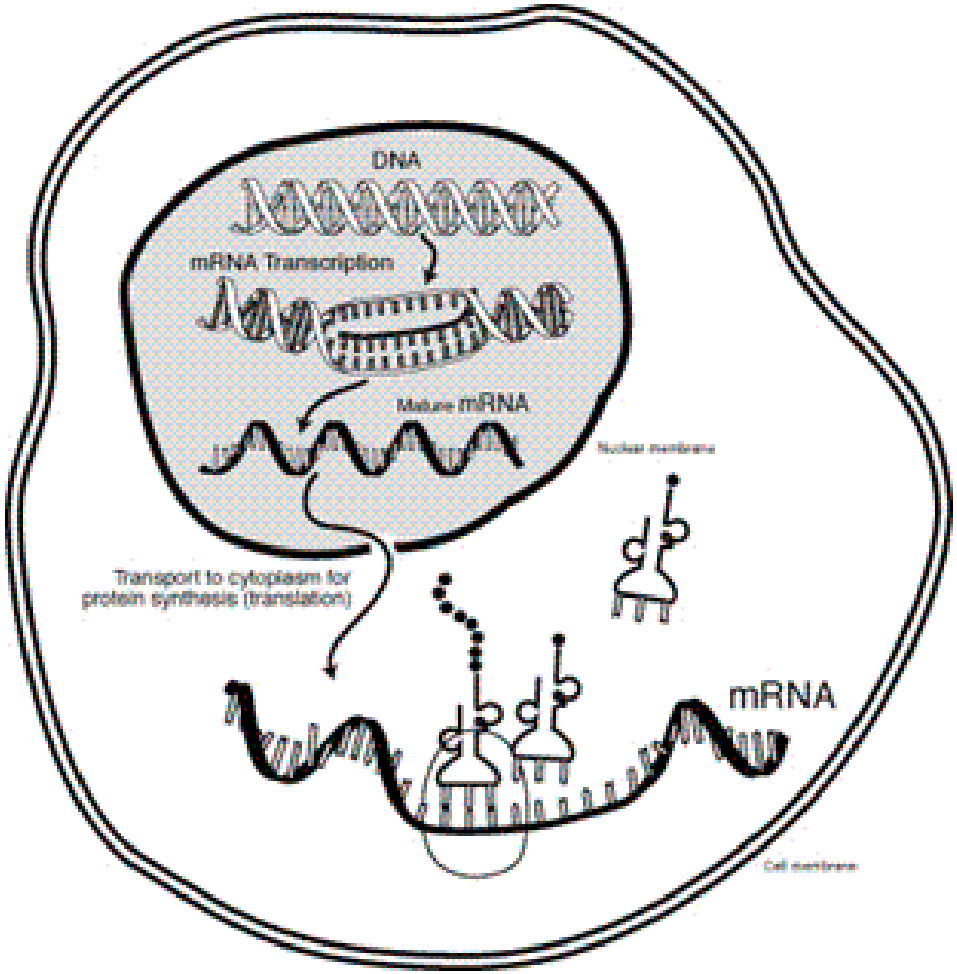
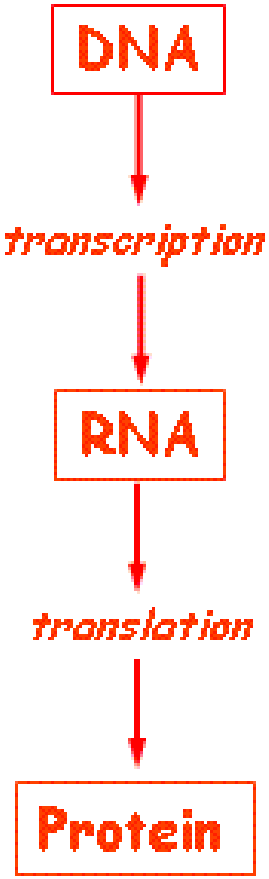
Flip-Flop: Fast lasso-based isoform prediction from RNA-seq data

Jean-Philippe Vert
(joint work with Elsa Bernard, Laurent Jacob, Julien Mairal)

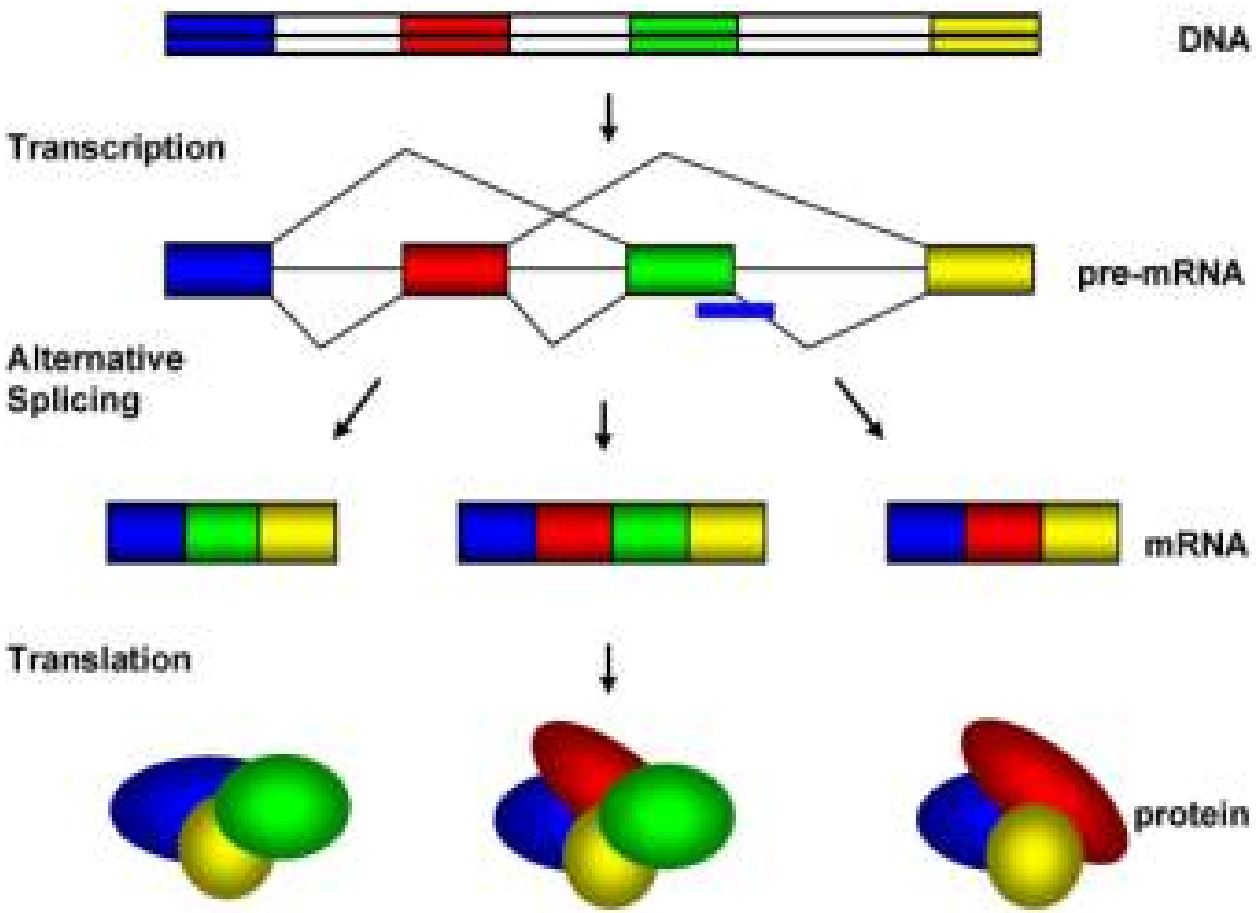
Kyoto University, Bioinformatics Center, July 12th, 2013

(old) Central dogma



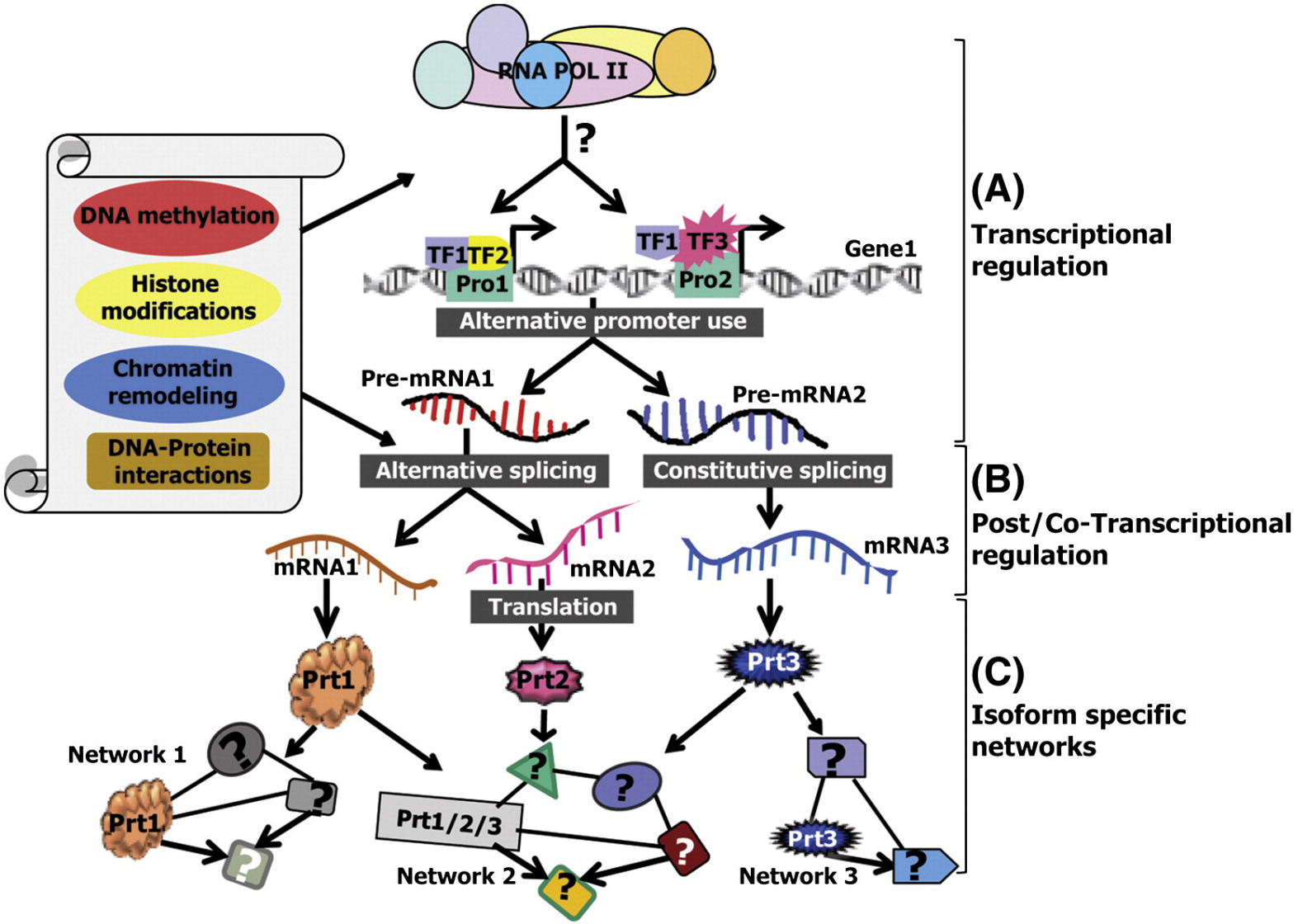


Alternative splicing: 1 gene = many proteins



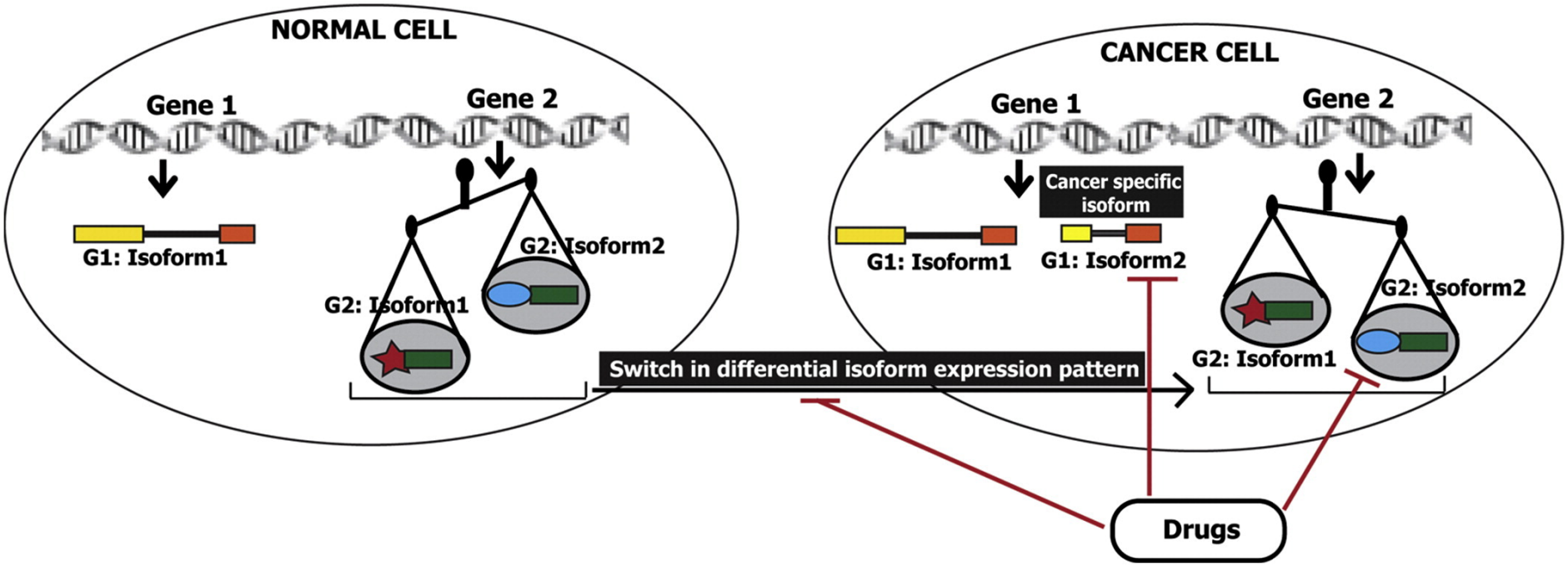
In human, 28k genes give 120k known transcripts (*Pal et al., 2012*)

Importance of alternative splicing



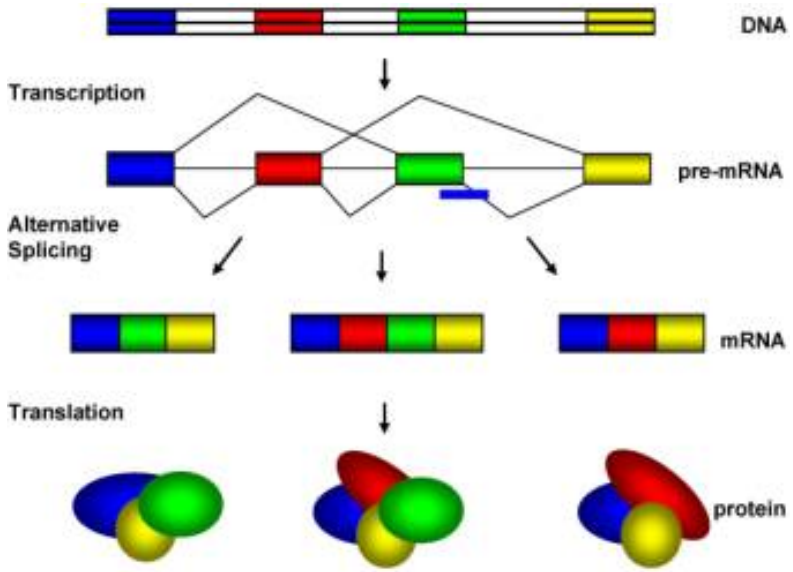
(*Pal et al., 2012*)

Opportunities for drug developments...



(*Pal et al., 2012*)

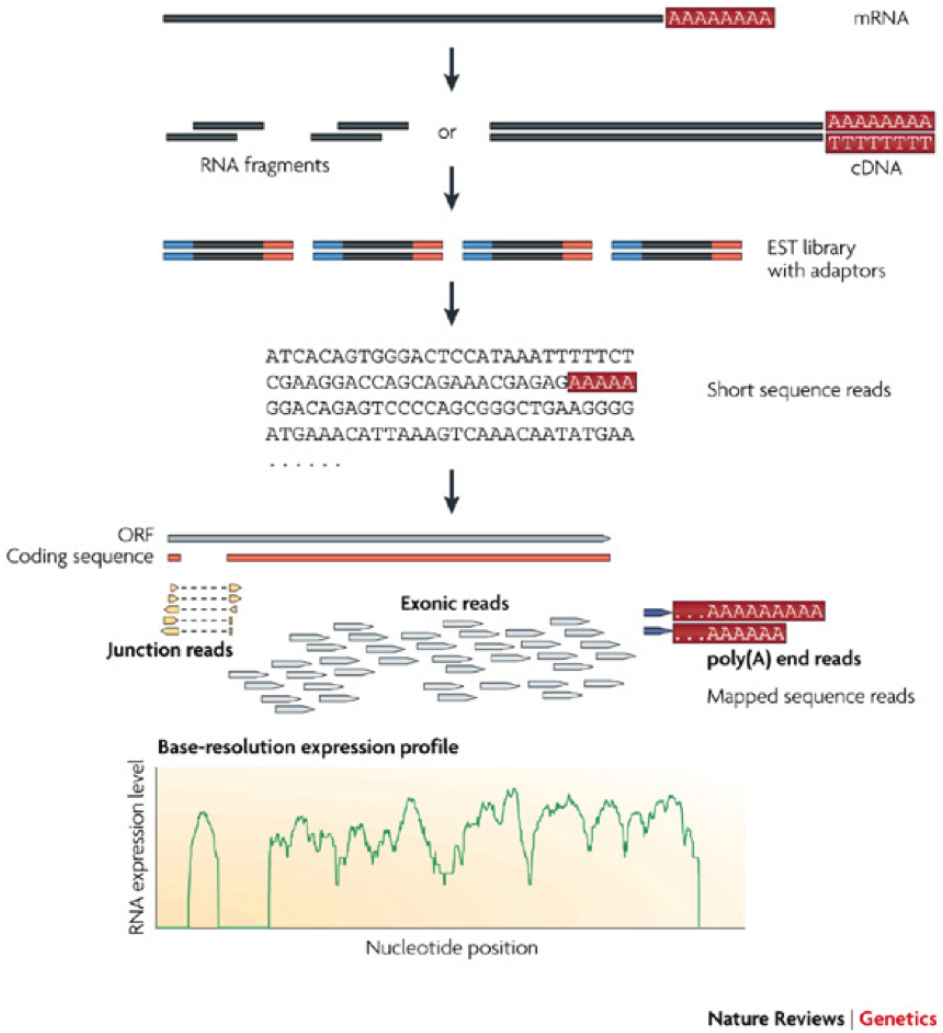
The isoform identification and quantification problem



Given a biological sample (e.g., cancer tissue), can we:

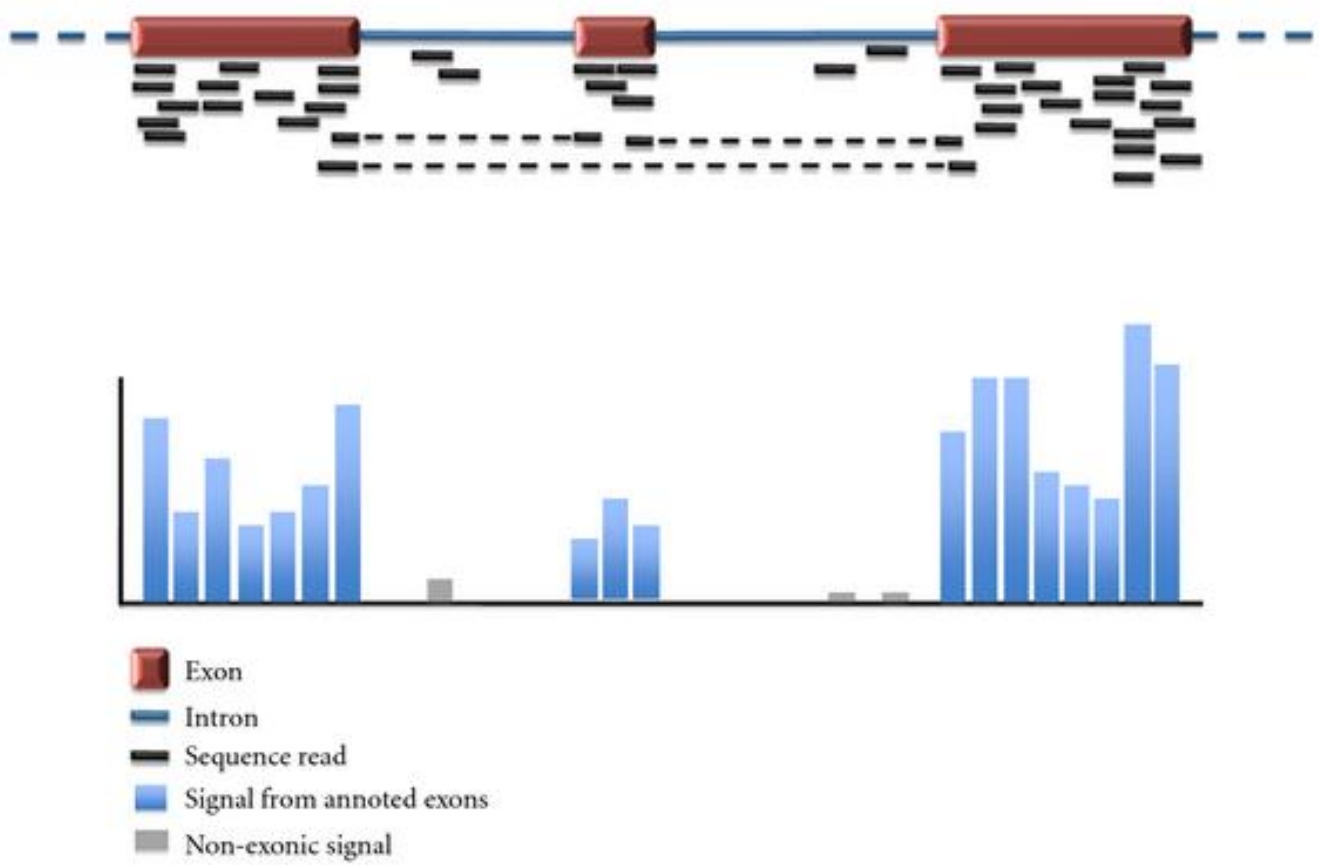
1. identify the isoform(s) of each gene present in the sample?
2. quantify their abundance?

RNA-seq measures mRNA abundance by sequencing short fragments



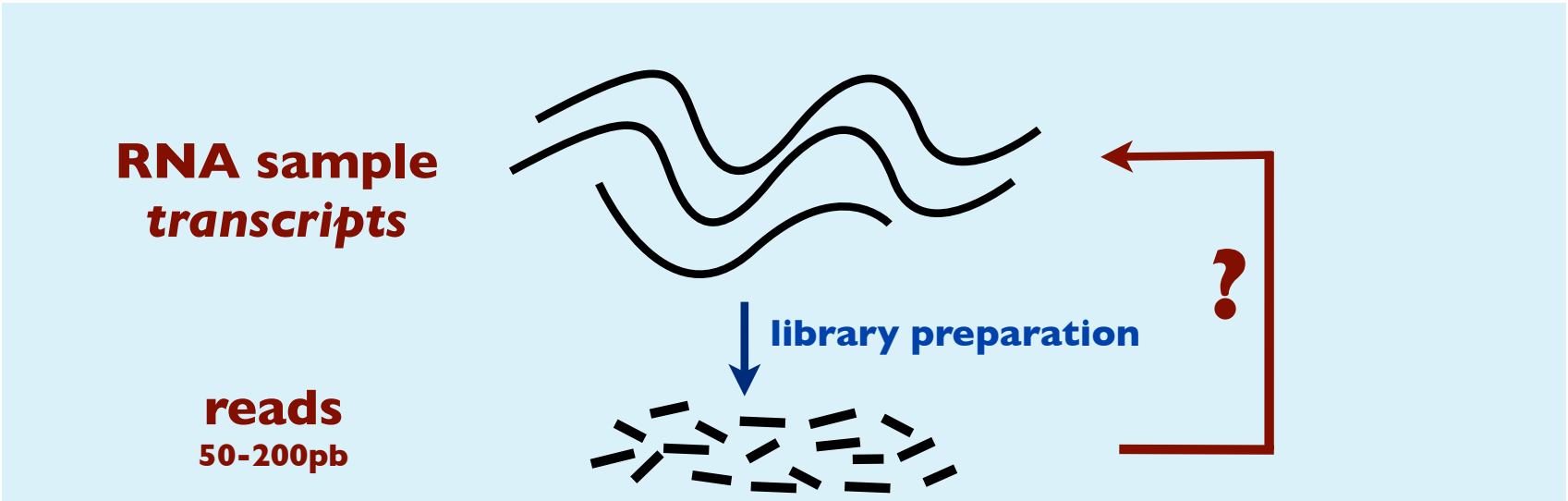
(*Wang et al., 2009*)

RNA-seq and alternative splicing



(Costa et al., 2011)

From RNA-seq to isoforms



Transcripts Quantification using annotations

- RQuant (Bohnert et al. 2009)
- FluxCapacitor (Montgomery et al. 2010)
- IsoEM (Nicolae et al. 2011)
- eXpress (Roberts et al. 2013)

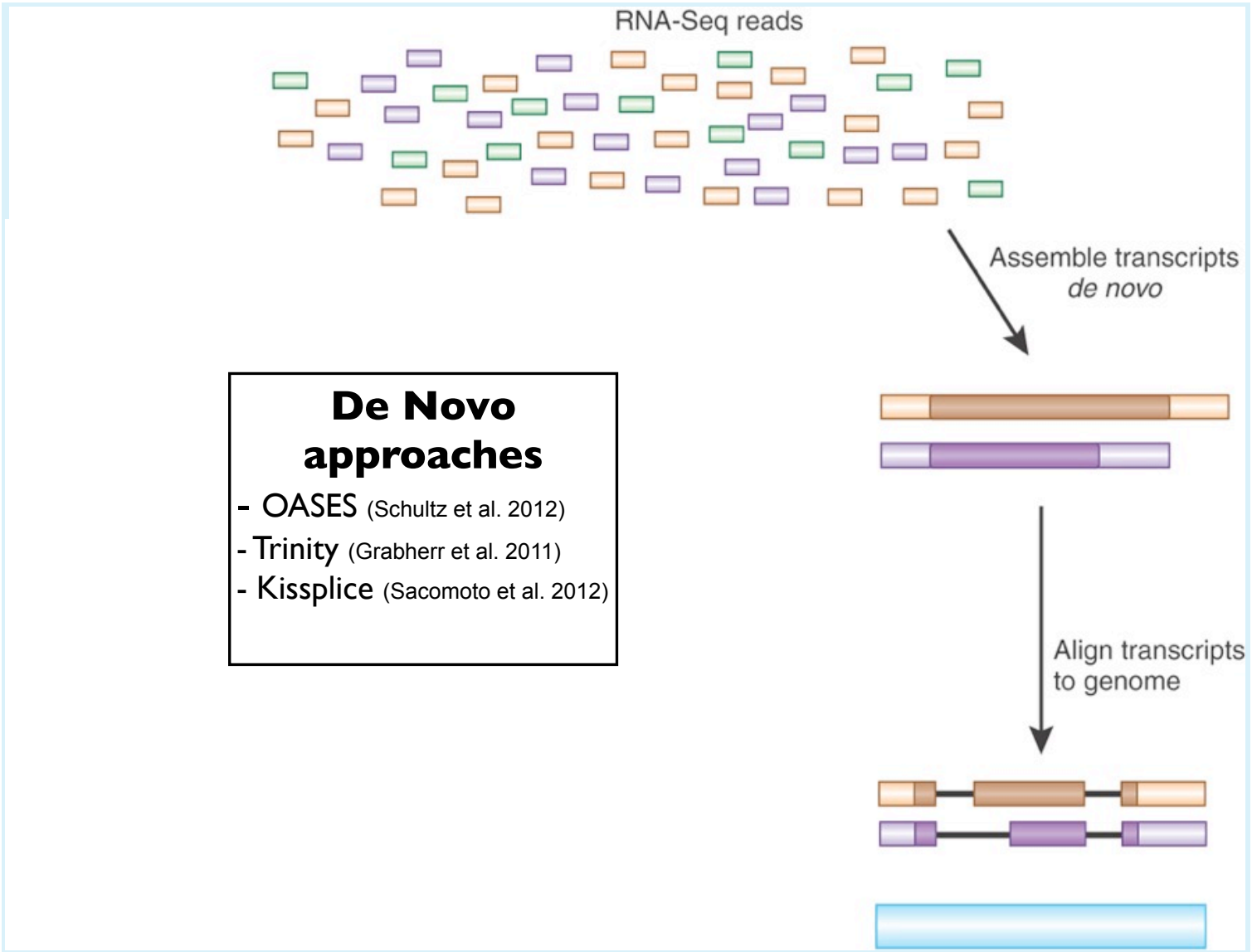
De Novo approaches

- OASES (Schultz et al. 2012)
- Trinity (Grabherr et al. 2011)
- Kissplice (Sacomoto et al. 2012)

Genome-based Transcripts Reconstruction

- Scripture (Guttman et al. 2010)
- Cufflinks (Trapnell et al. 2010)
- IsoLasso (Li et al. 2011a)
- NSMAP (Xia et al. 2011)
- SLIDE (Li et al. 2011b)
- iReckon (Mezlini et al. 2012)
- **FlipFlop**

De Novo methods



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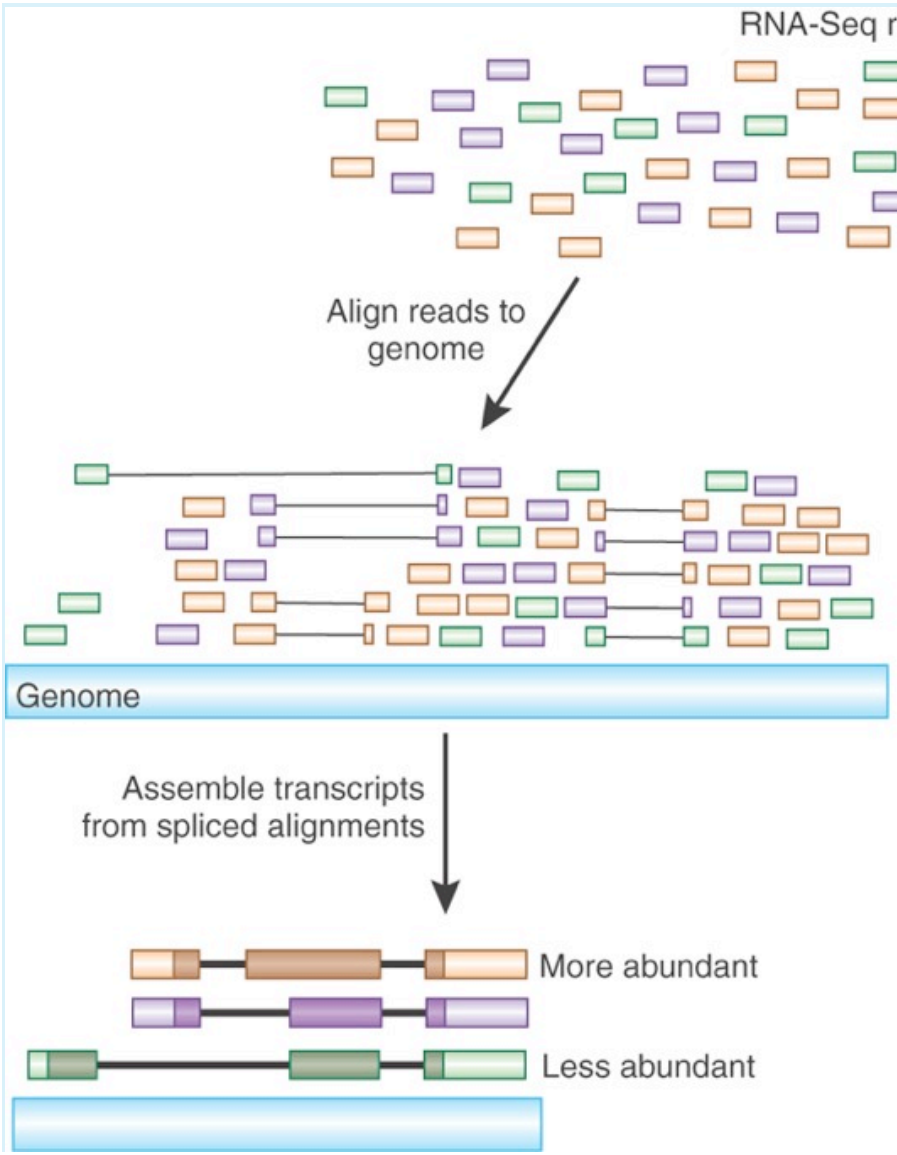
Genome-based methods



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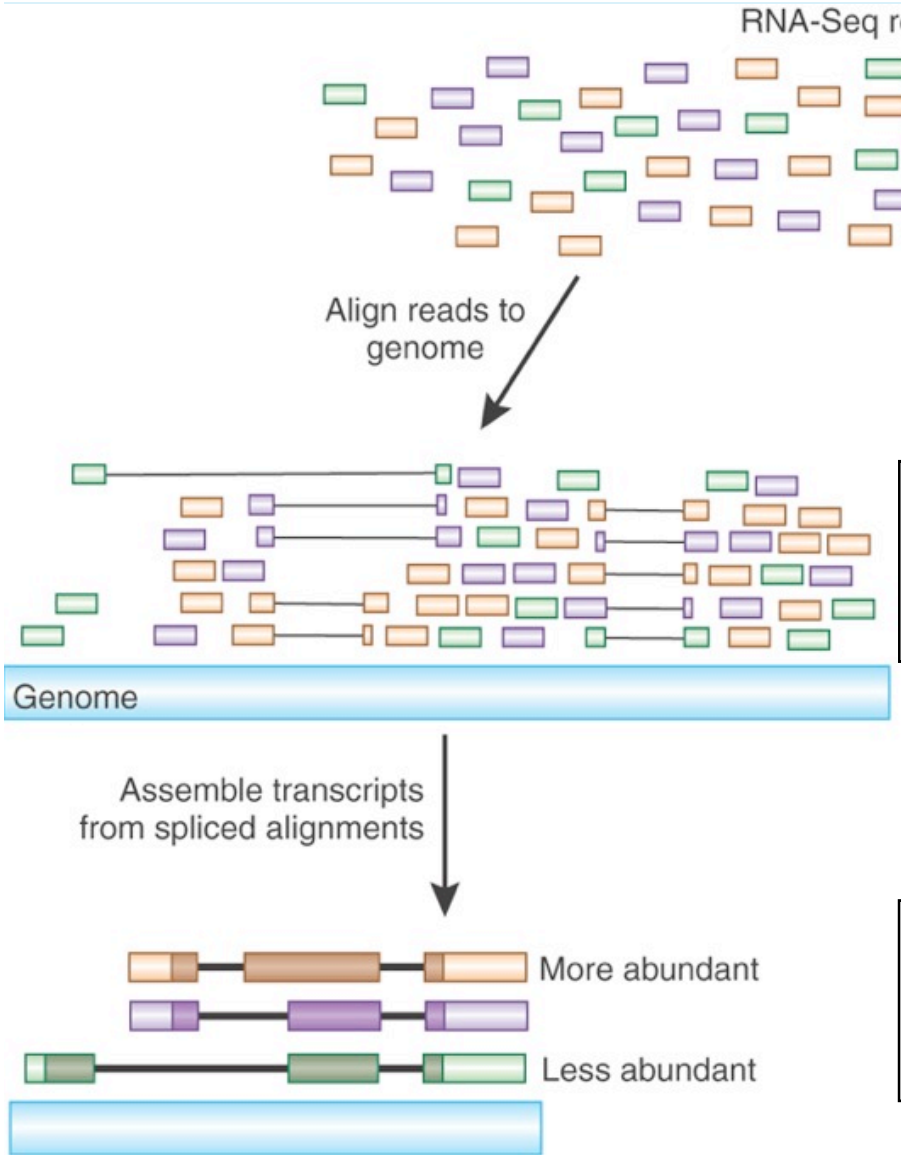
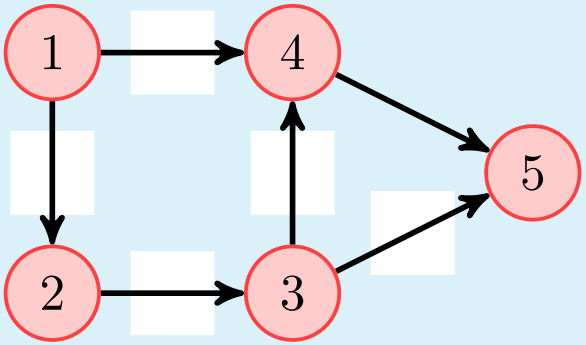
Genome-based



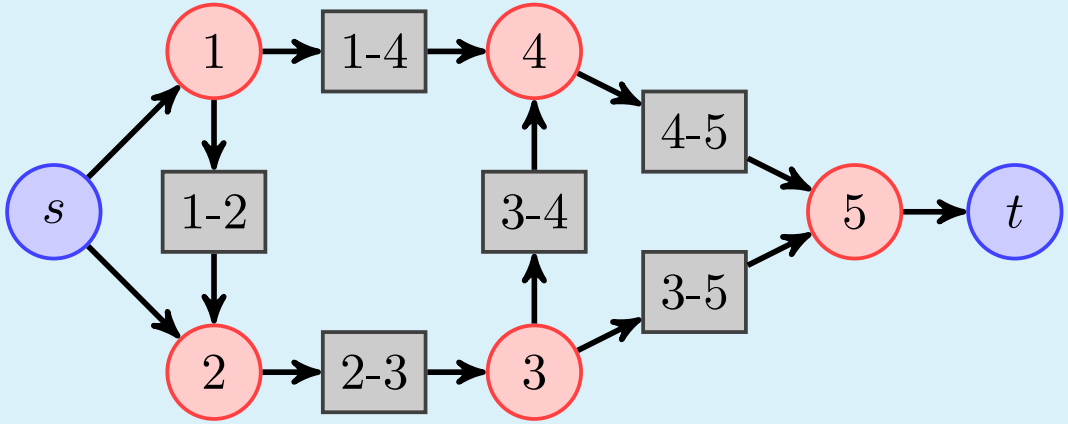
Input:
spliced alignment of reads against reference genome

Job:
reconstruct transcripts multi-assembly problem

Isoforms are Paths in a Graph



(a) Splicing graph for a gene with 5 exons.



(b) Graph G' with junctions, source s and sink t nodes.

- Cufflinks → *overlap graph*
- Scripture, IsoLasso → *connectivity graph*
- SLIDE, NSMAP, iReckon → *splicing graph*
- **FlipFlop → *'customized' splicing graph***

How to select a small number of paths?

n exons $\rightarrow\sim 2^n$ paths/candidate isoforms

$\sim$ 1000 candidates paths for 10 exons and $\sim$ 1000000 for 20 exons

Minimum Path Cover

- Cufflinks, IsoLasso.

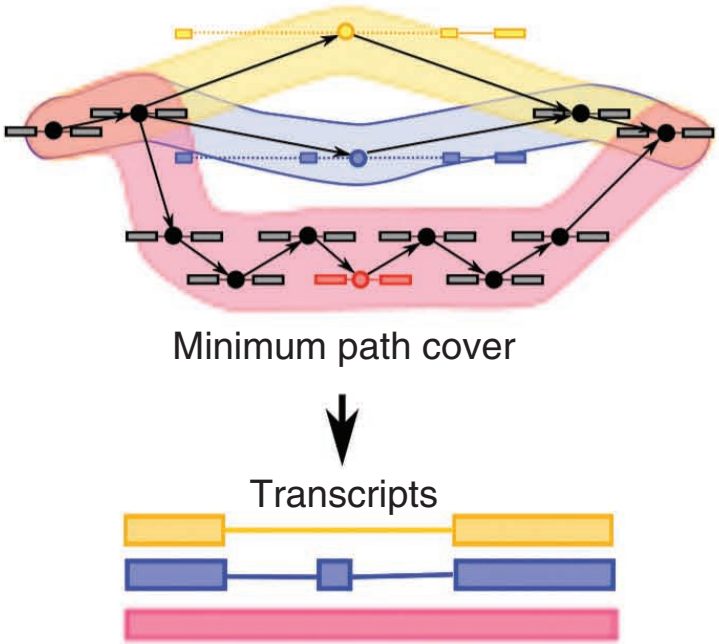
Regularization approaches

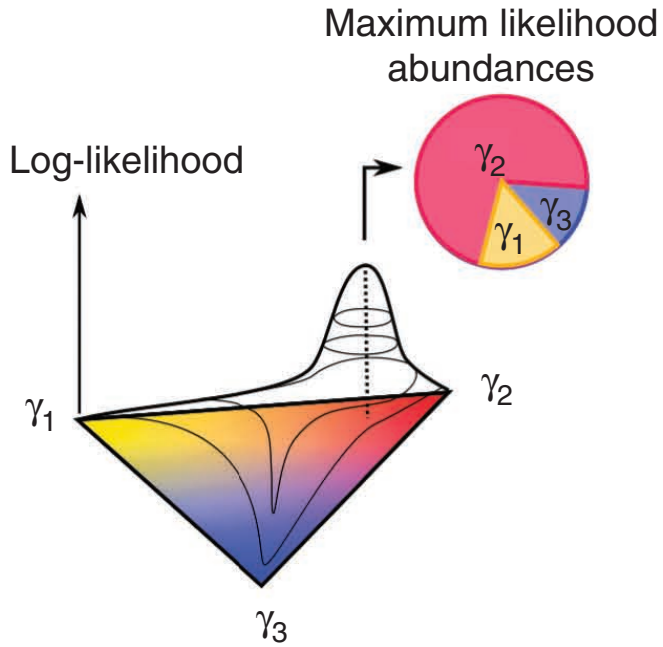
- NSMAP, SLIDE, iReckon, FlipFlop.

Cufflink strategy

A two-step approach:

1. Find a set of *minimal paths* in the graph (independently from the read abundance value) to identify a good set of isoforms
2. Estimate isoform abundance using read abundance





(*Trapnell et al., 2010)*

Regularization approach

- Suppose there are c candidate isoform (c large)
- Let ϕ the unknown c-dimensional vector of abundance
- Let $L(\phi)$ quantify whether ϕ explains well the observed read counts (e.g., minus log-likelihood)
- Regularization approach solve a problem:

$$\min_{\phi} L(\phi) \quad \text{such that} \quad \phi \text{ is sparse.}$$

Pros and cons of both paradigms

Separate identification and abundance estimation

- Find a small set of transcripts which covers all reads, *then* estimate ϕ.
- Cufflinks, Isolasso.

Simultaneous identification and abundance estimation

- Estimate sparse ϕ over set of all possible transcripts.
- NSMAP, SLIDE, iReckon, Flip-Flop

Pros and cons of both paradigms

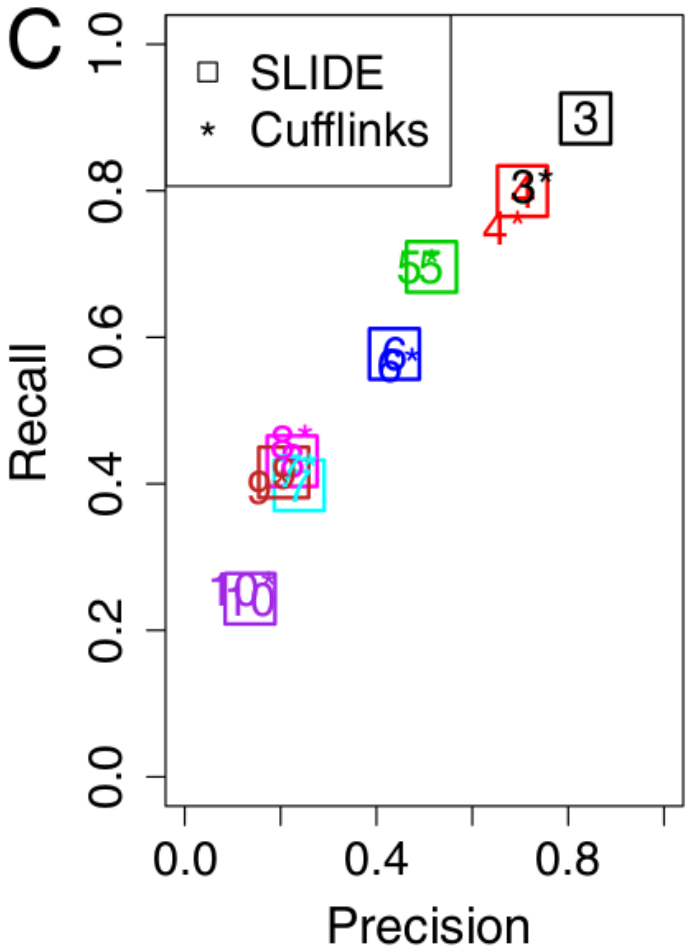
Separate identification and abundance estimation

- Find a small set of transcripts which covers all reads, *then* estimate ϕ.
- Cufflinks, Isolasso.
- Pros : fast.
- Cons : loss of power.

Simultaneous identification and abundance estimation

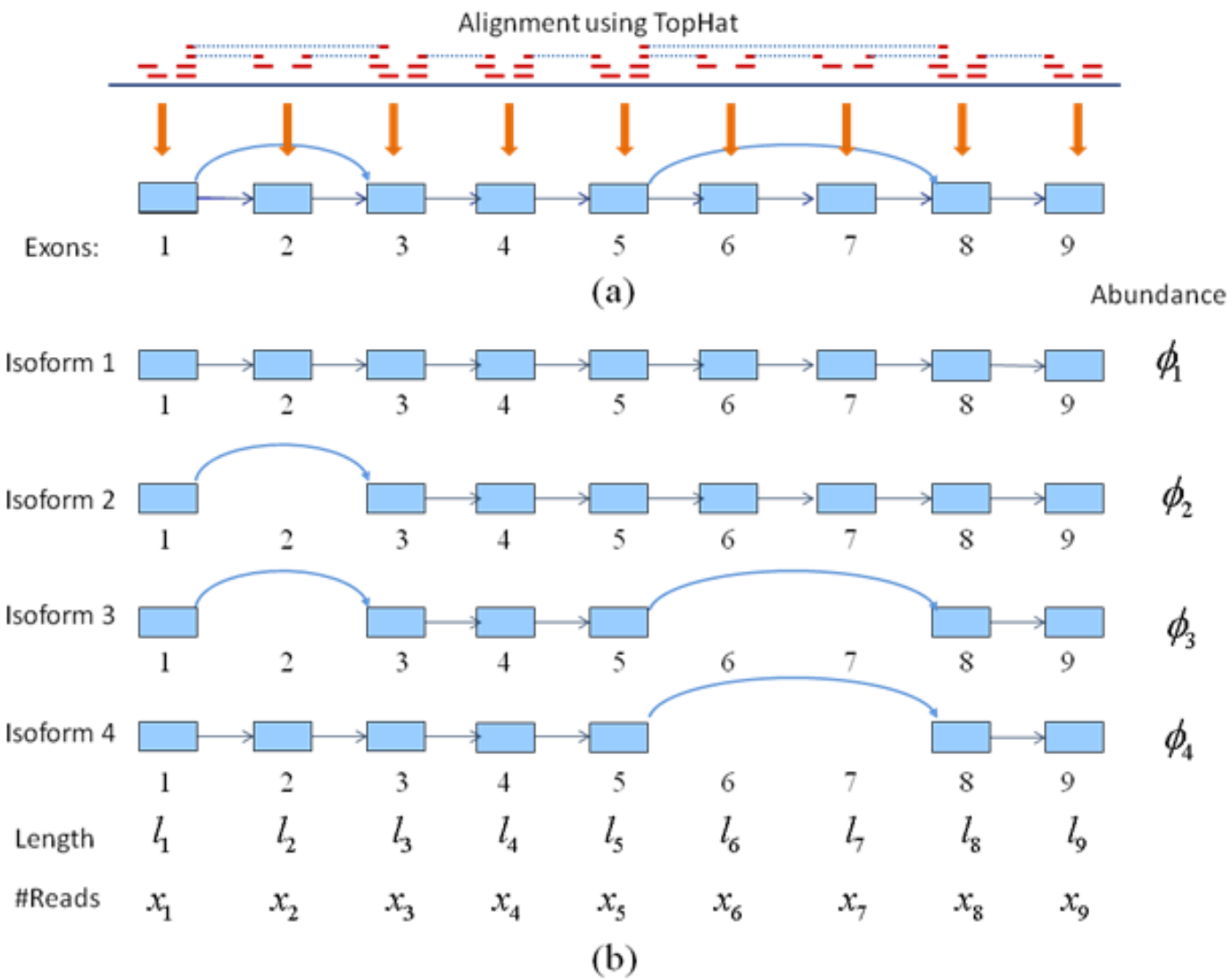
- Estimate sparse ϕ over set of all possible transcripts.
- NSMAP, SLIDE, iReckon, Flip-Flop
- Pros : More powerful.
- Cons : Exponential complexity (up to $2^n - 1$ candidates).

Simultaneous identification and abundance estimation : more power



(Li et al., 2011)

The isoform deconvolution problem



(Xia et al., 2011)

More formally

e exons, n "bins" (exons+junctions)
c candidate isoforms (up to $2^e - 1$)
$\phi \in \mathbb{R}_+^c$ the vector of abundance of isoforms (unknown!)
U binary matrix:

$$
\begin{array}{c}
 \\
\mathit{isoform}_1 \\
\mathit{isoform}_2 \\
\vdots \\
\mathit{isoform}_c
\end{array}
\begin{array}{c}
\begin{array}{ccccccc}
\mathit{exon}_1 & \cdots & \mathit{exon}_e & \mathit{junction}_{1,2} & \cdots & \mathit{junction}_{e_1,e}
\end{array} \\
\begin{pmatrix}
1 & \cdots & 1 & 1 & \cdots & 1 \\
1 & \cdots & 0 & 1 & \cdots & 0 \\
 & \cdots & & & \cdots & \\
0 & \cdots & 1 & 0 & \cdots & 0
\end{pmatrix}
\end{array}
$$

$U^\top \phi$ the abundance of each exon/junction.

Goal: estimate ϕ from the observed reads on each exon/junction

Regularization approach

- The log likelihood of $\phi \in \mathbb{R}^c$ only depends on the abundance of each exon/junction in $U^\top \phi \in \mathbb{R}^n$
- Example: Gaussian (IsoLasos, SLIDE) or Poisson (NSMAP, FlipFlop) negative log-likelihood
- Regularization-based approaches try to solve:

$$\min_{\phi \in \mathbb{R}^c} R(U^\top \phi) \quad \text{such that} \quad \phi \text{ is sparse,}$$

where $R : \mathbb{R}^n \to \mathbb{R}$ is convex

- This is generally a NP-hard problem, so we use a convex relaxation akin to Lasso regression

The Lasso idea

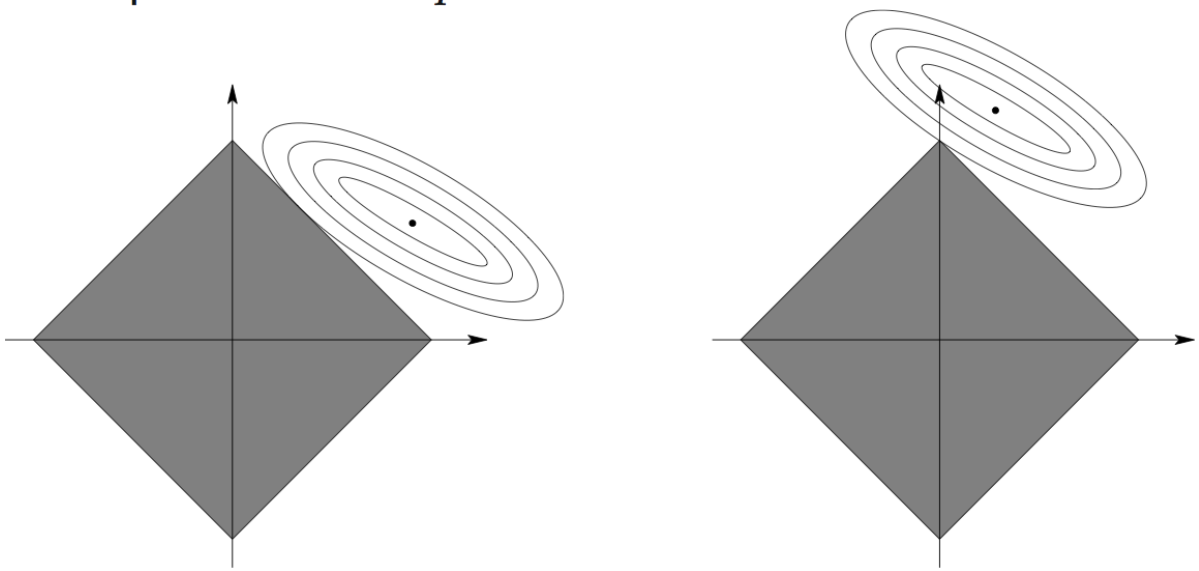
The ℓ_1 penalty (Tibshirani, 1996; Chen et al., 1998)

If $R(\beta)$ is convex and "smooth", the solution of

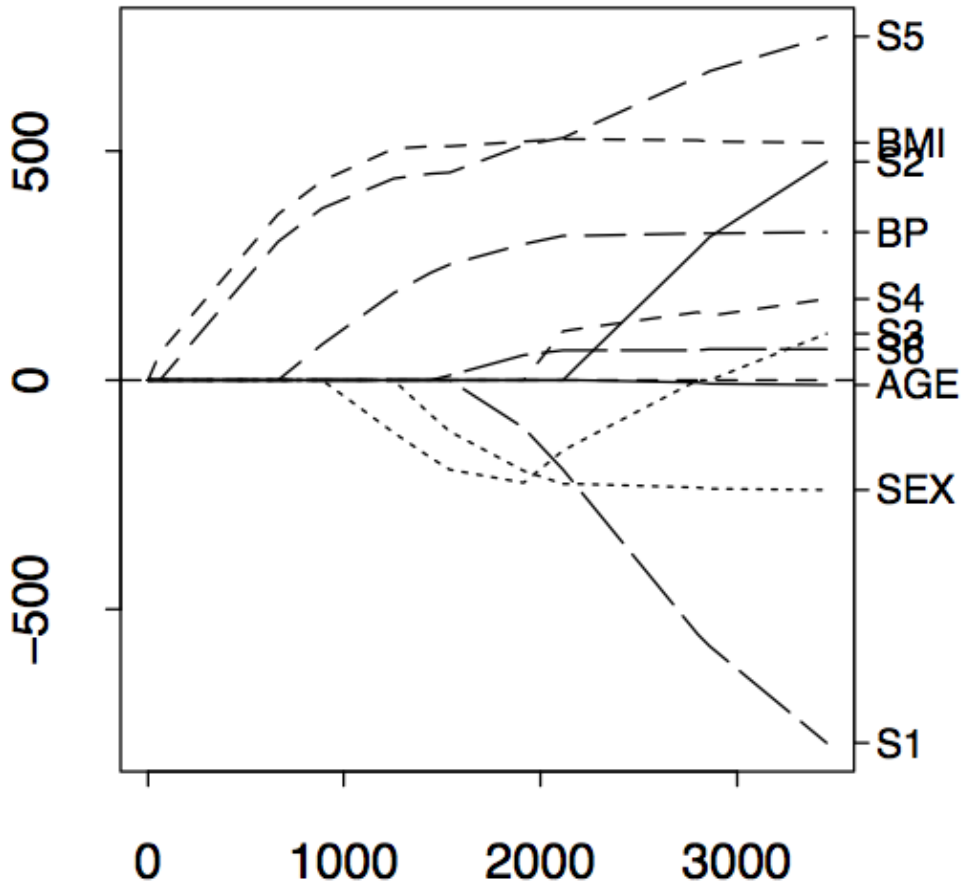
$$\min_{\beta \in \mathbb{R}^p} R(\beta) + \lambda \sum_{i=1}^{p} |\beta_i|$$

is usually sparse.

Geometric interpretation with $p = 2$



Lasso example



Typically solved in $O(n^3)$

Isoform deconvolution with the Lasso

Estimate ϕ sparse by solving (IsoLasso, NSMAP, SLIDE):

$$\min_{\phi \in \mathbb{R}^c_+} R(U^\top \phi) + \lambda \| \phi \|_1$$

Complexity $O(c^3) = O(2^{3e})$...

Works well BUT computationally challenging to work with all candidate isoforms for large genes!

Fast isoform deconvolution with the Lasso (FlipFlop)

Theorem (Bernard, Mairal, Jacob and V., 2012)

The isoform deconvolution problem

$$\min_{\phi \in \mathbb{R}_+^c} R(U^\top \phi) + \lambda \| \phi \|_1$$

can be solved in polynomial time in the number of exon.

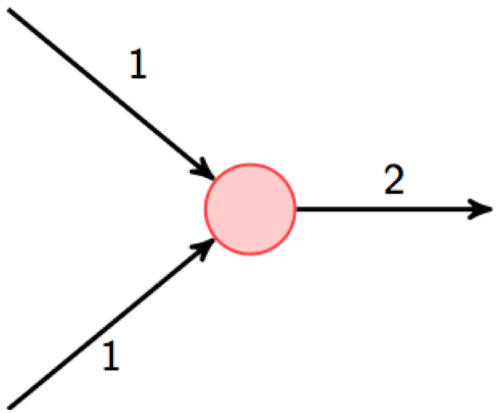
Key ideas

1. $U^\top \phi$ corresponds to a flow on the graph
2. Reformulation as a convex cost flow problem (Mairal and Yu, 2012)
3. Recover isoforms by flow decomposition algorithm

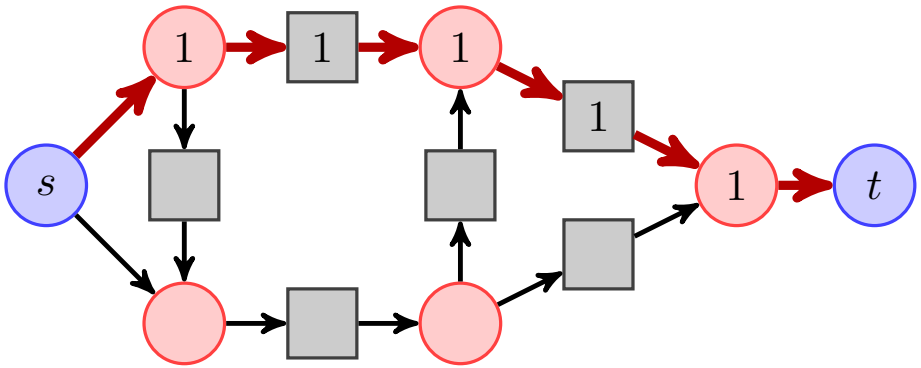
"Feature selection on an exponential number of features in polynomial time"

Flow concept

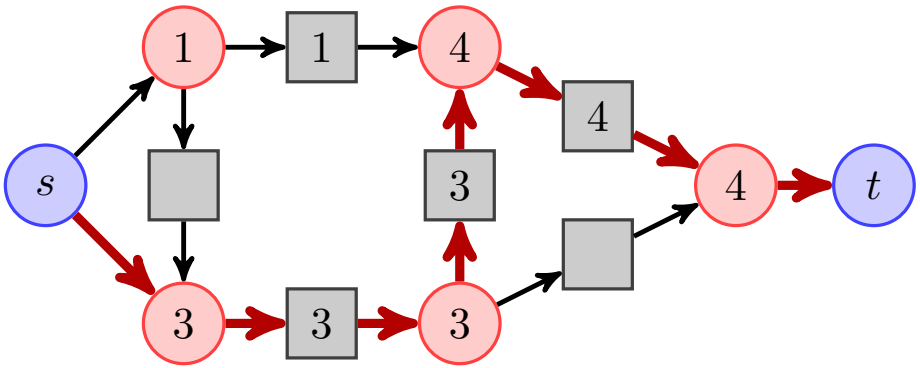
A **flow** f is a nonnegative function on arcs that respects conservation constraints (Kirchhoff's law)



Combinations of isoforms are flows



(a) Reads at every node corresponding to one isoform.

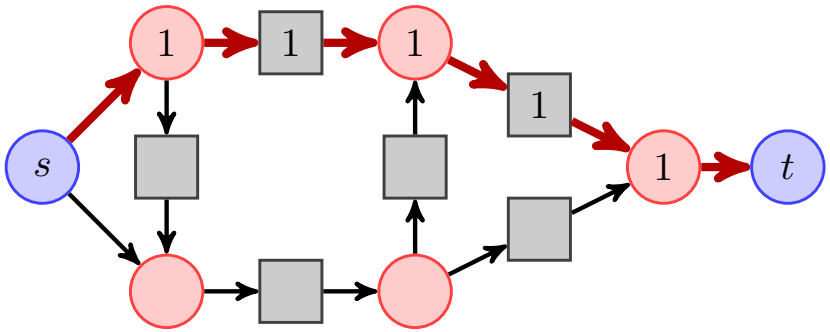


(b) Reads at every node after adding another isoform.

- **Linear combinations of isoforms** $\Rightarrow$ **Flow value on every nodes**
- **Flow value on every nodes** $\Rightarrow$ **Paths with given value/abundance**

Flow Decomposition
(linear time algorithm)

From isoforms to flow (key trick!)



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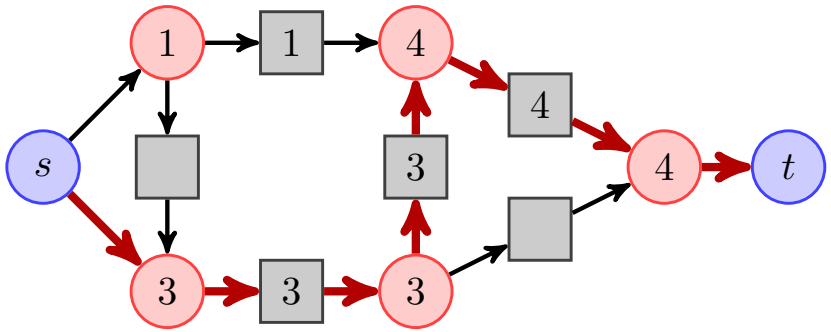


(b) Reads at every node after adding another isoform.

- $U^\top \phi \in \mathbb{R}^n$ when $\phi \in \mathbb{R}^c$ is the set of flows
- Moreover, $||\phi||_1 = f_t$!

Therefore,

$$\min_{\phi \in \mathbb{R}^c_+} R(U^\top \phi) + \lambda \| \phi \|_1$$

is equivalent to

$$\min_{\text{f flow}} R(f) + \lambda f_t$$

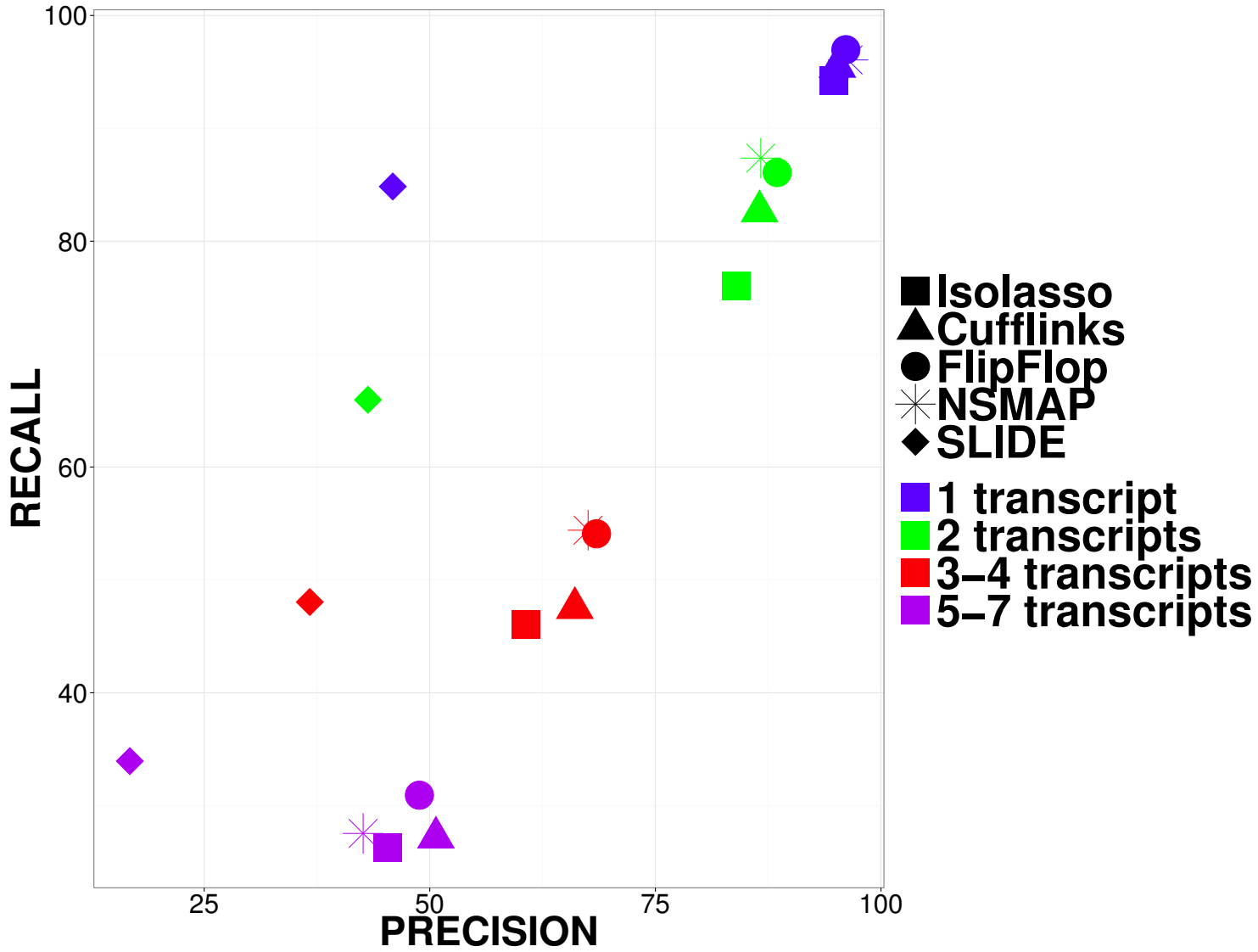
Summary

$$\min_{\phi \in \mathbb{R}^c_+} R(U^\top \phi) + \lambda \| \phi \|_1$$

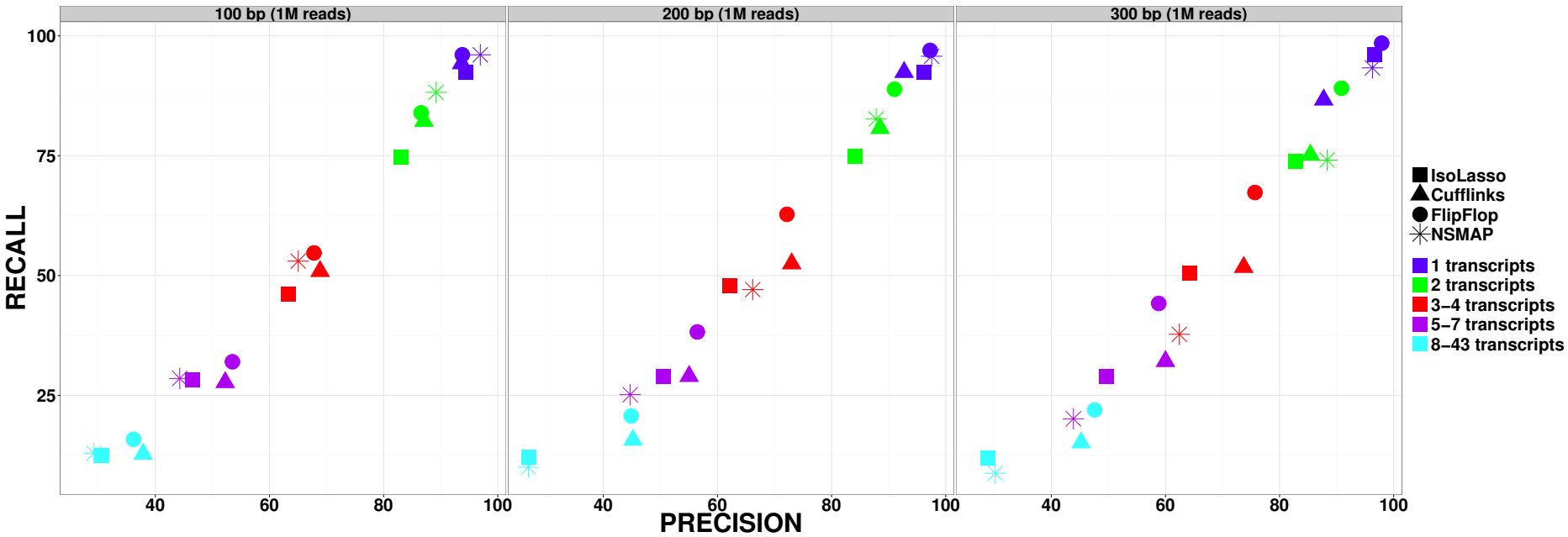
- Cufflink : *a priori* selection of isoforms (minimum graph cover)
- IsoLasso : pre-filtering of candidate isoforms using various heuristics
- NSMAP, SLIDE : limit the maximum number of exons
- FlipFlop : exact optimization without pre-filtering in polynomial time, by solving a convex problem in the space of flows (dimension n) and recovering path with the flow decomposition algorithm.

Human Simulation: Precision/Recall

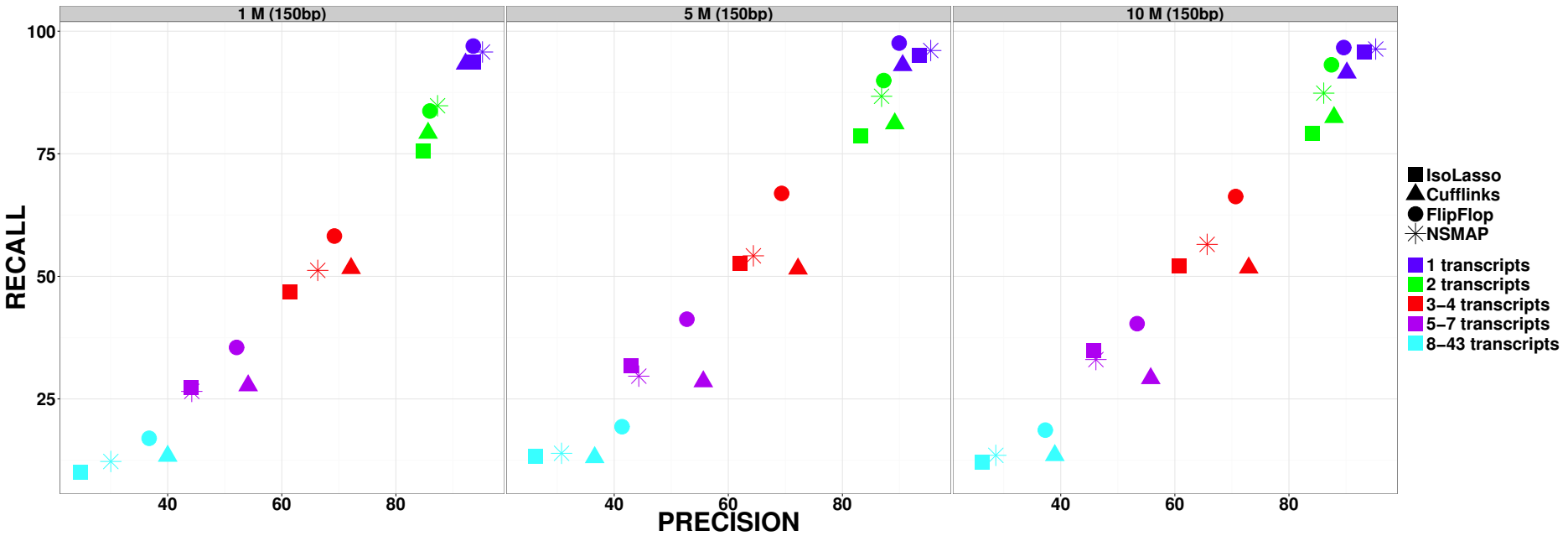
hg19, 1137 genes on chr1, 1million 75 bp single-end reads by transcript levels.
Simulator: `http://alumni.cs.ucr.edu/~liw/rnaseqreadsimulator.html`



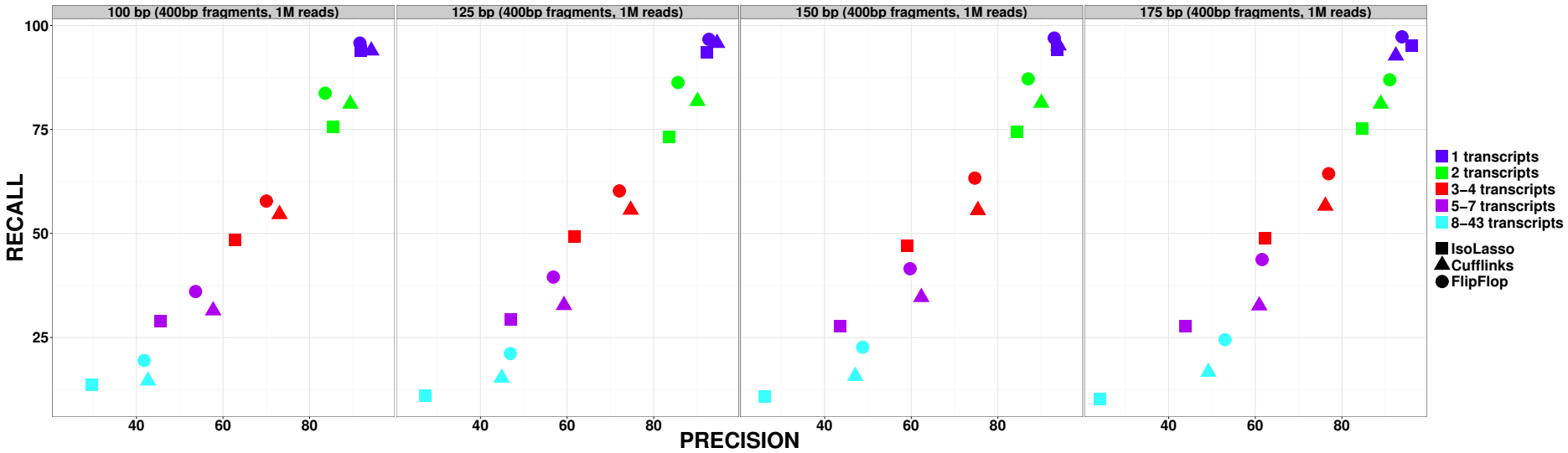
Performance increases with read length



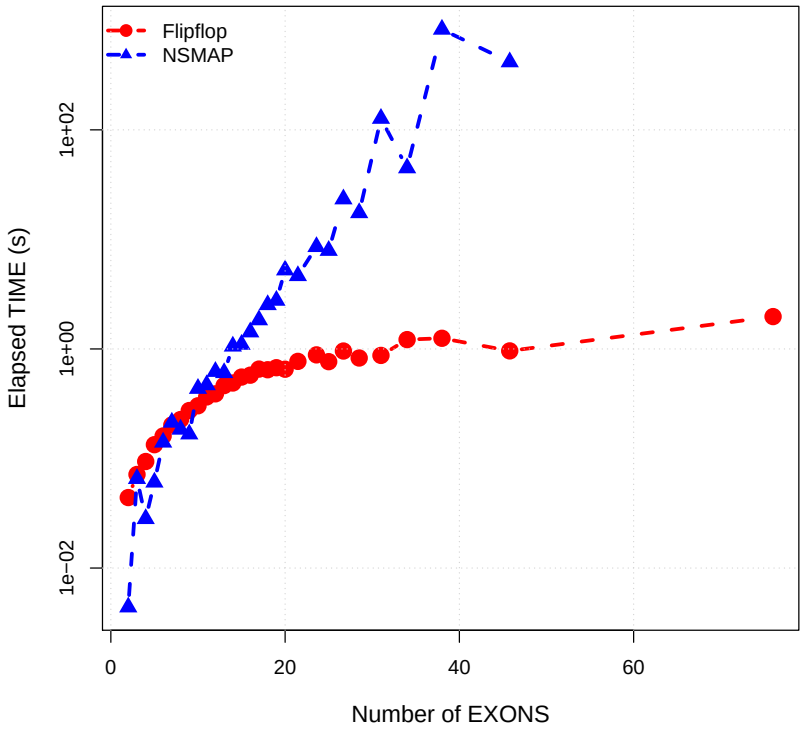
Performance increases with coverage

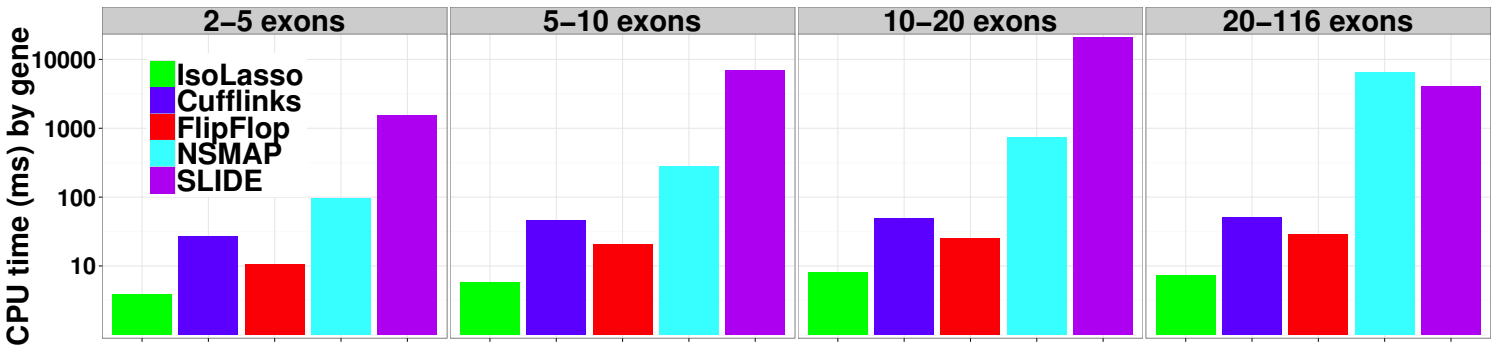


Extension to paired-end reads OK.



Speed trial


Flipflop
NSMAP
Elapsed TIME (s)
1e+02
1e+00
1e−02
0
20
40
60
Number of EXONS


2–5 exons
5–10 exons
10–20 exons
20–116 exons
CPU time (ms) by gene
10000
1000
100
10
IsoLasso
Cufflinks
FlipFlop
NSMAP
SLIDE

Conclusion

http://cbio.mines-paristech.fr/flipflop

Summmary

- Transcript selection over all possible candidates is hard.
- We show the problem is equivalent to a simpler one.
- With our approach, the full problem is solved as quickly as the more heuristic one (Cufflinks approach).

Future work

- Some loose ends : GC content, decomposition, post-processing...
- Ongoing : abundance estimation comparison.
- Adapt framework to paired-end reads,
- Applications : differential expression, classification, clustering.

Acknowledgements

Elsa Bernard (Mines ParisTech / Institut Curie), Laurent Jacob (UC Berkeley / CNRS), Julien Mairal (INRIA)

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