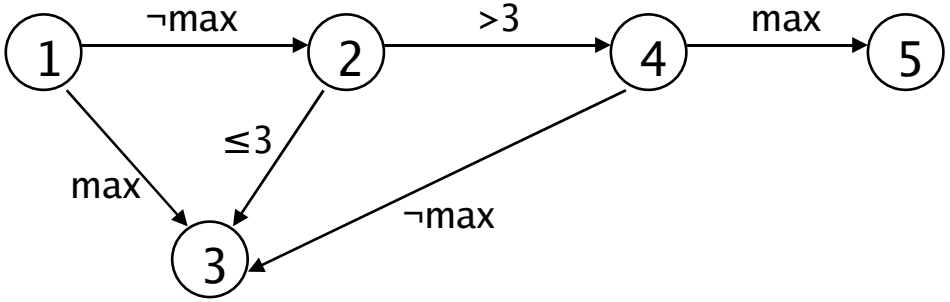
Example

aaqbb
XXY
ApZ

XXbb
aaqY

aapZ
AqY

XXZ
aapbb



1:

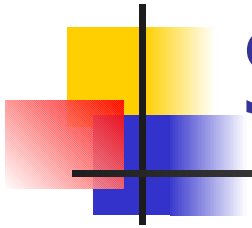
q	b
XX	Y

2:

a	qY
A	pZ

4:

XX	b
ap	Z



Similarities

As one can see the model is similar to splicing test tube systems or tissue-like P systems.

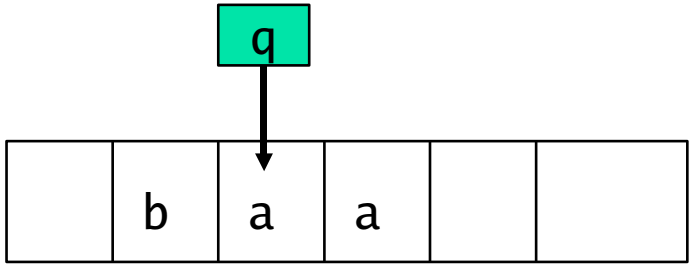
However the communication (and filtering) mechanism is significantly different.

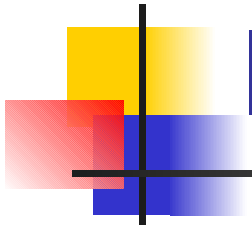
Universality

The obtained model is universal.

It is possible to simulate a Turing machine with 11 nodes.

Not very surprising, as splicing is too powerful.





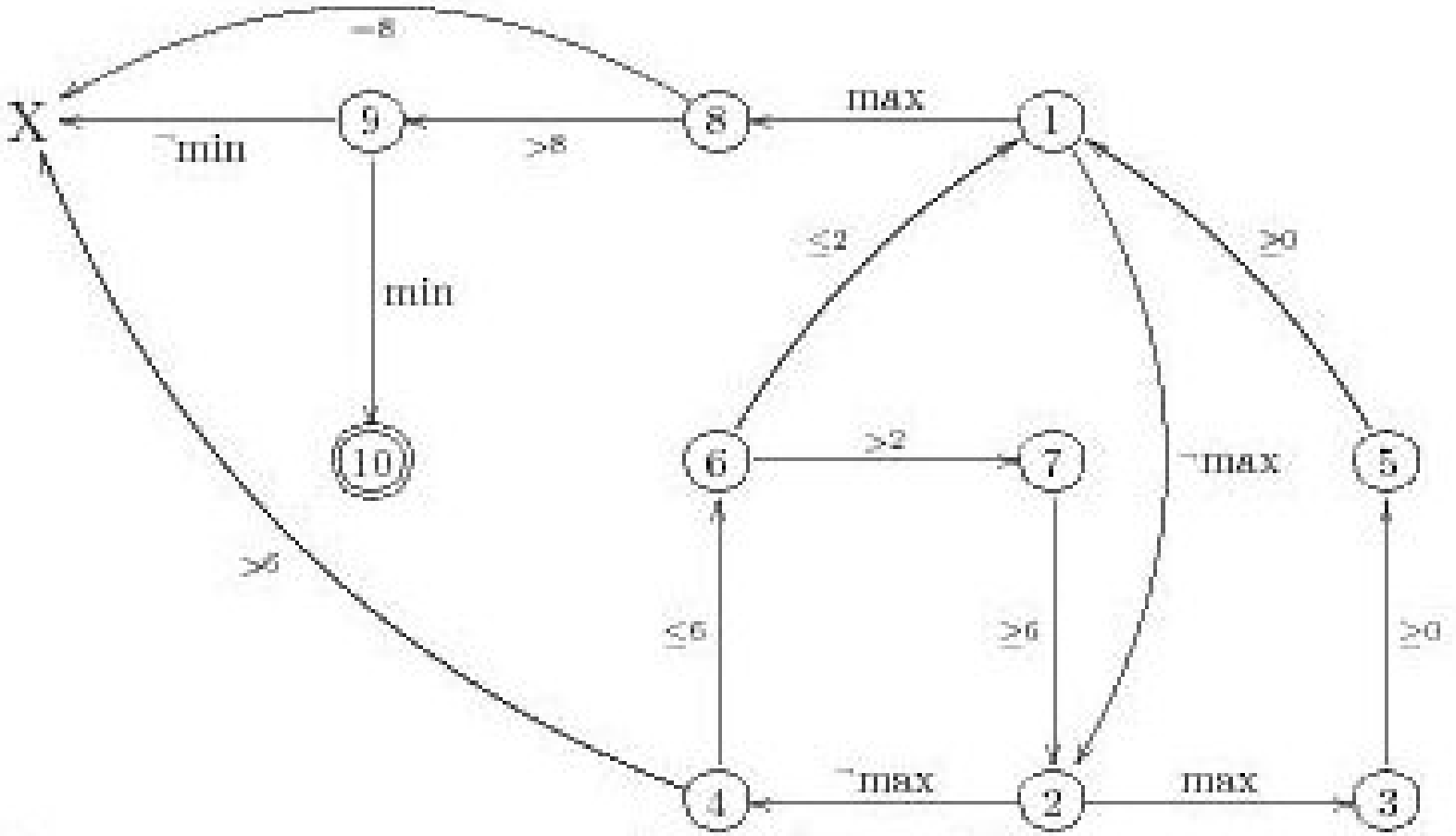
Ideas of the proof

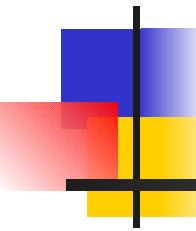
A configuration of a Turing machine is encoded as a string.

A move of a Turing machine is simulated in 3 steps (cut, replace, paste).

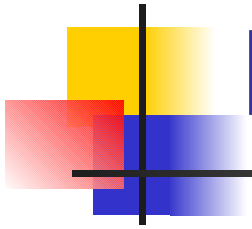
Using length separation we eliminate unwanted strings.

Ideas of the proof





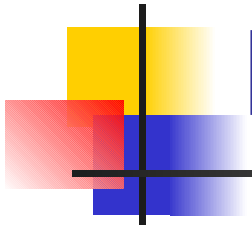
Remarks & Extensions



Predicates

All predicates (except min/max) may be expressed by **<k** and **>k** predicates.

In most of the cases only min/max predicates are sufficient (in particular for the universality).



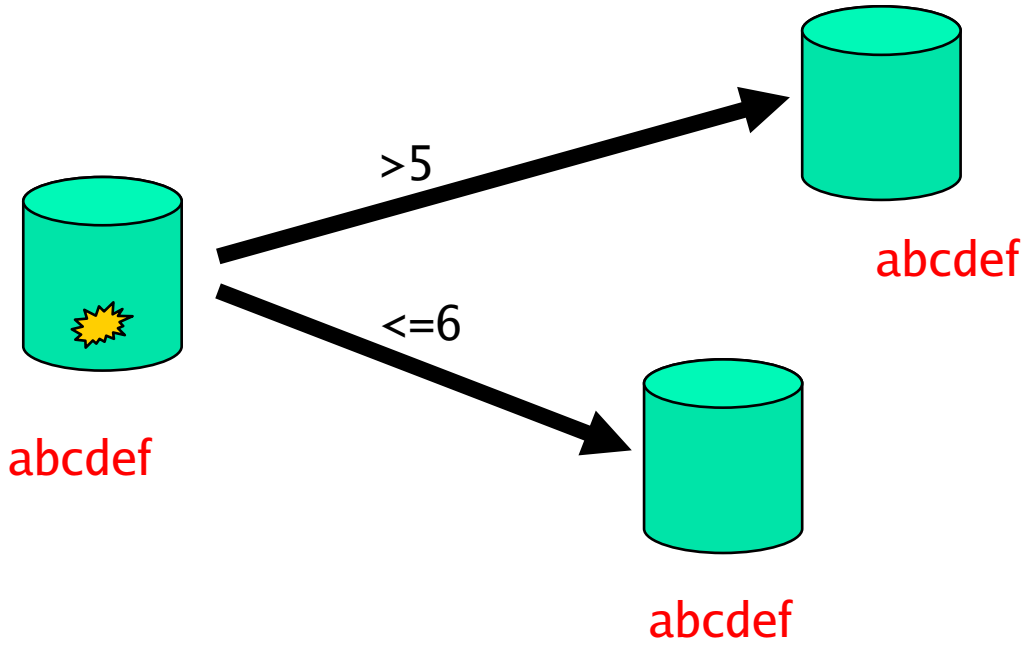
Finite length predicates

If no min/max predicates are used, then corresponding systems are regular (conjecture)

In particular, words of length greater than some constant k cannot be distinguished by such systems…

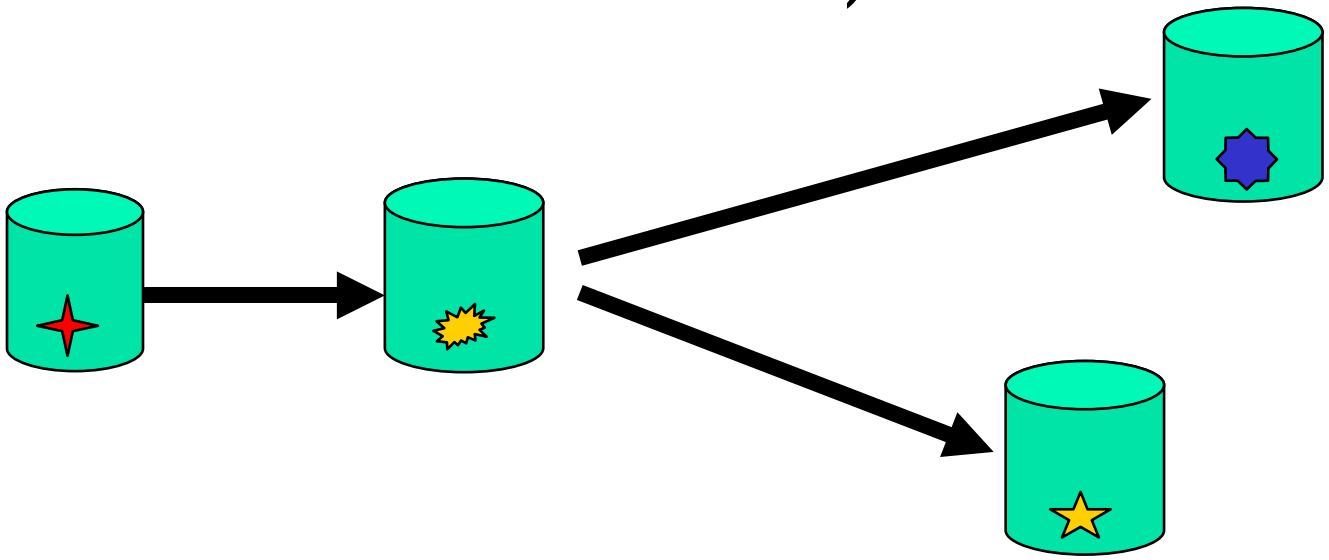
Contradictory predicates

What means to allow contradictory predicates?



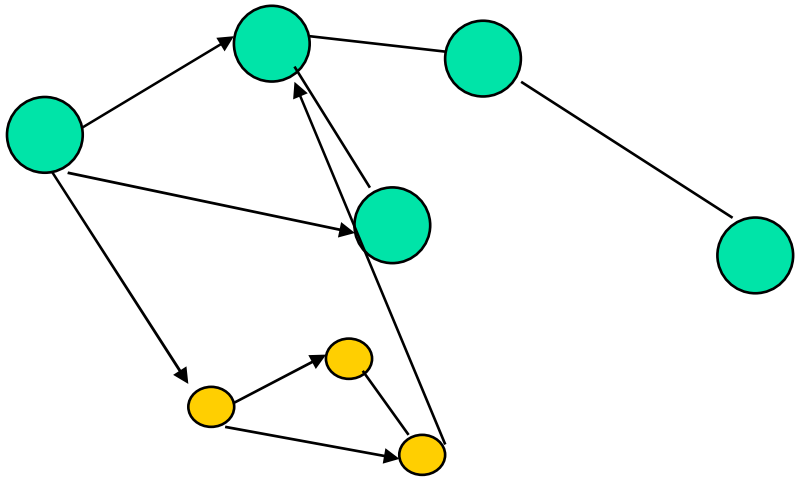
Hybrid systems

We may consider hybrid systems (by associating different operations to different test tubes).



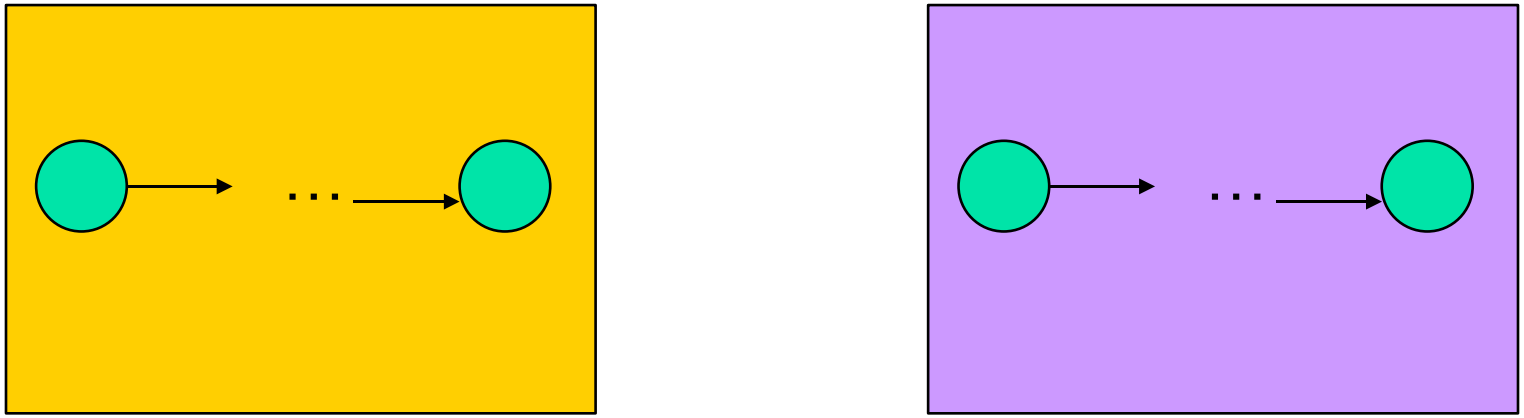
Composition

Moreover, each node may correspond to another system:



Chaining

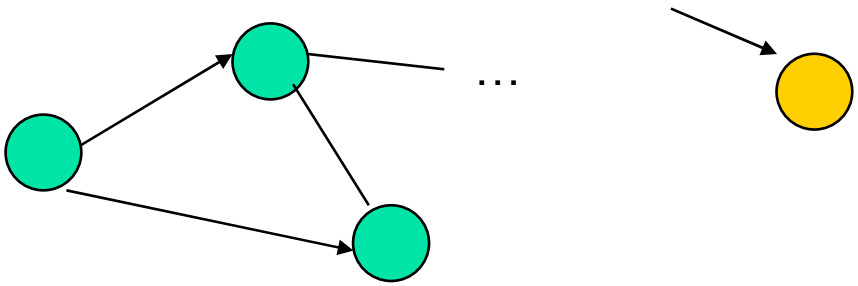
Terminal filtering may be omitted and this gives the possibility to chain different systems



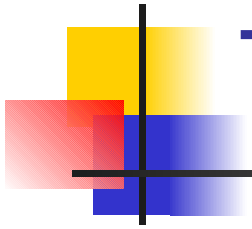
Halting

Generally, the end of the computation occurs when there is no rule applicable.

However, since this condition is not easy to test, we may use a special acknowledgement tube for halting.



Halt

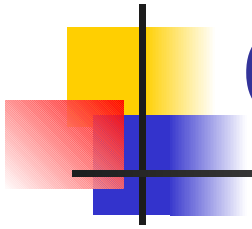


The result

The result may be taken in

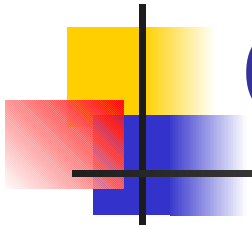
- grammar systems style (all terminals that transit the output node).
- P systems style (the terminals are collected only at the halting configuration).

Communication function



It might be possible (although with no biological motivation) to use other functions instead of the length function.

$|x|_a$, $|x| \bmod 3$, …



Conclusions

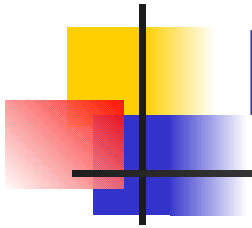
A theoretical model based on a commonly used lab technique.

Many variants.

Gives an interesting filtering mechanism.

Universal…

It can be used to design in vitro systems (transducers) that will do a desired transformation on a string (DNA).

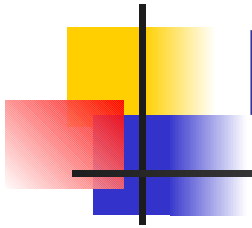


Further work

Use another operations.

Restrictions:

- One elementary rule per test tube.
- Determinism.
- Using only max (min) predicate.
- Using only min_k and max_k predicates.
- Predicates with a threshold.
- …



Further work

Applications to the theory of formal languages.

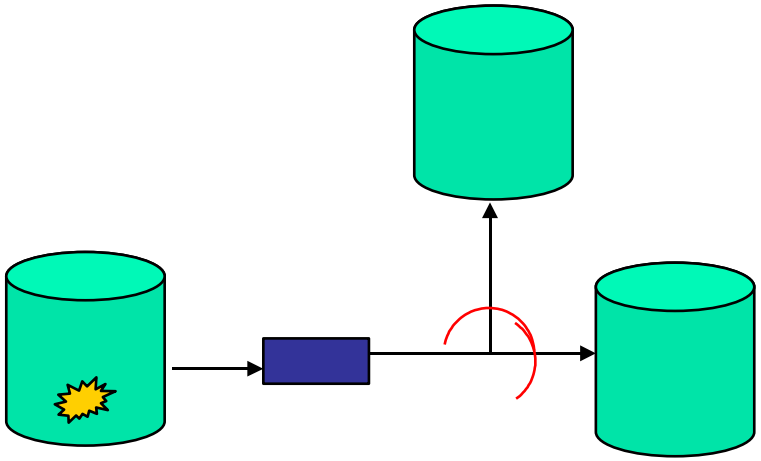
Investigation of the efficiency of predicates.

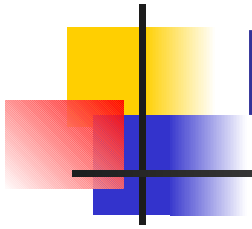
Find examples of "interesting" transformations (happening in biology).

Design of transducers for real DNA transformations.

Implementation?

Implementation





Bibliography

E. Csuhaj-Varju, S. Verlan, On Length-Separating Test Tube Systems, in Proceedings of DNA12, 2006, vol. 4287 of *LNCS*, 58-70 (also in publication in *Natural Computing*).