Graphs and polytopes: learning Bayesian networks with LP relaxations

Tommi Jaakkola MIT CSAIL

based on joint work with David Sontag, MIT Amir Globerson, HUJI Marina Meila, U Washington

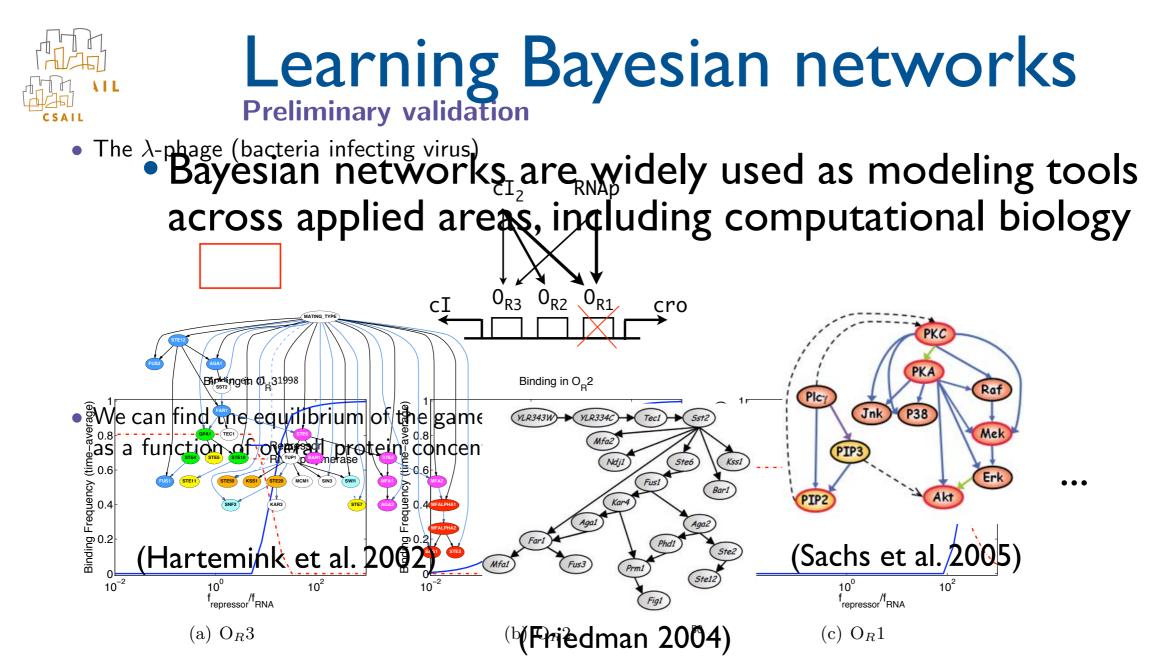


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Discussion 7 Wednesday, March 10, 2010

References

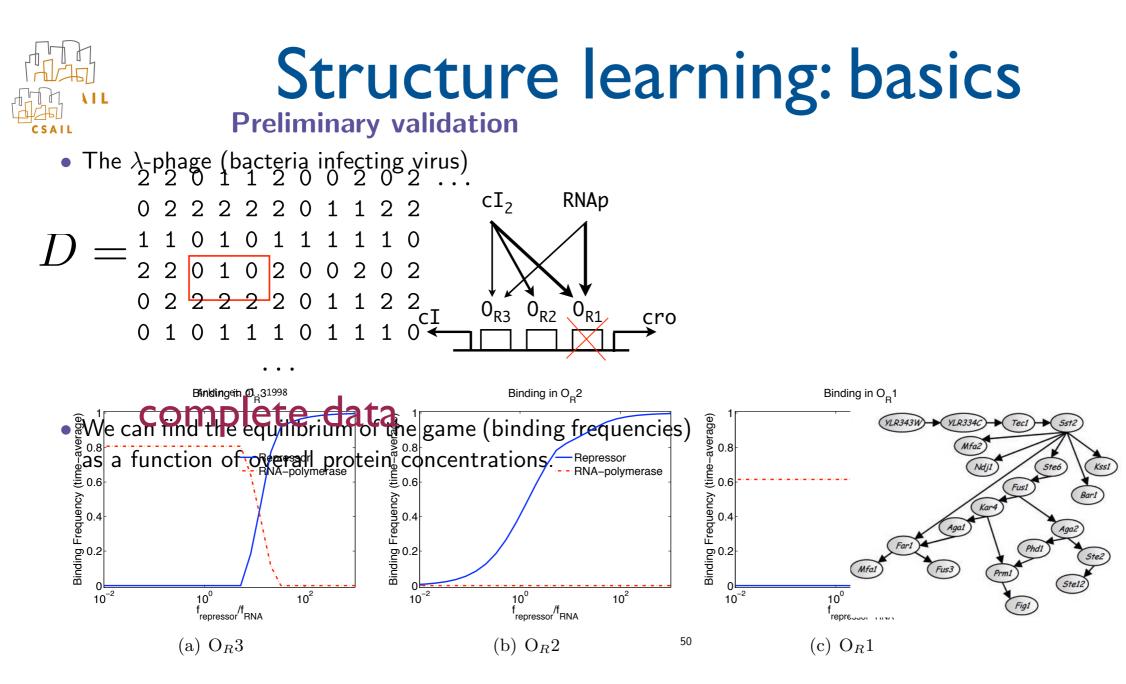


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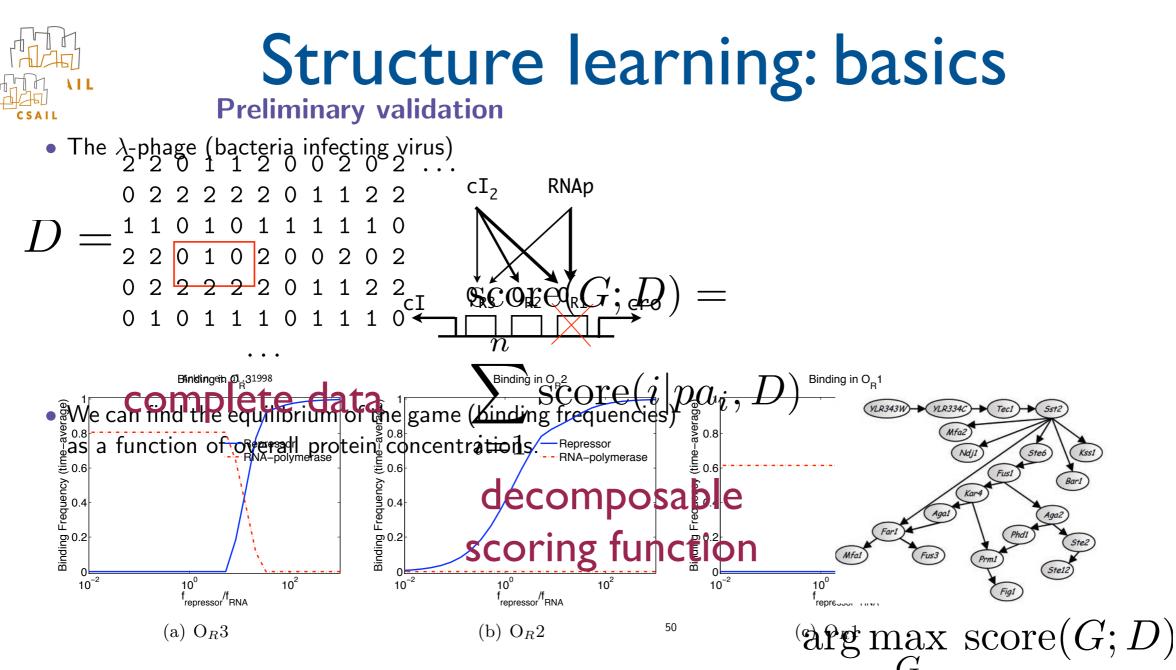


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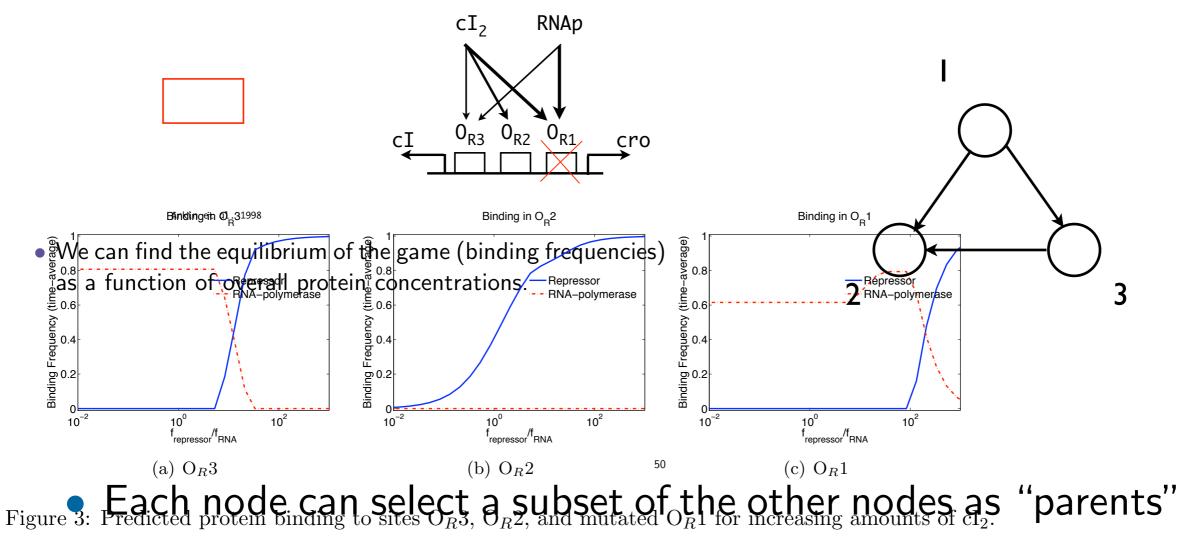
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References

Structure learning as inference

Preliminary validation

• The λ -phage (bacteria infecting virus)



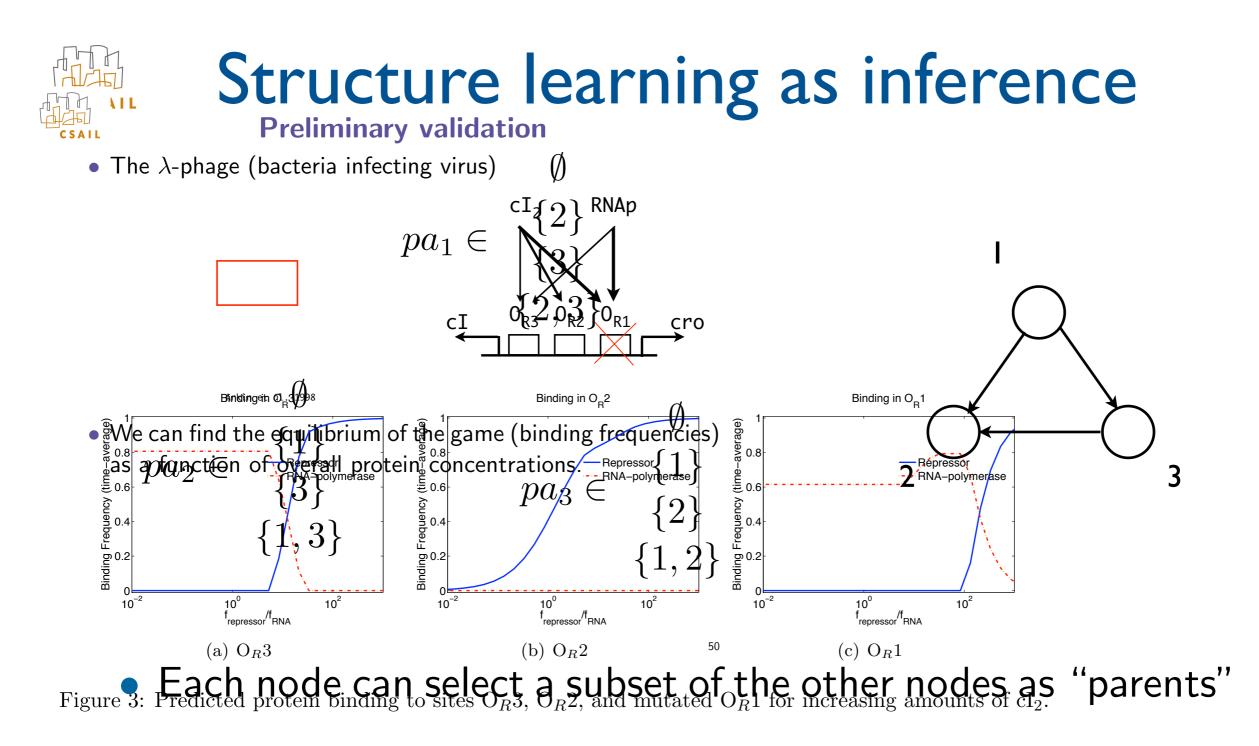
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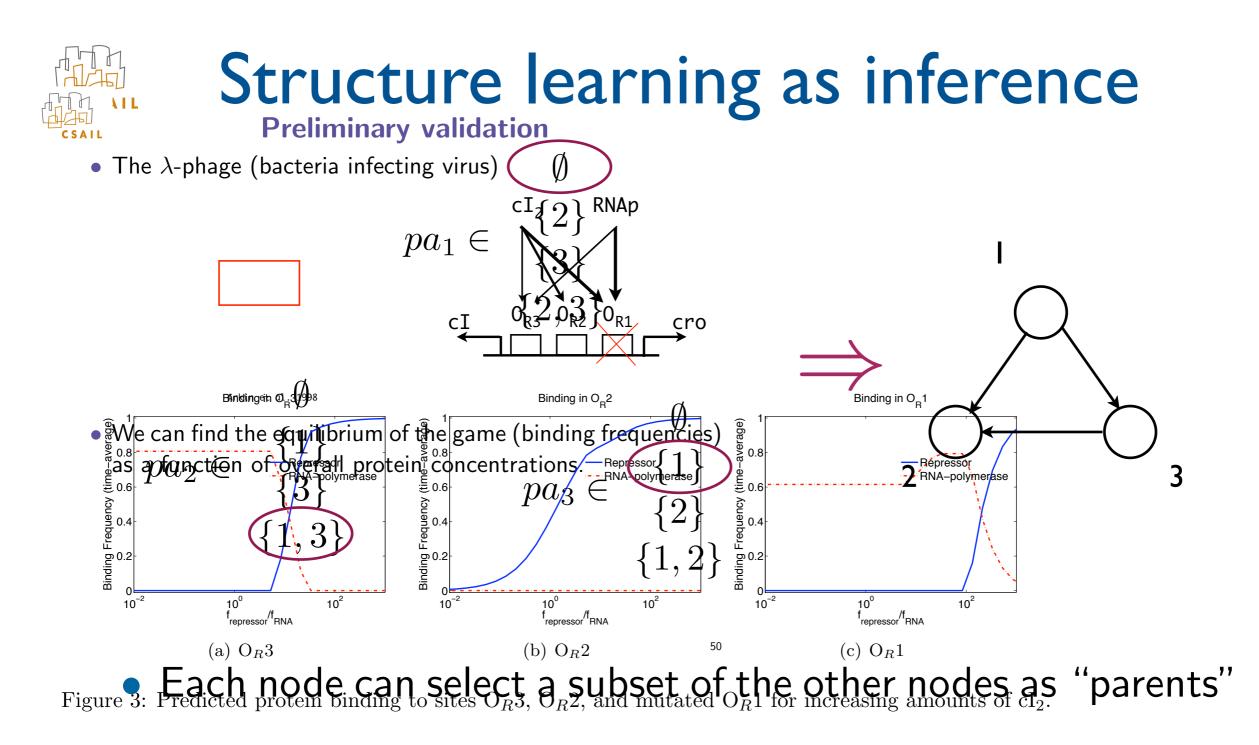
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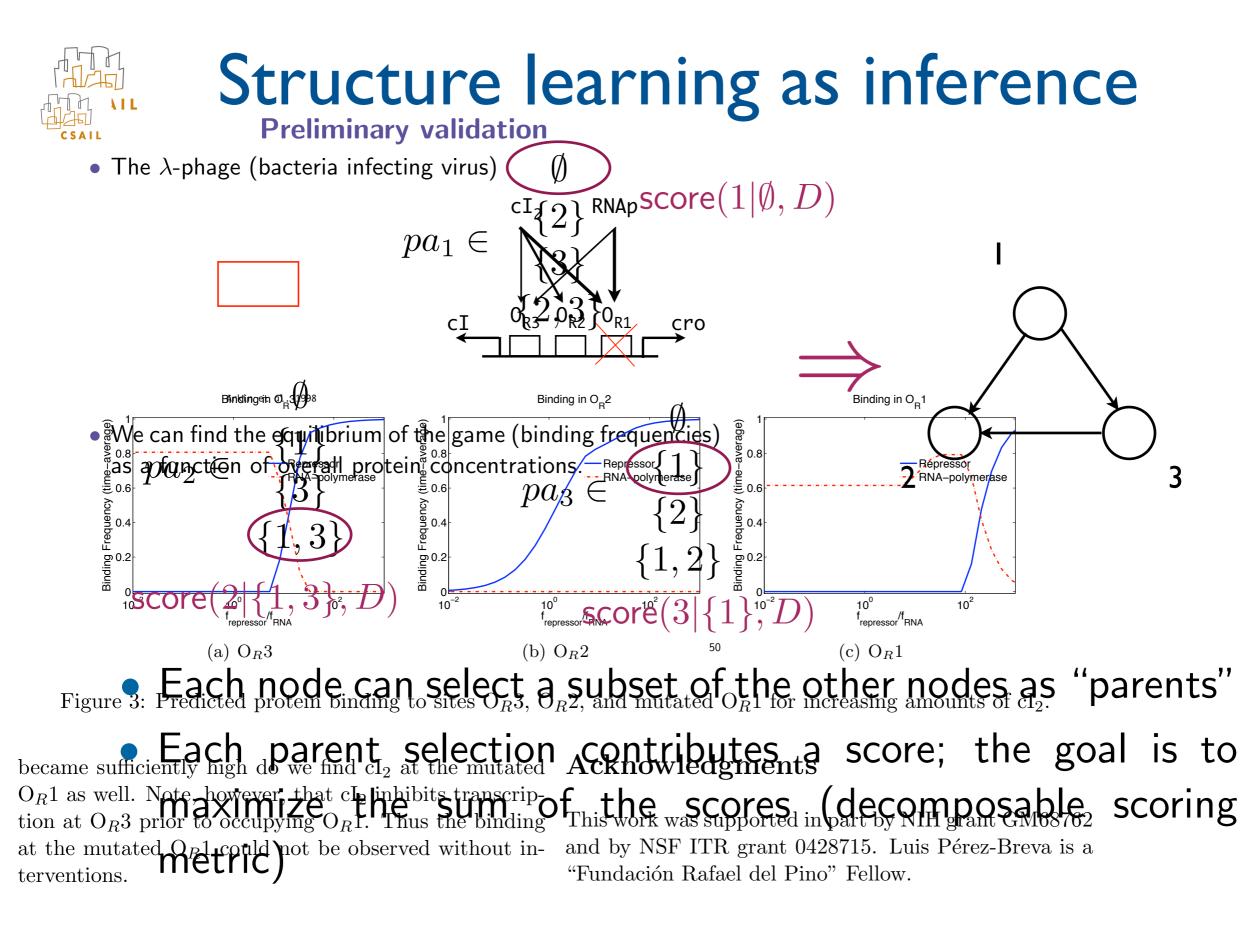
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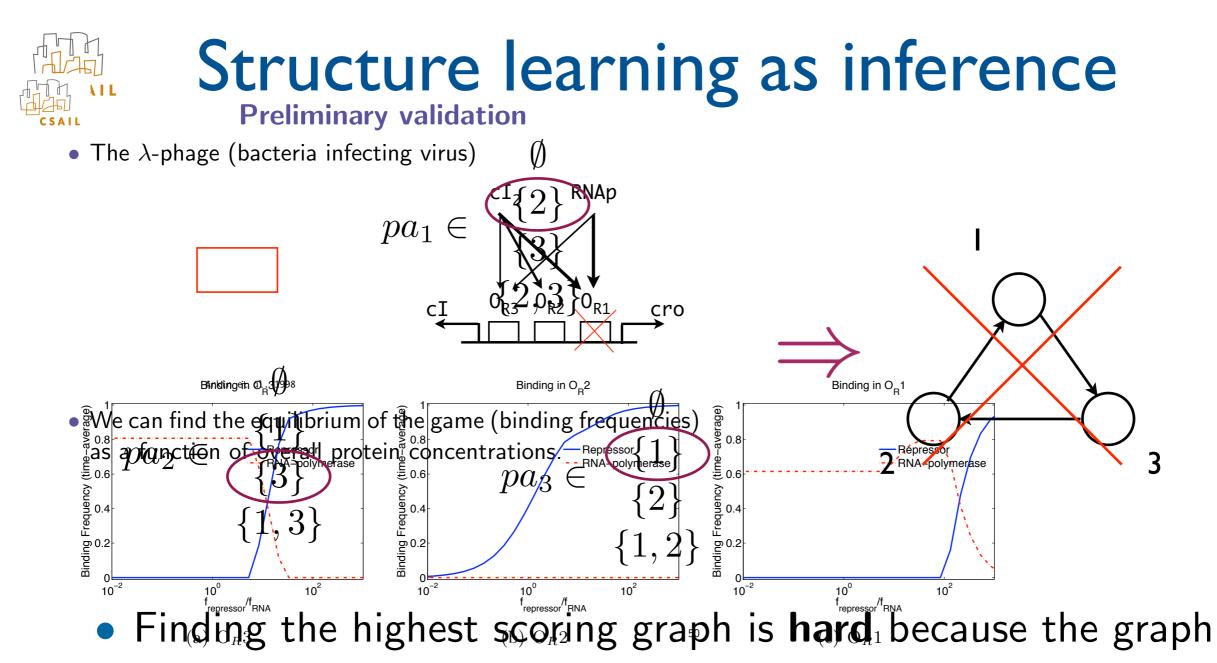


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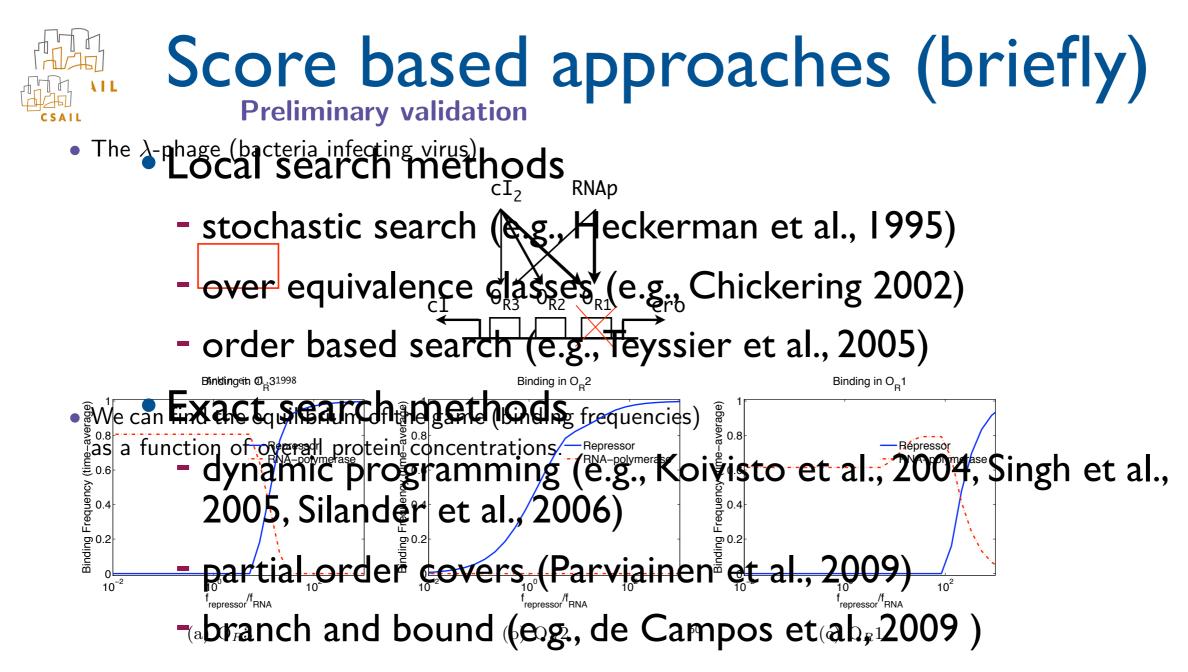


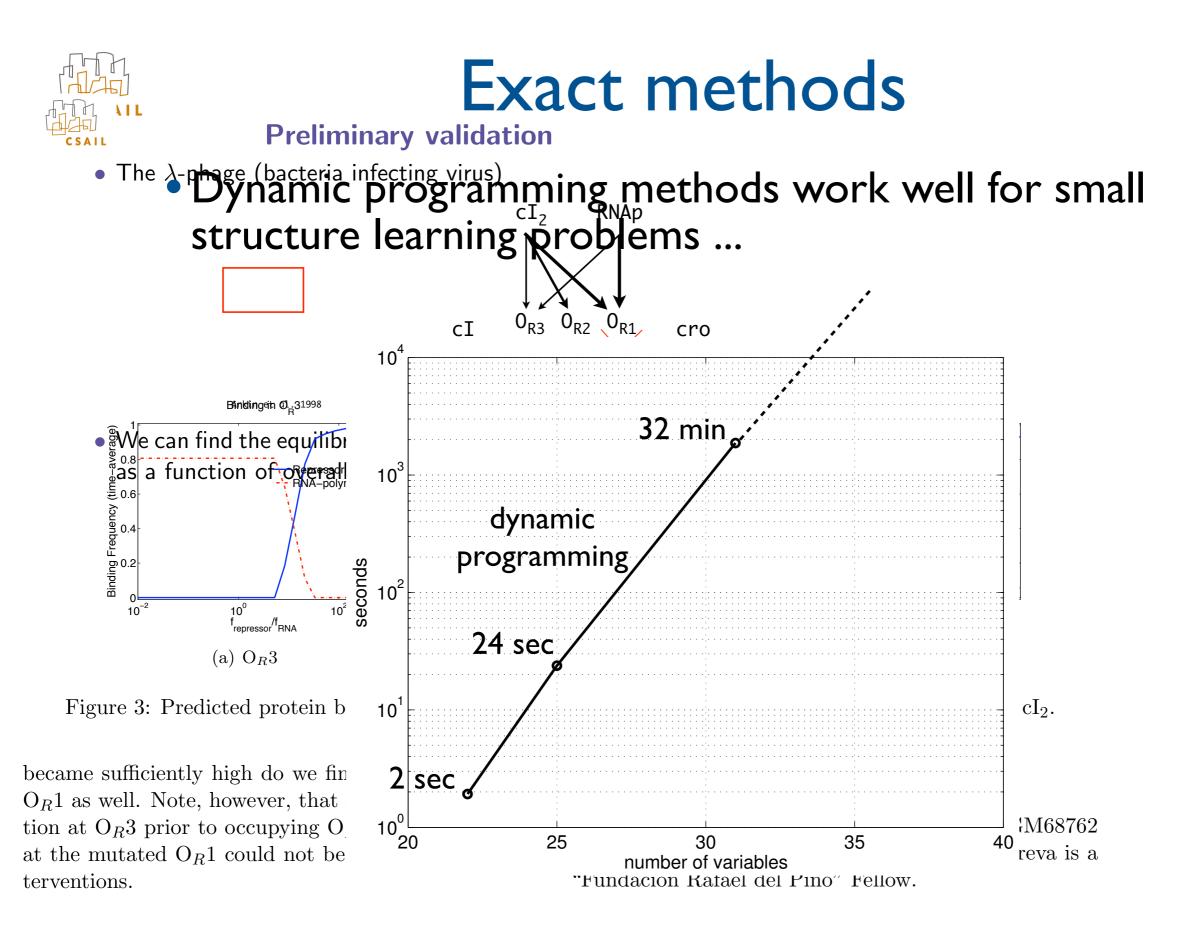
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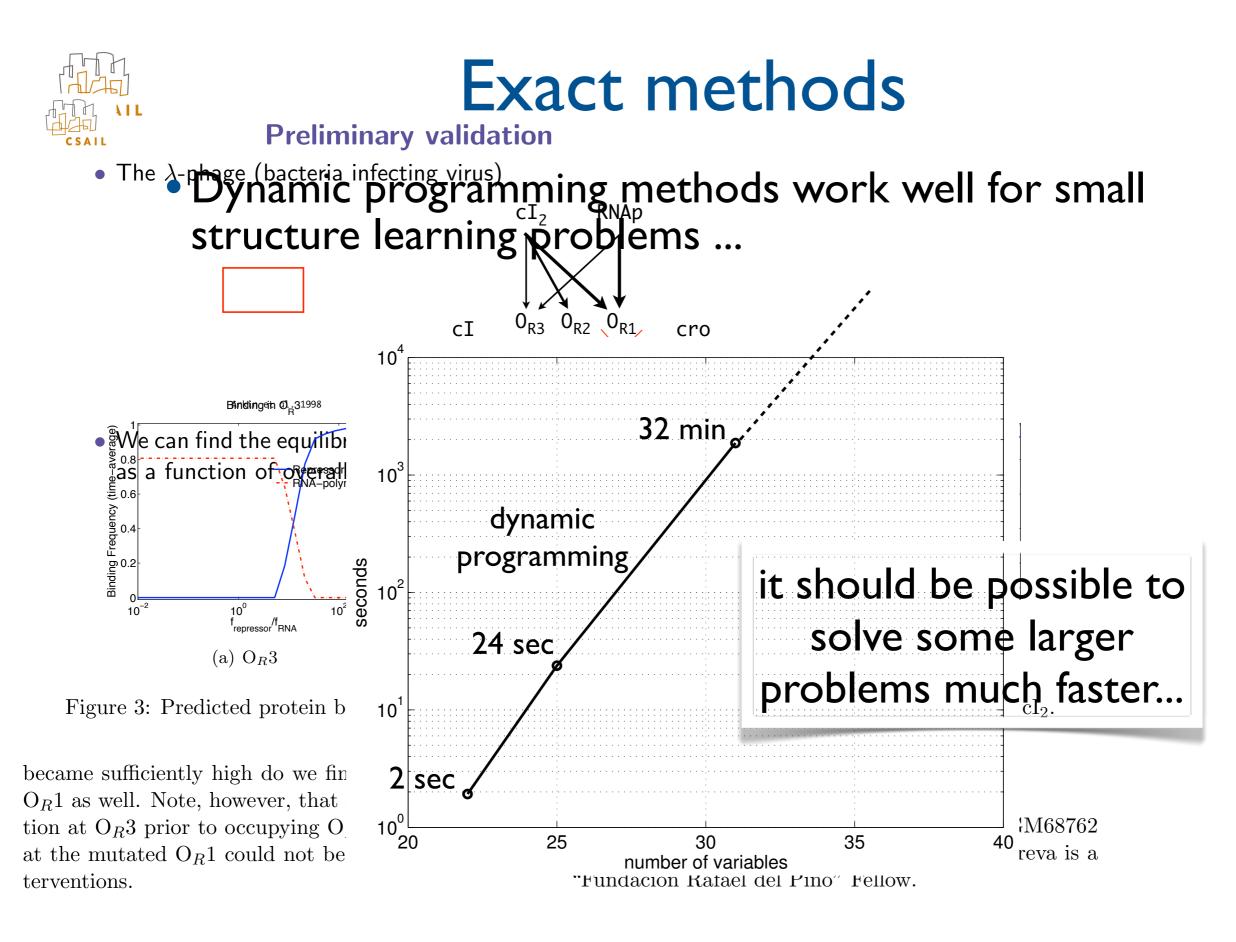
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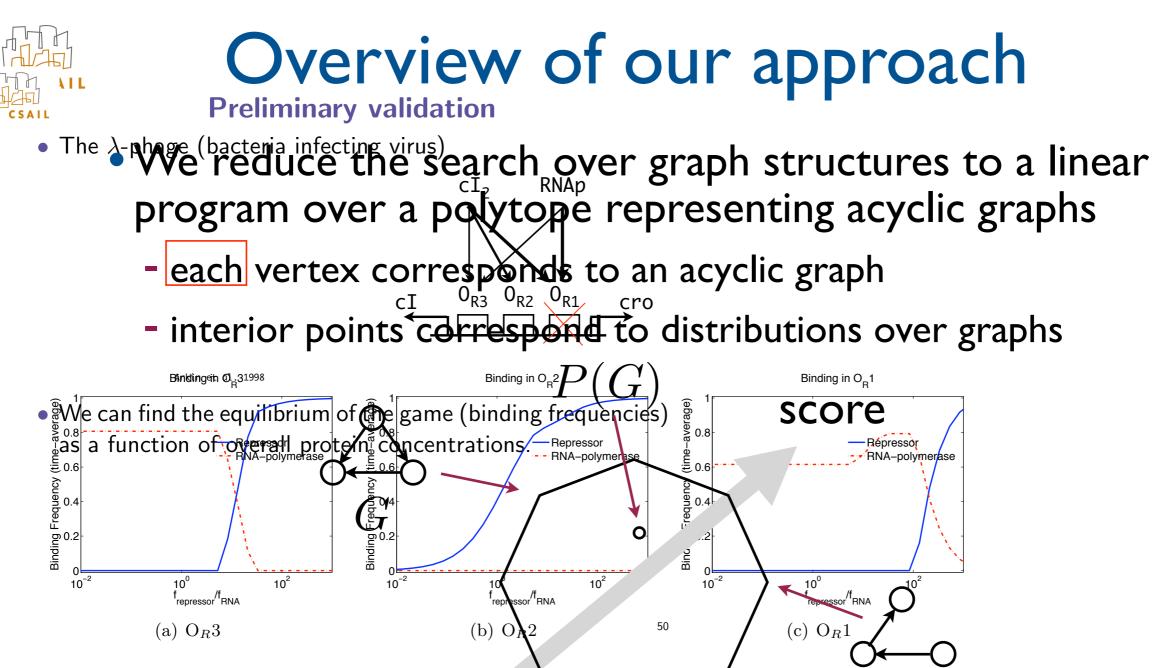


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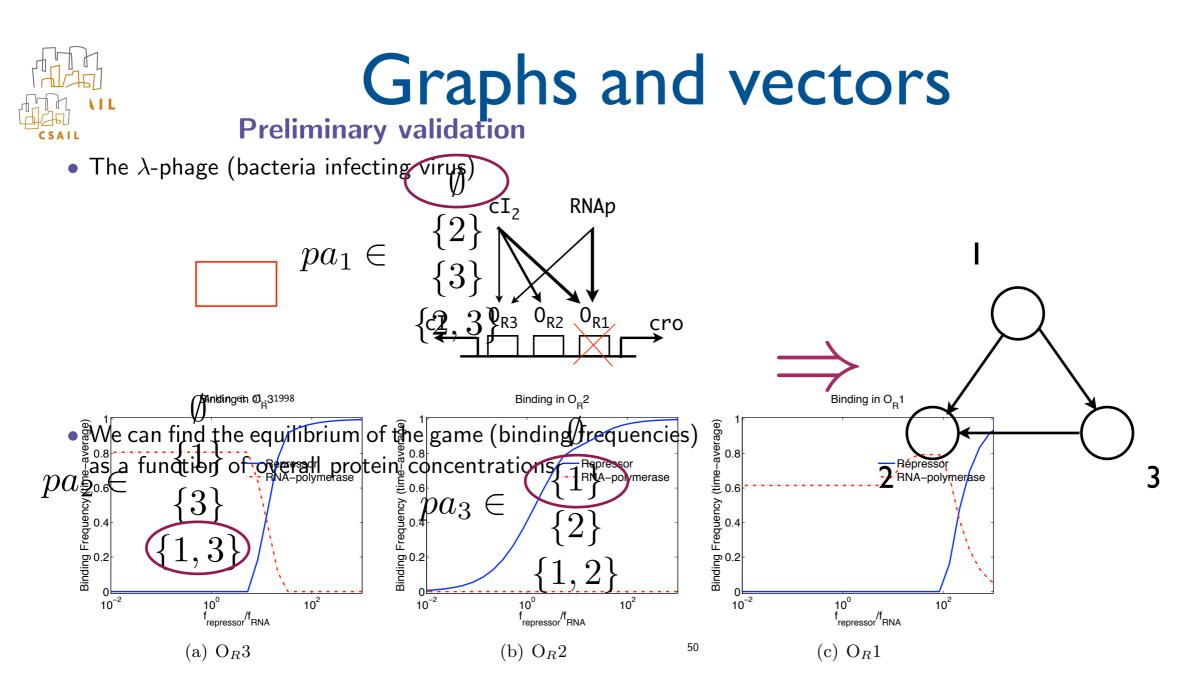


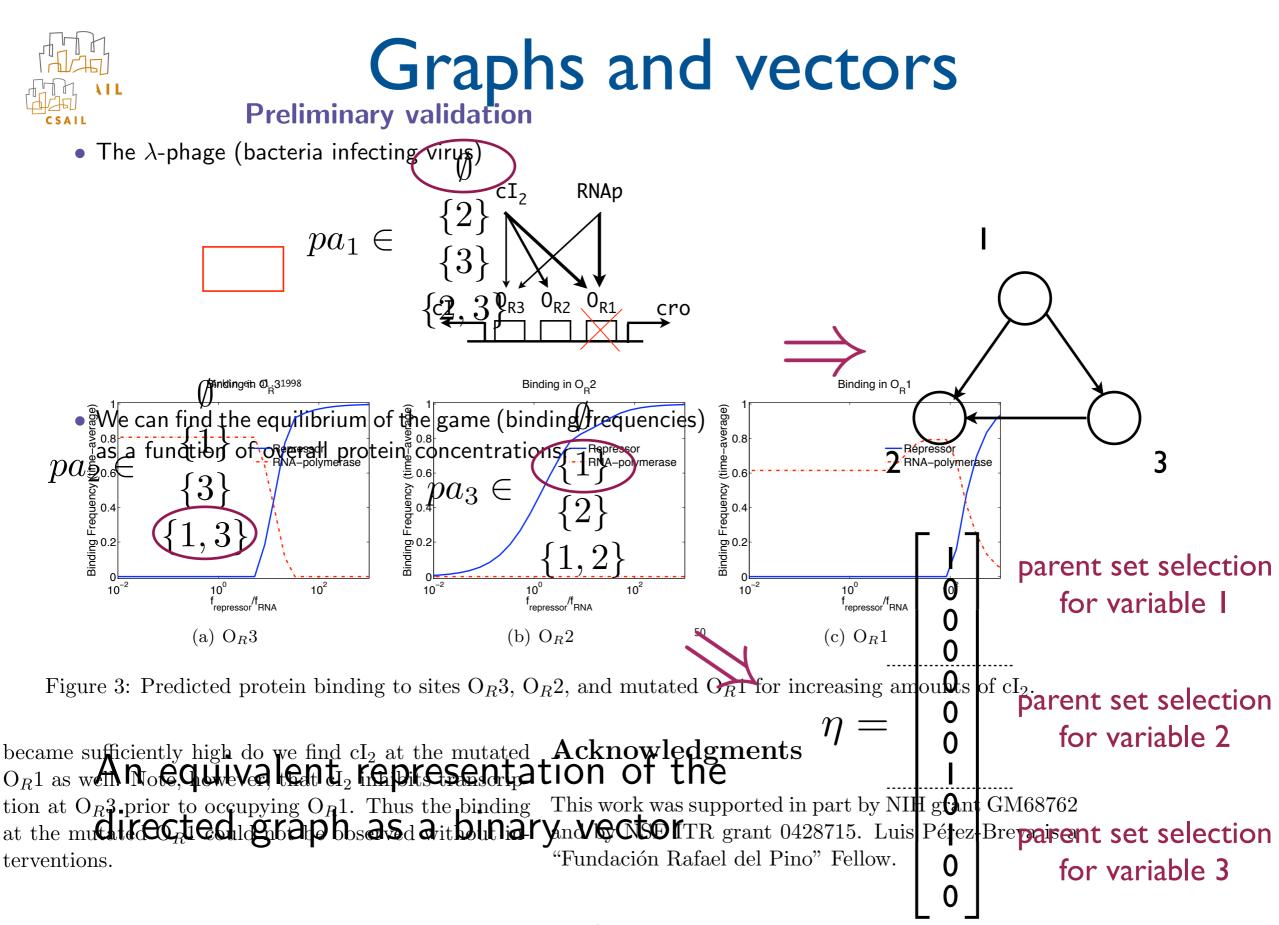
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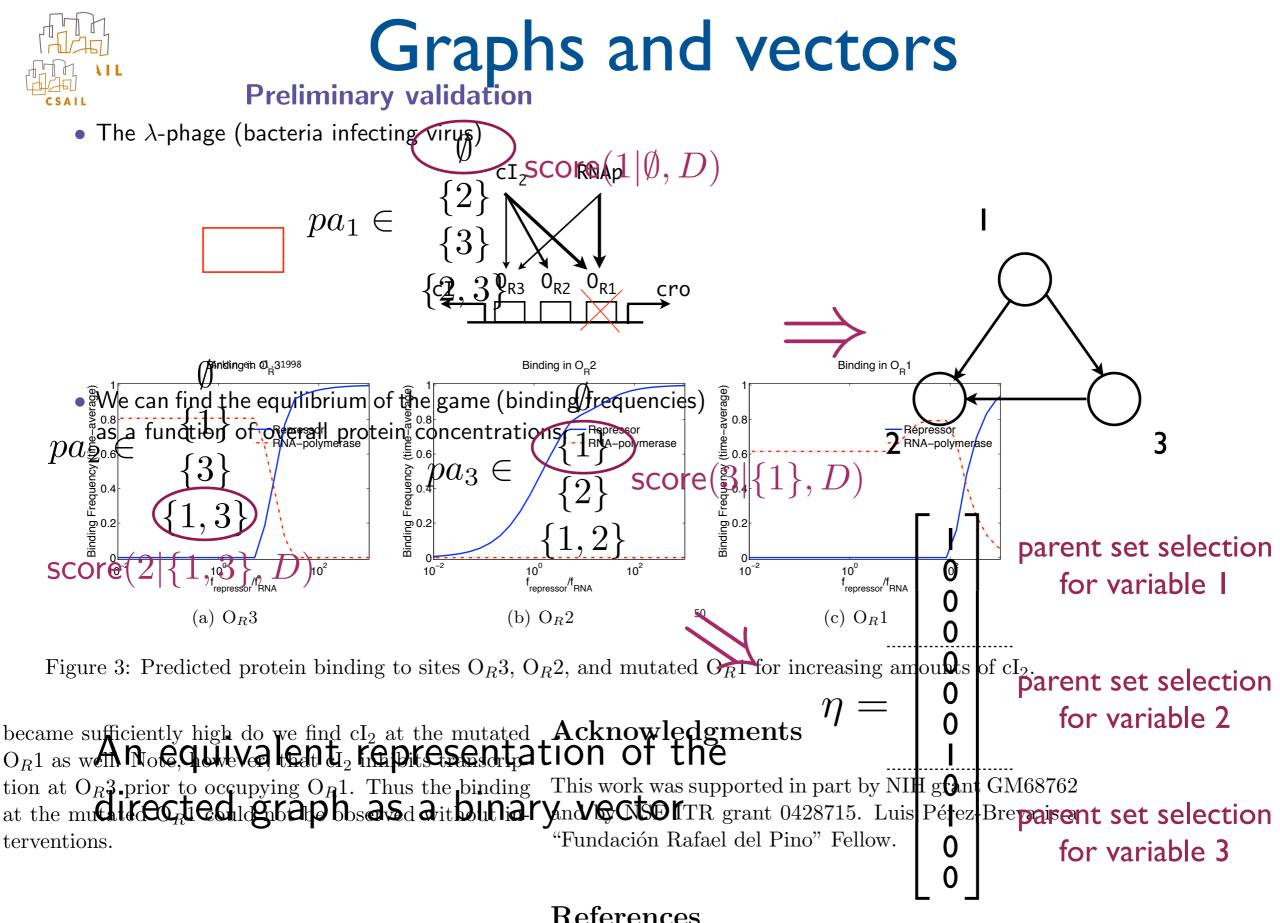
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Preliminary validation

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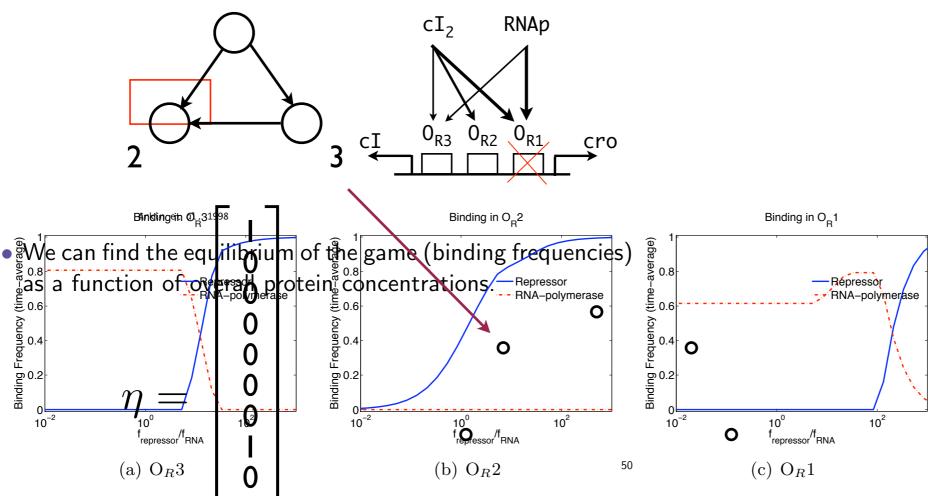


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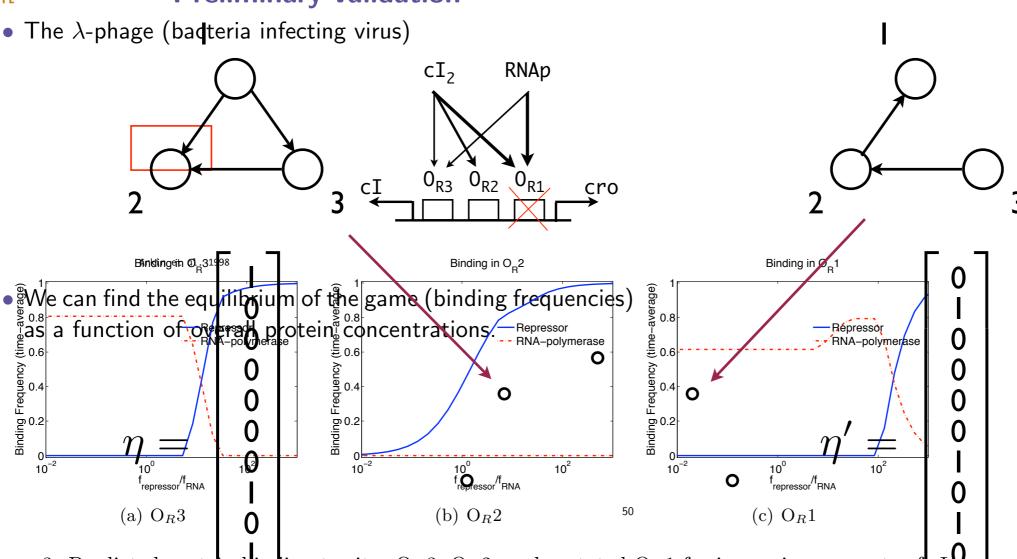
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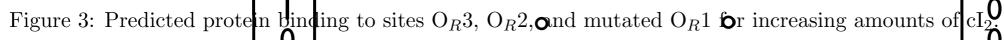
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Discussion 7 Wednesday, March 10, 2010

Graphs and polytopes **Preliminary validation**





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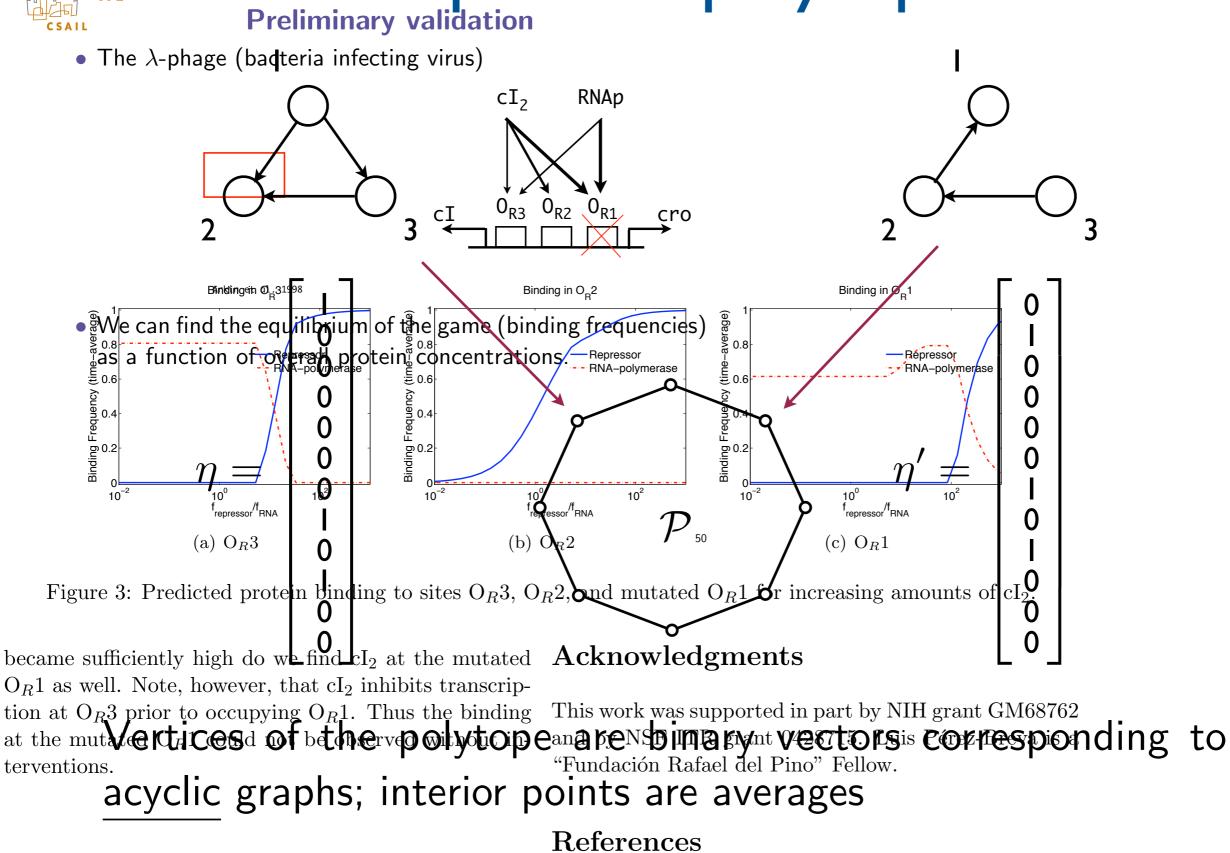
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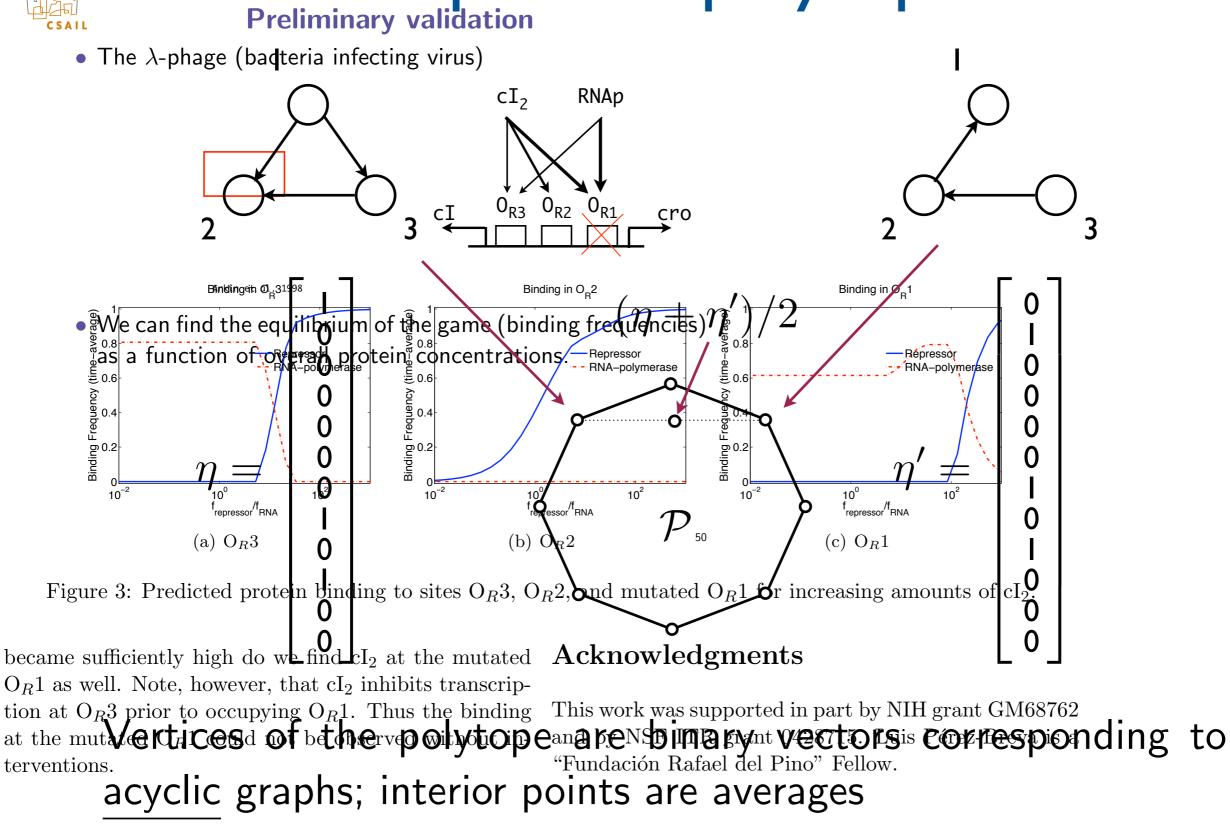
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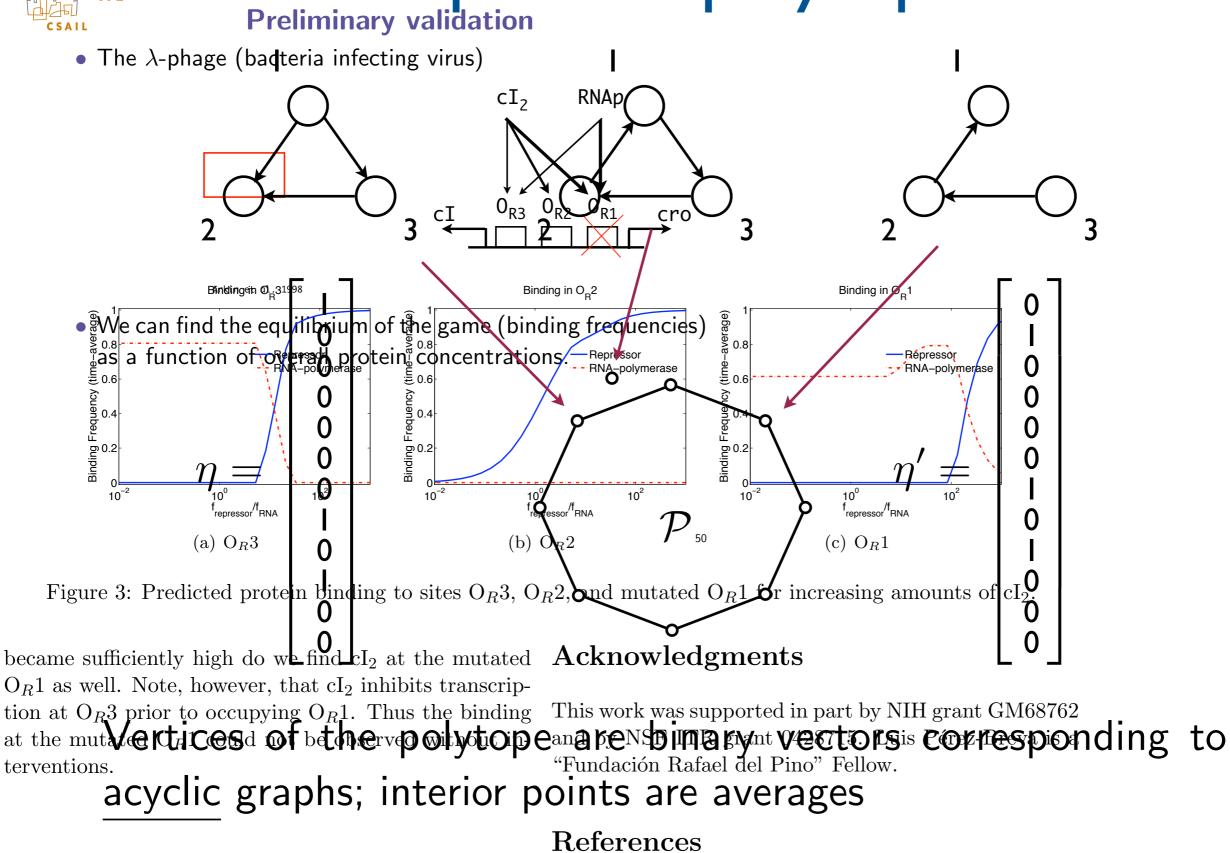


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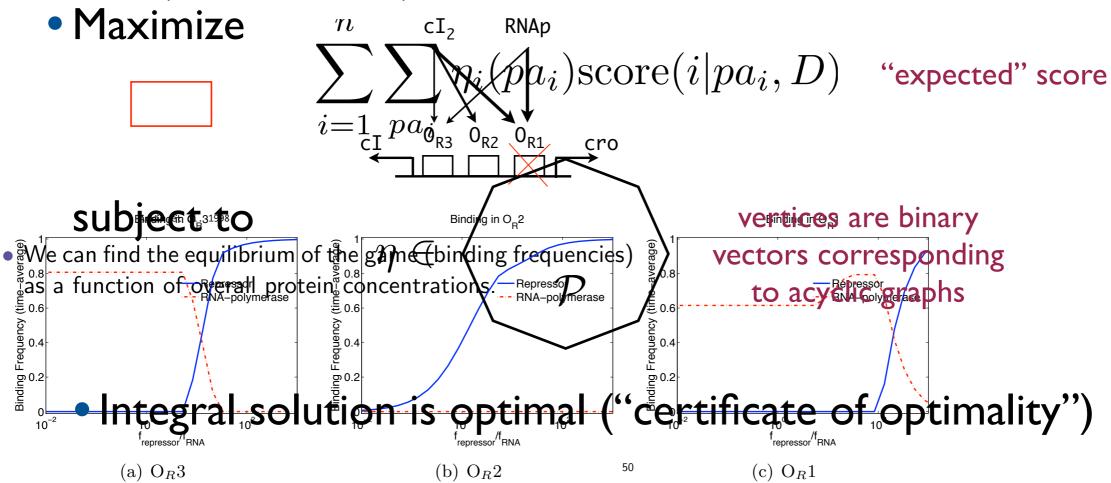


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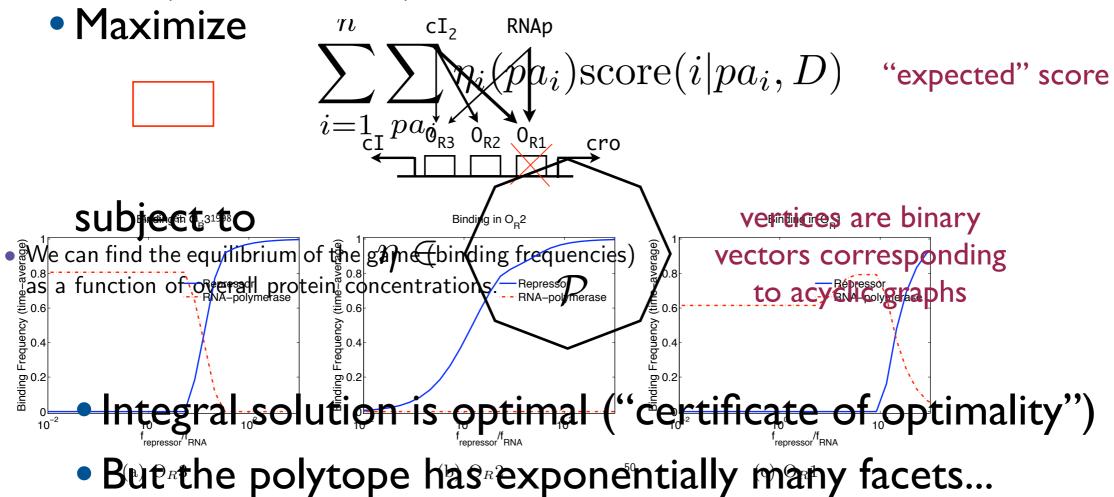


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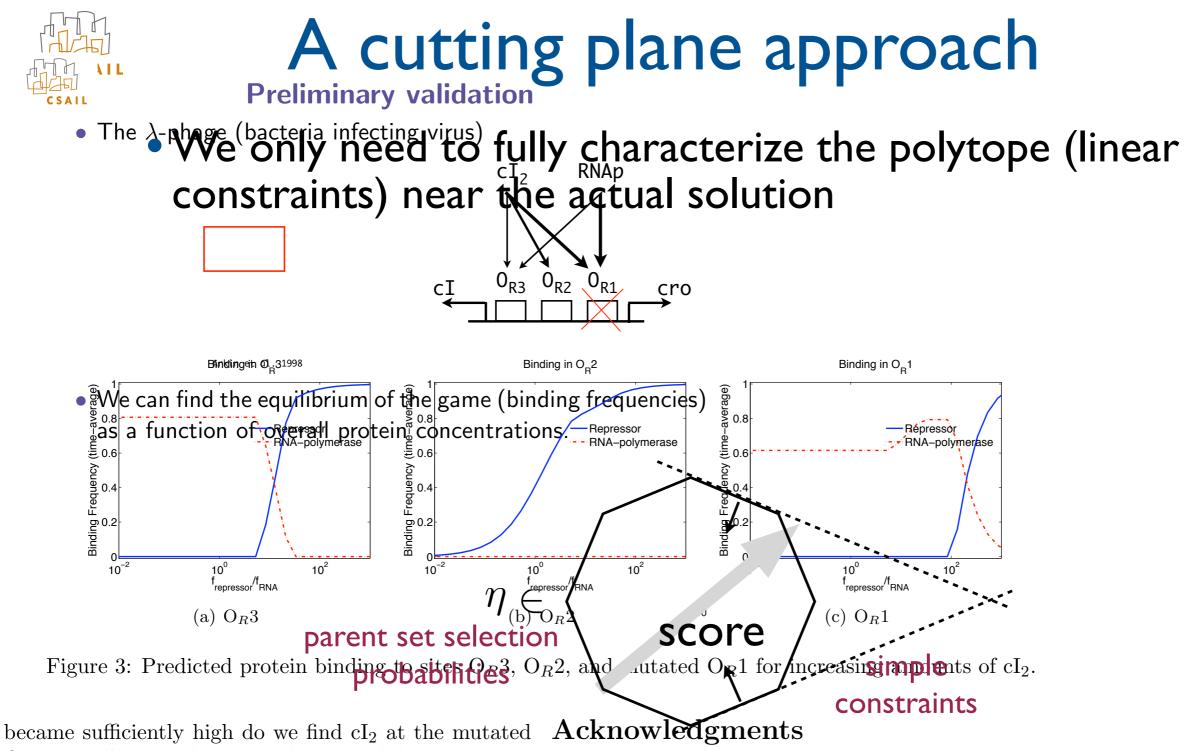
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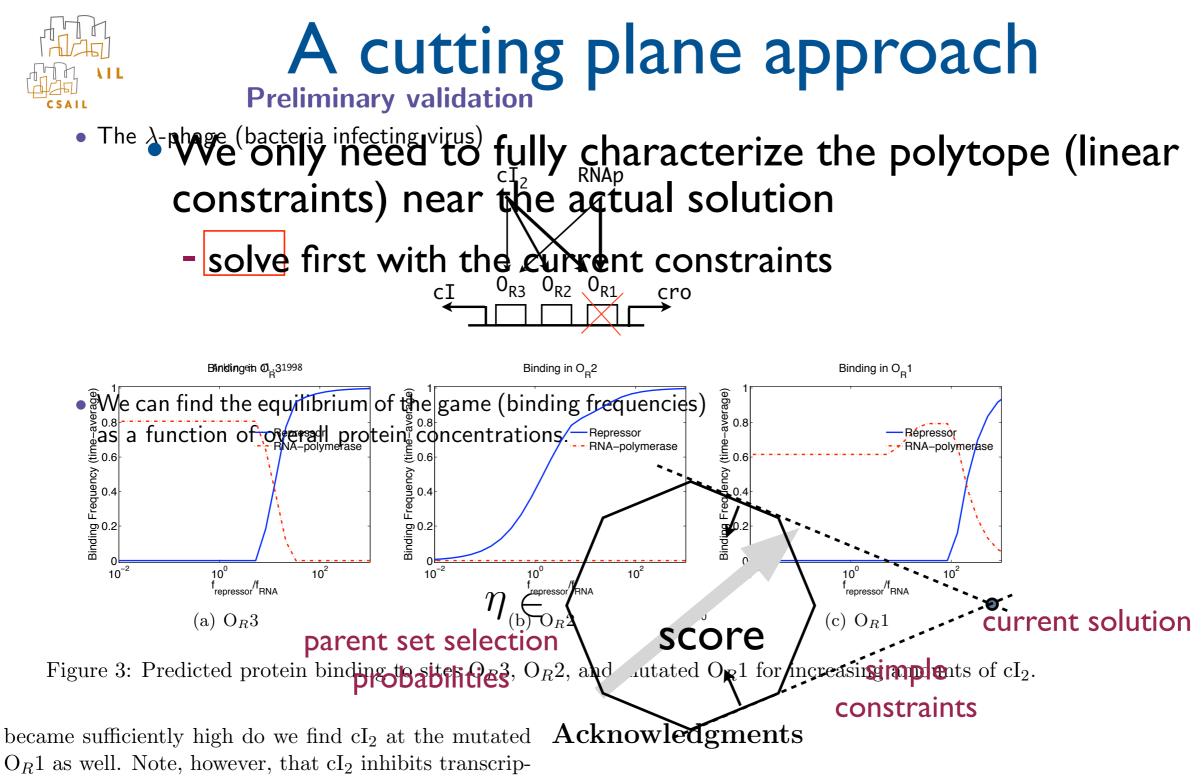
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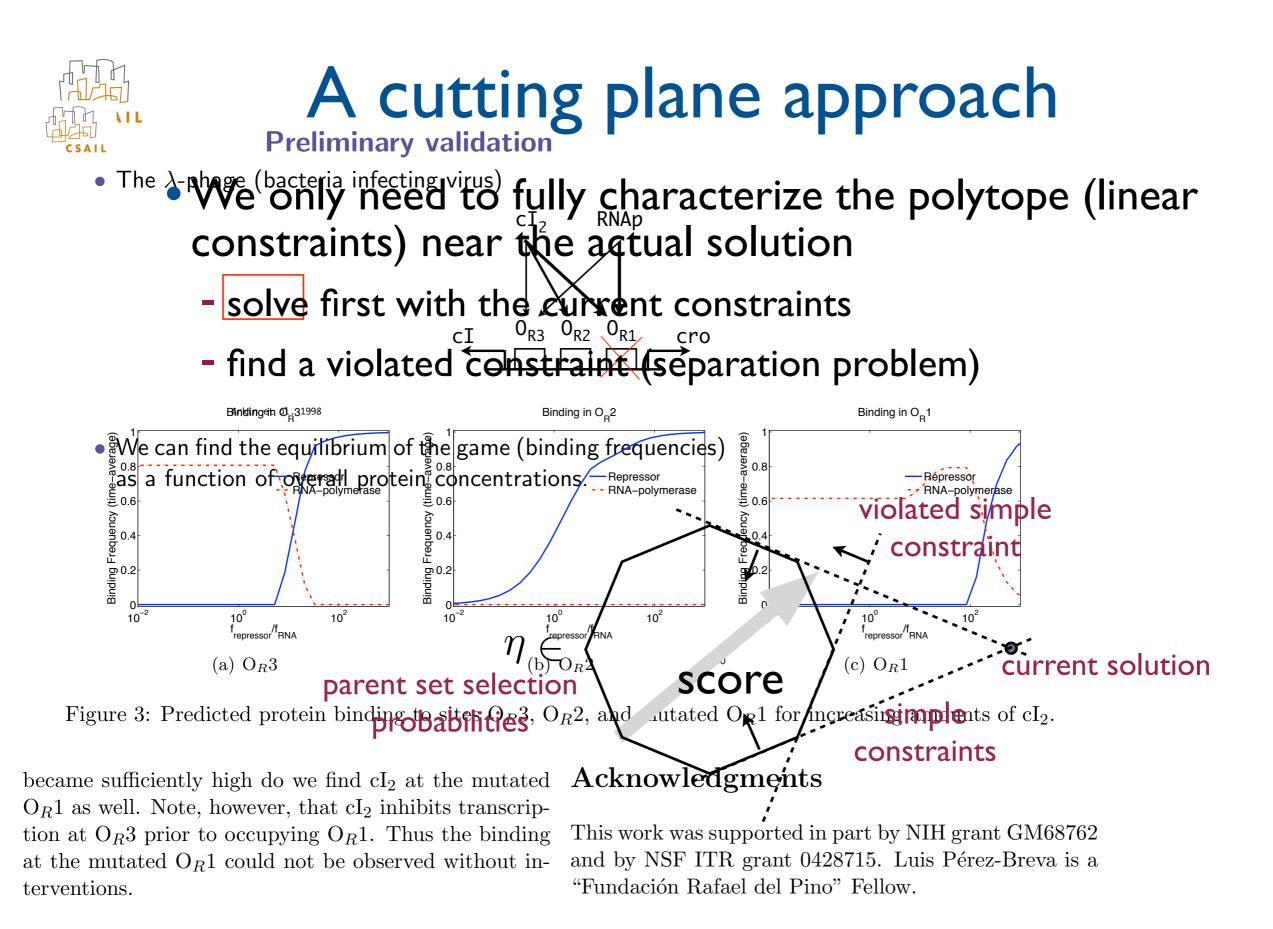
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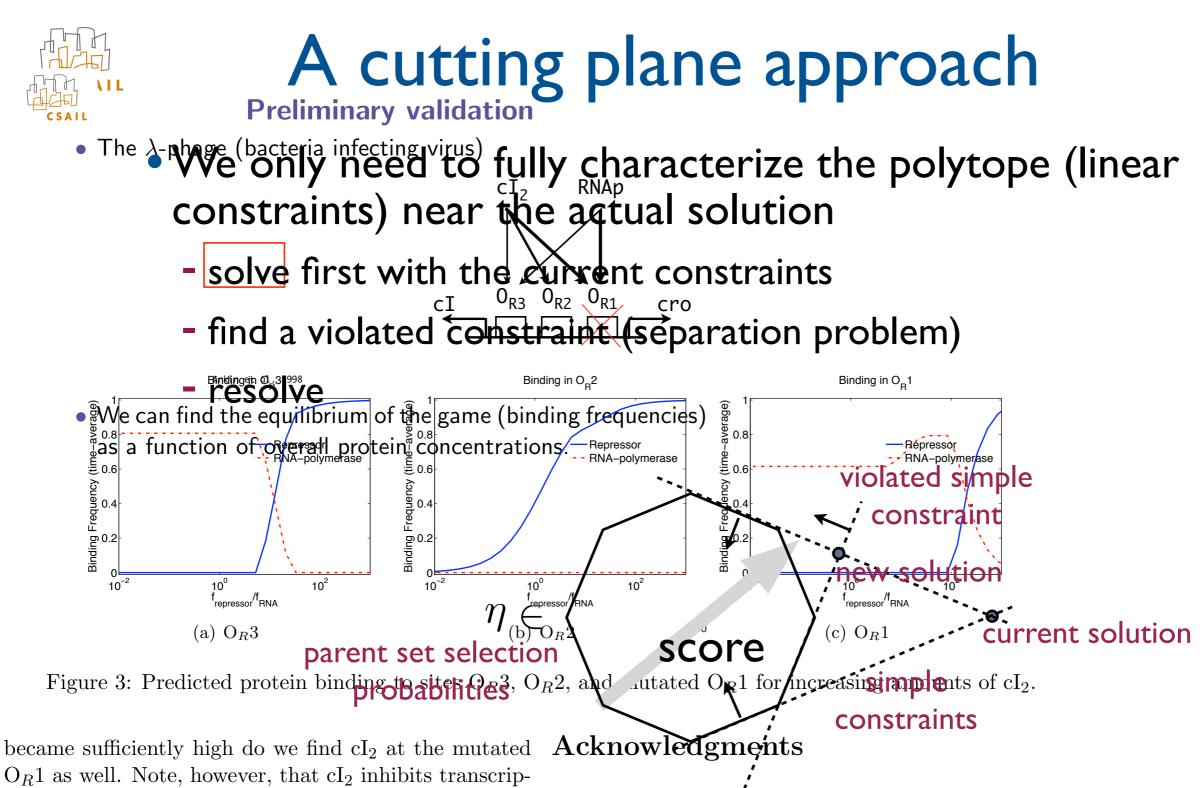
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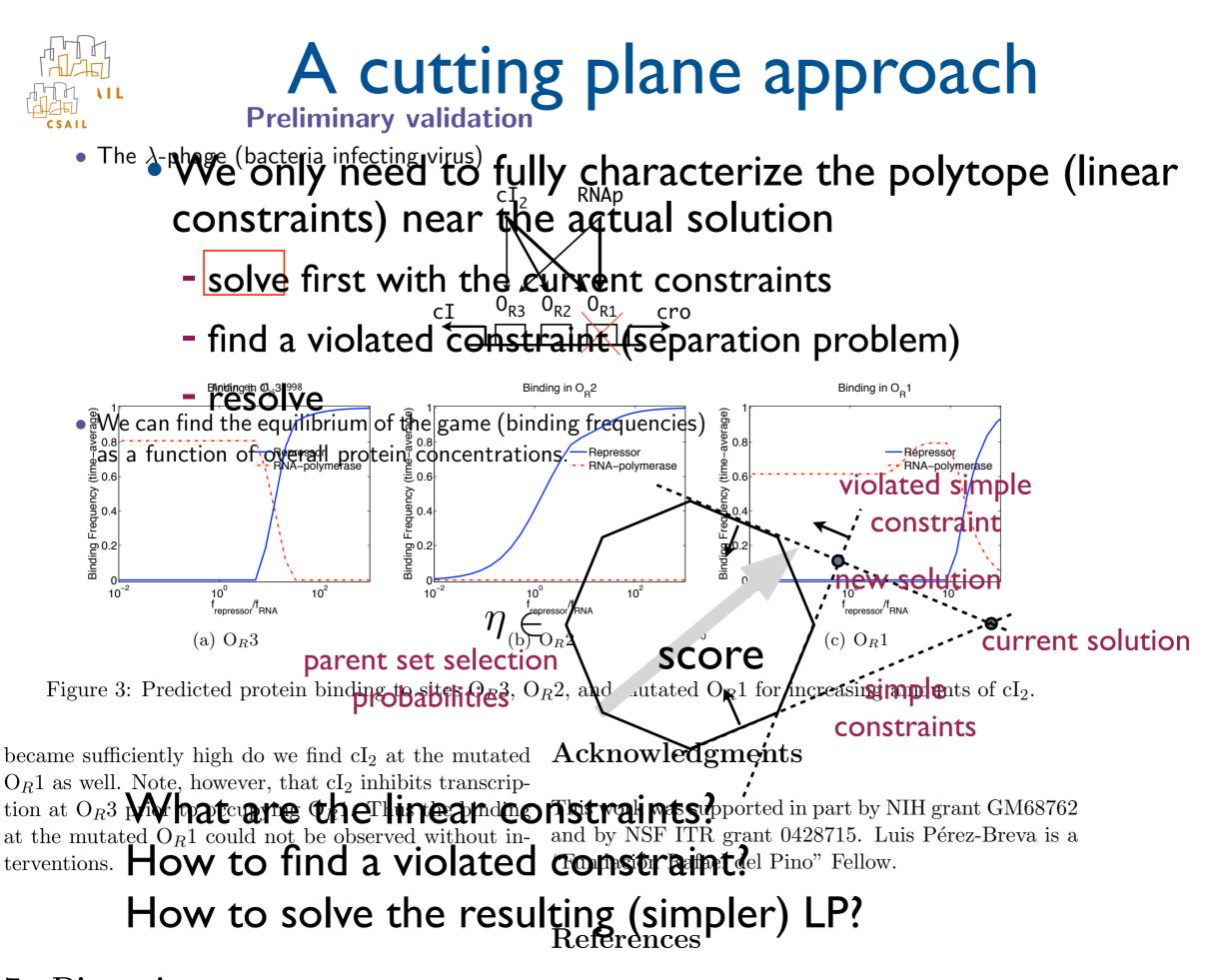
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Discussion

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The separation problem Preliminary validation

• The λ -phage (bacteria infecting virus)

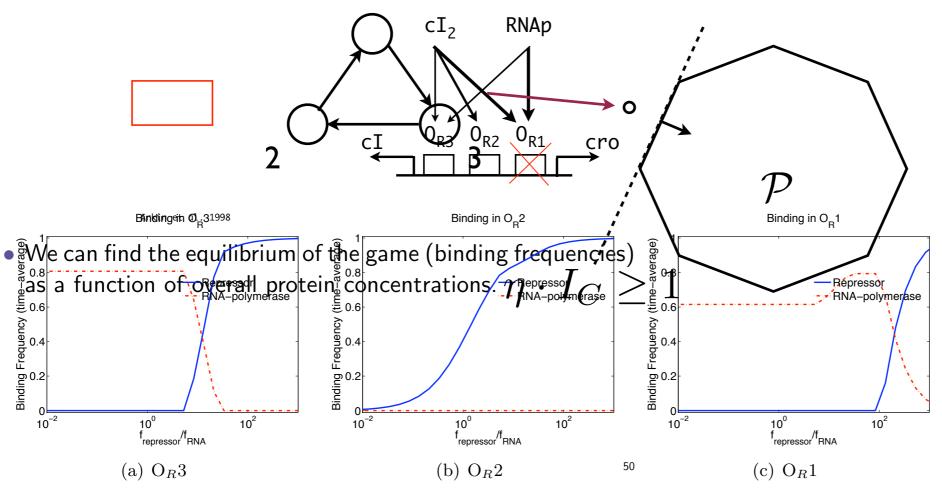


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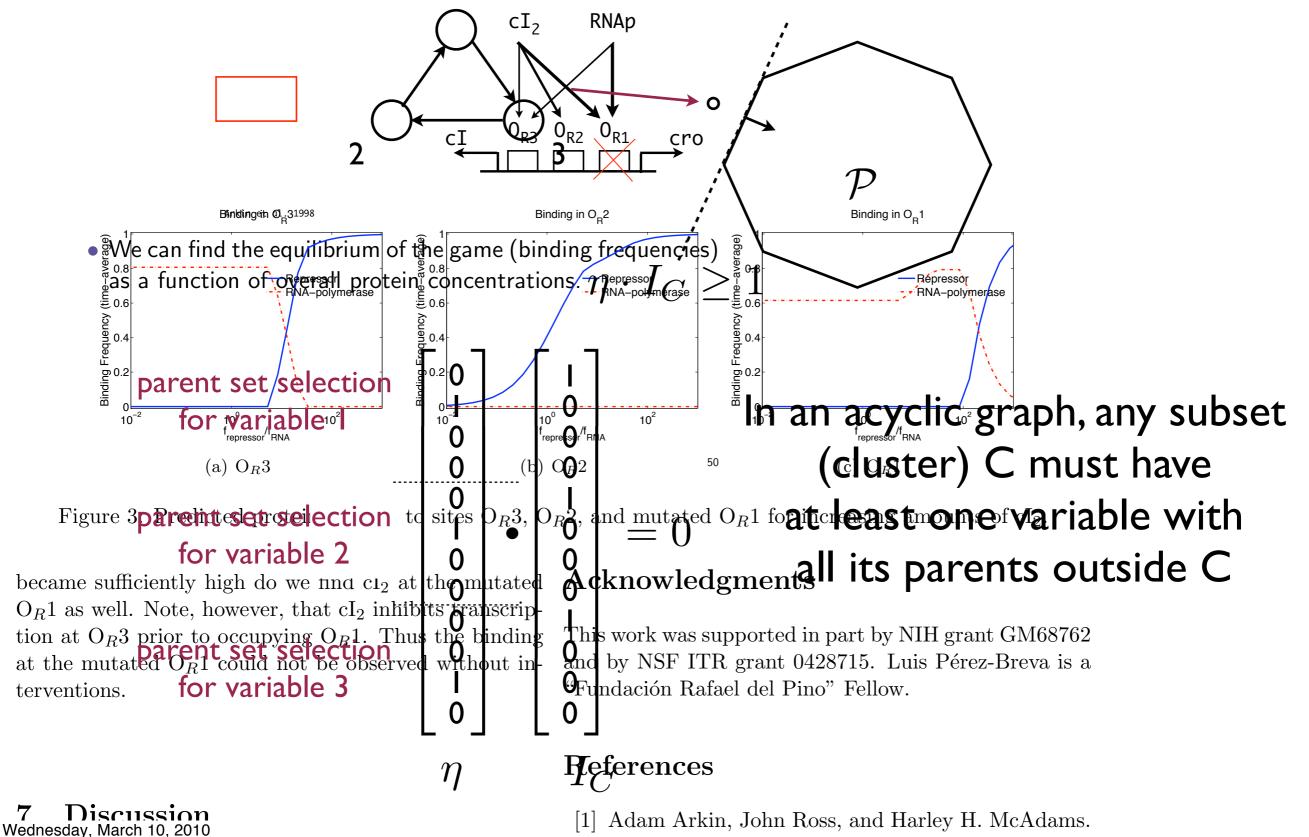
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Preliminary validation

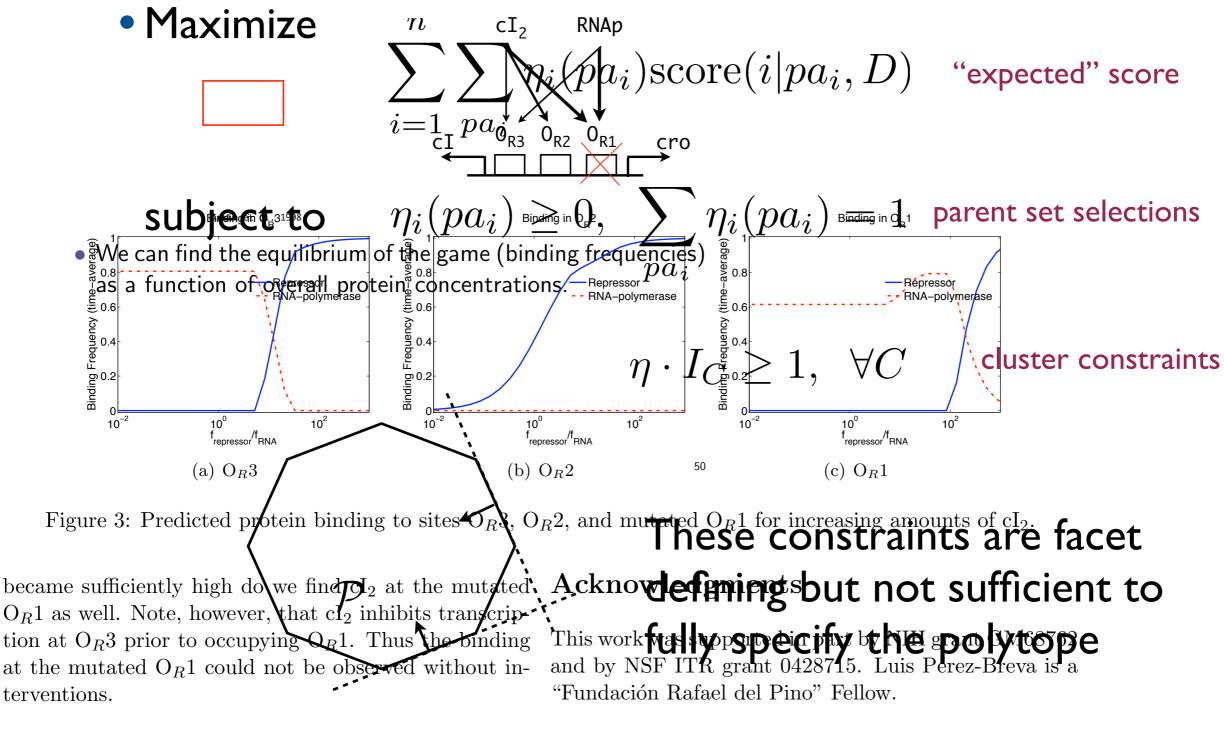
The λ-phage (bacteria infecting virus)

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LP relaxation for structure learning

• The λ -phage (bacteria infecting virus)



7 Discussion Wednesday, March 10, 2010

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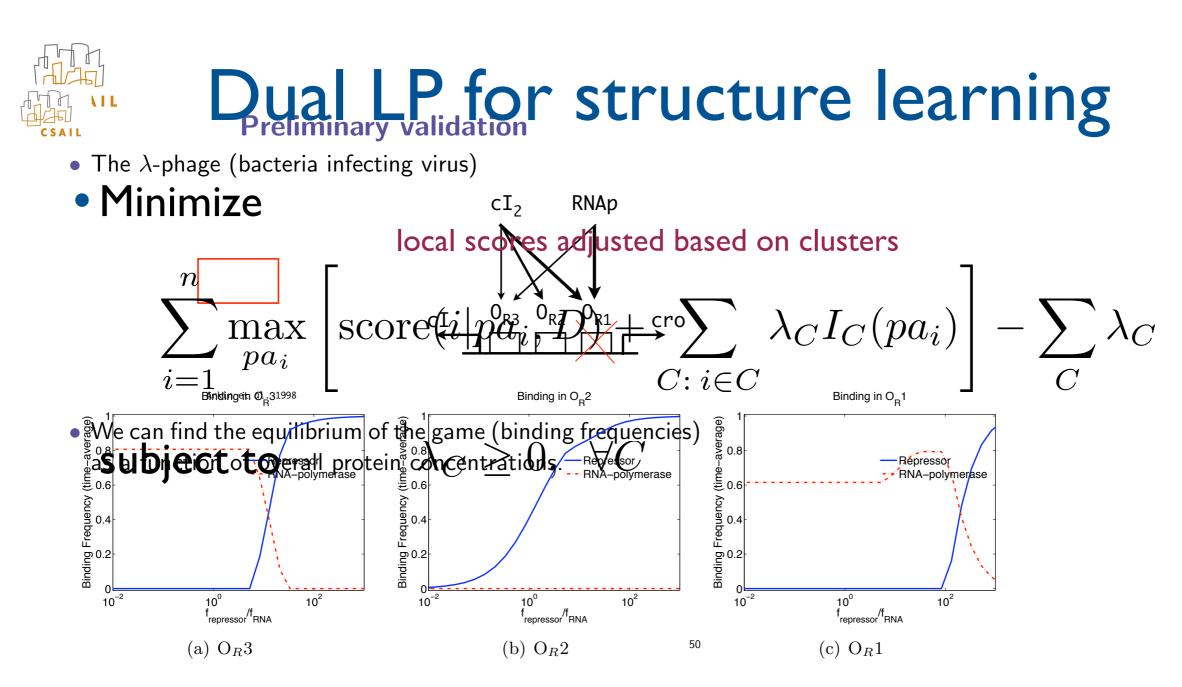


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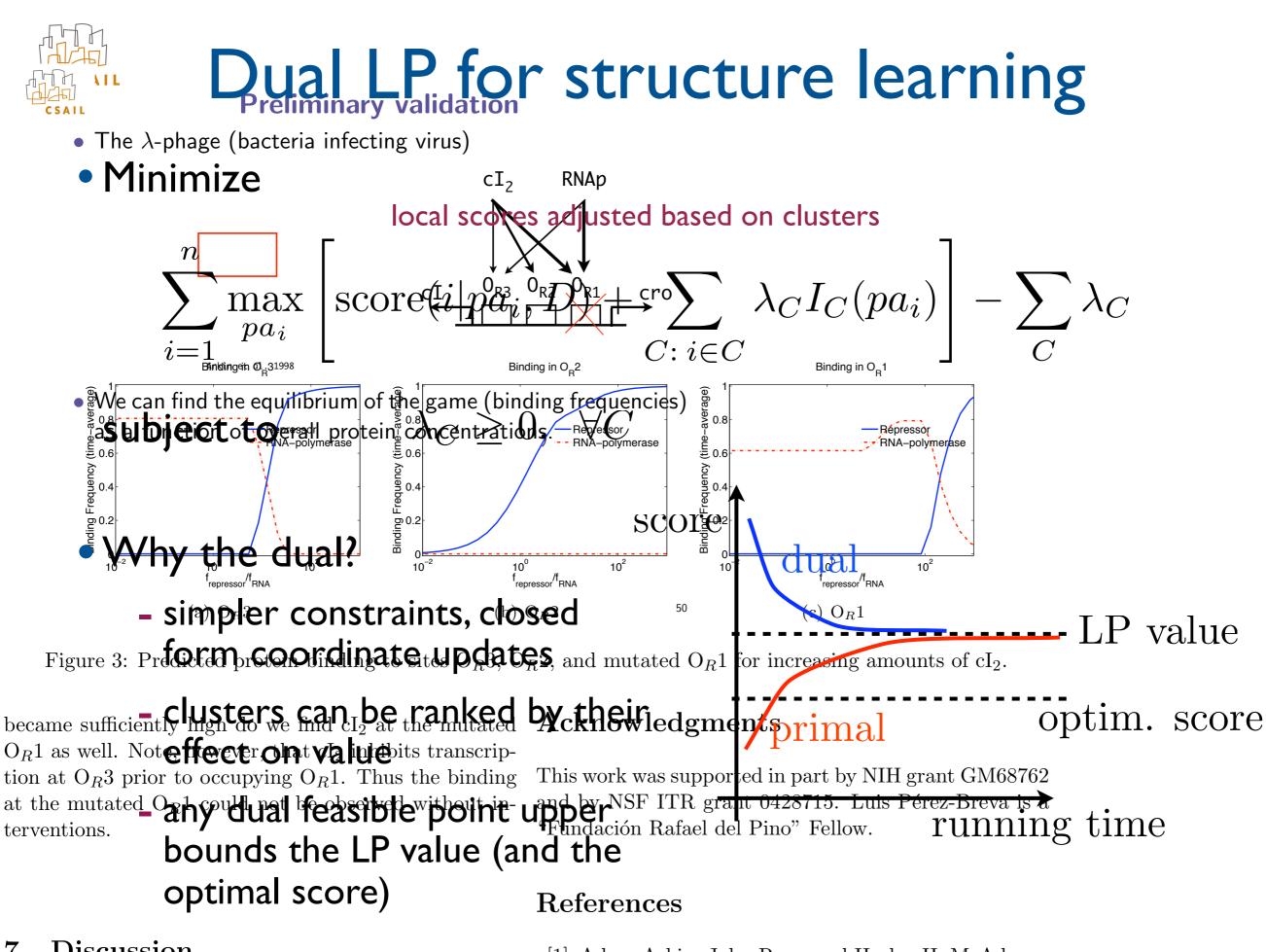
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• The -phage (hacteria infecting virus) ing experiments in C. elegans

- 25 phenotypic indicators/markers that characterize each experimental outcome
- We seek to build a Bayesian network model over the

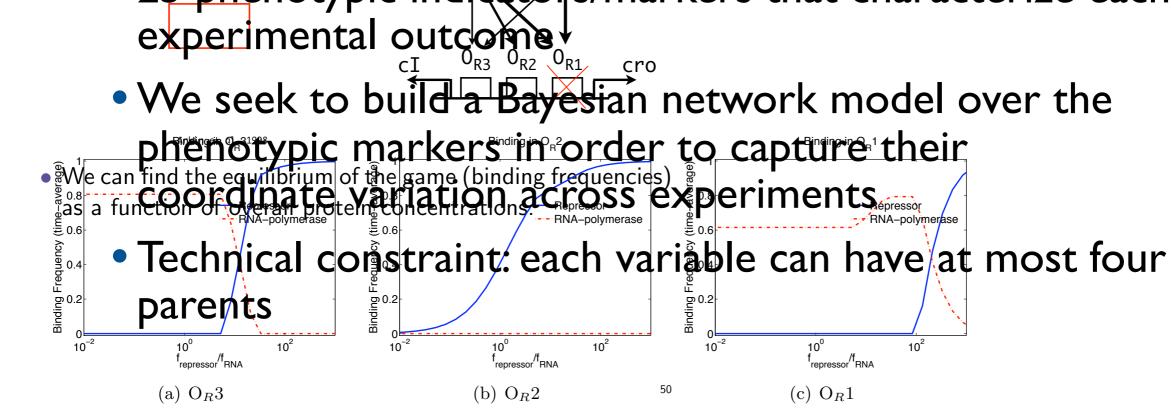


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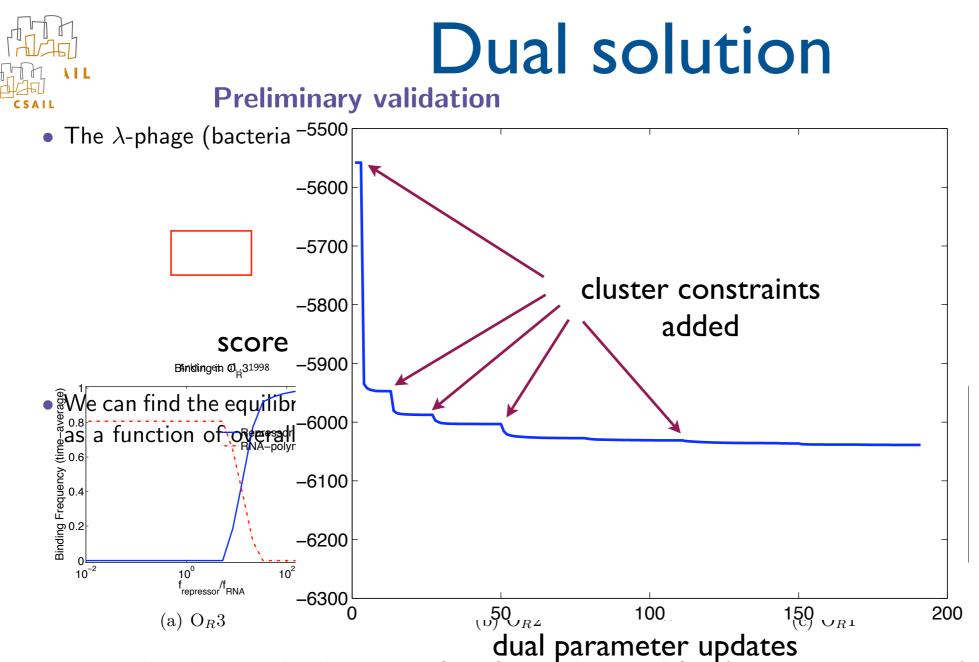
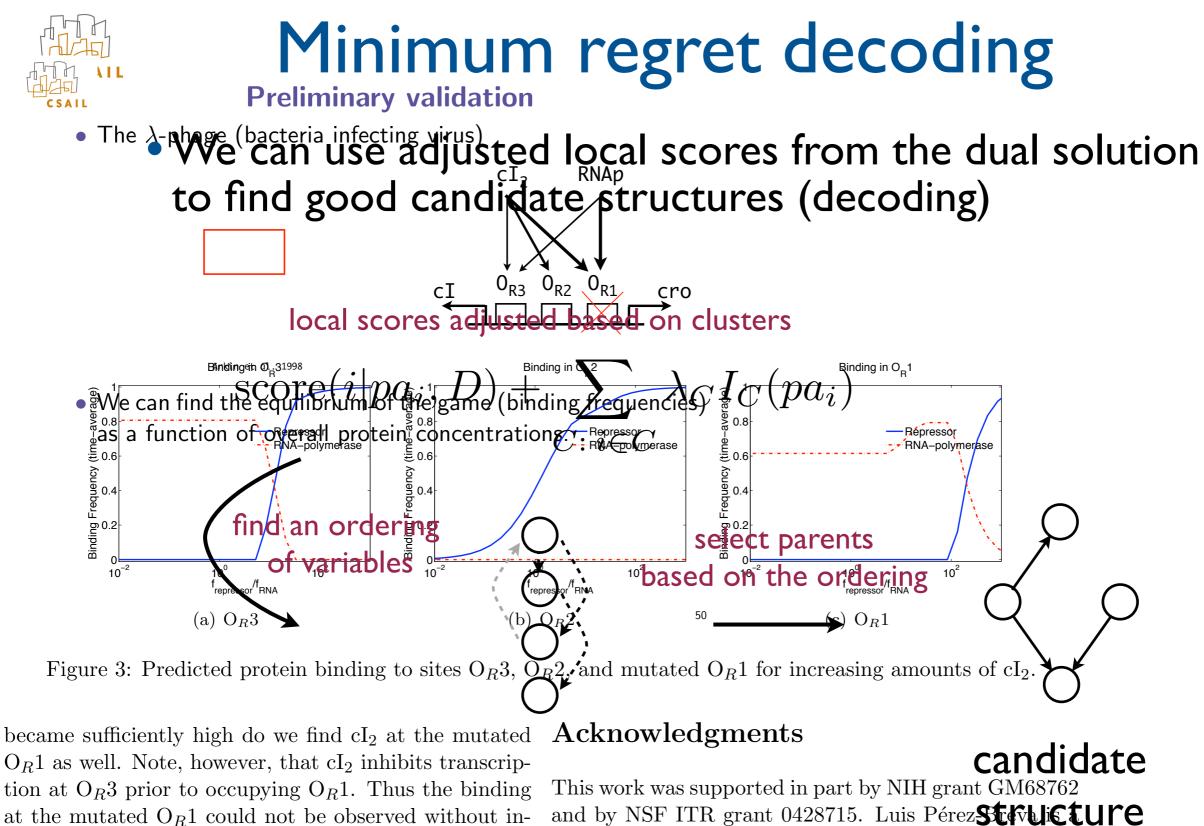


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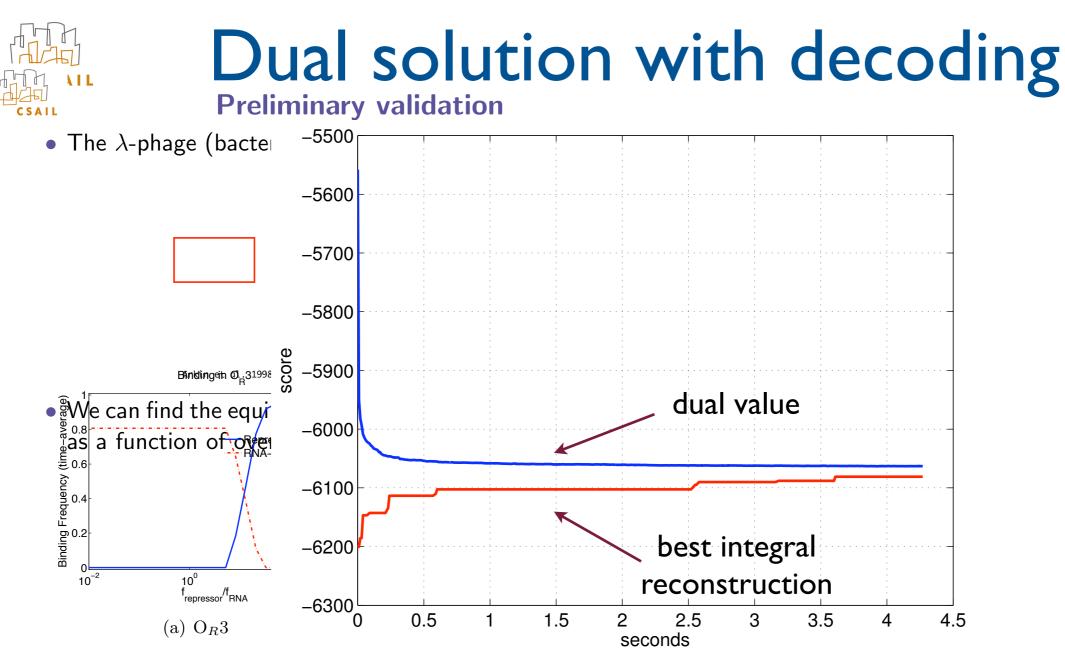


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References

Branch and Bound

Preliminary validation

- The We can further tighten the approximation by iteratively partitioning the space of possible solutions and using the LP relaxation separately for each partition
 - The dual LP (upper bound) is particularly effective for determining how the tree of partitions should be

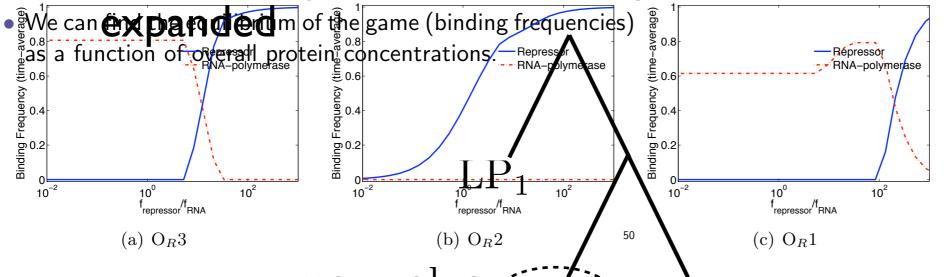


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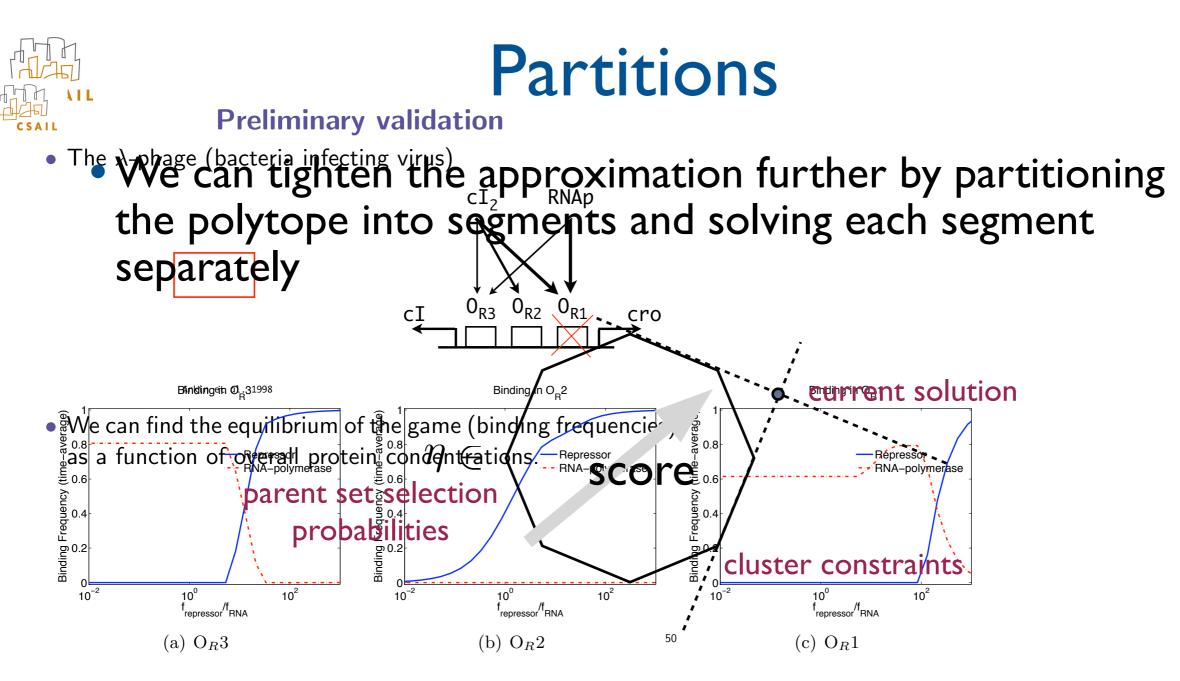


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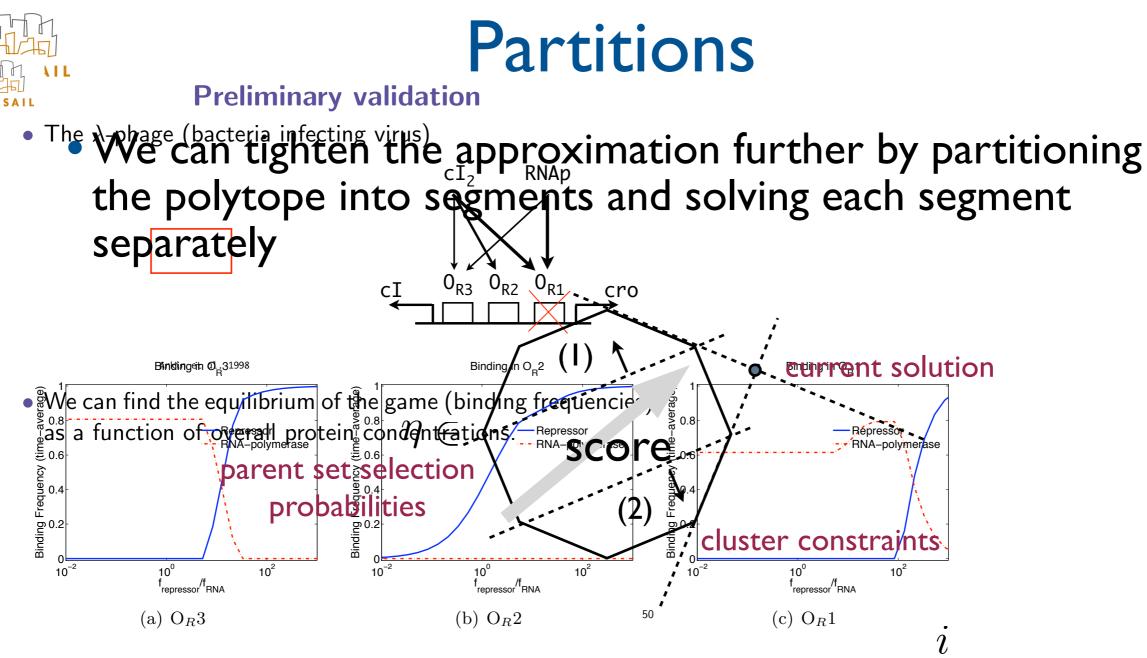


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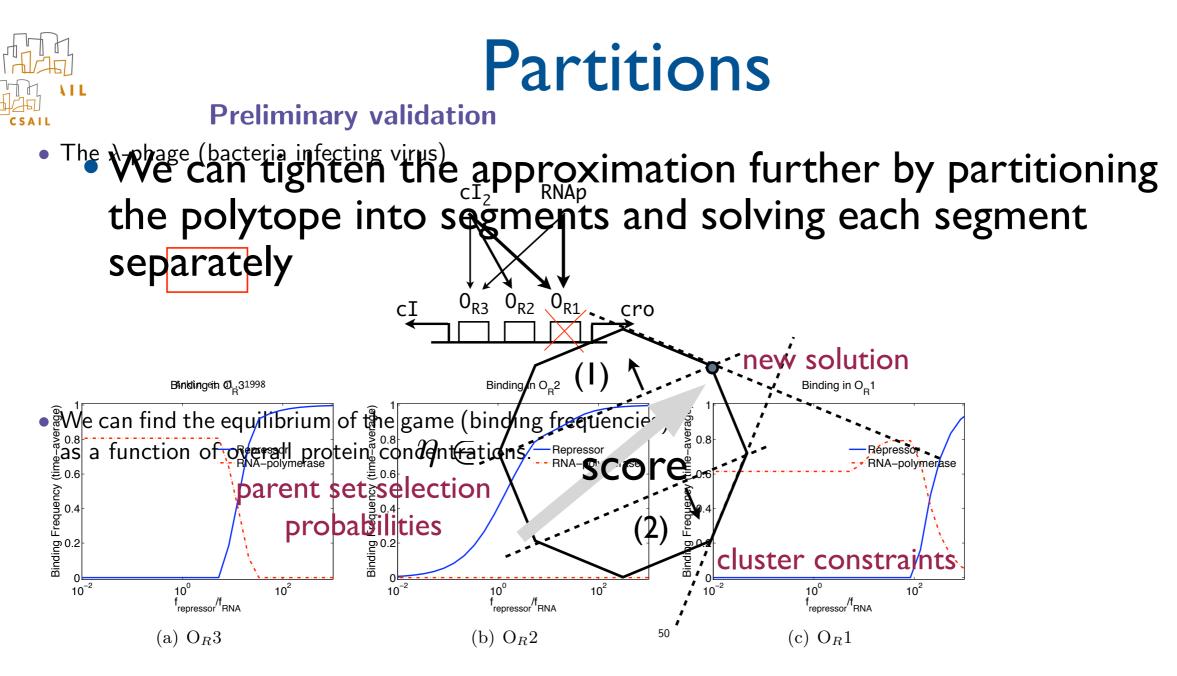


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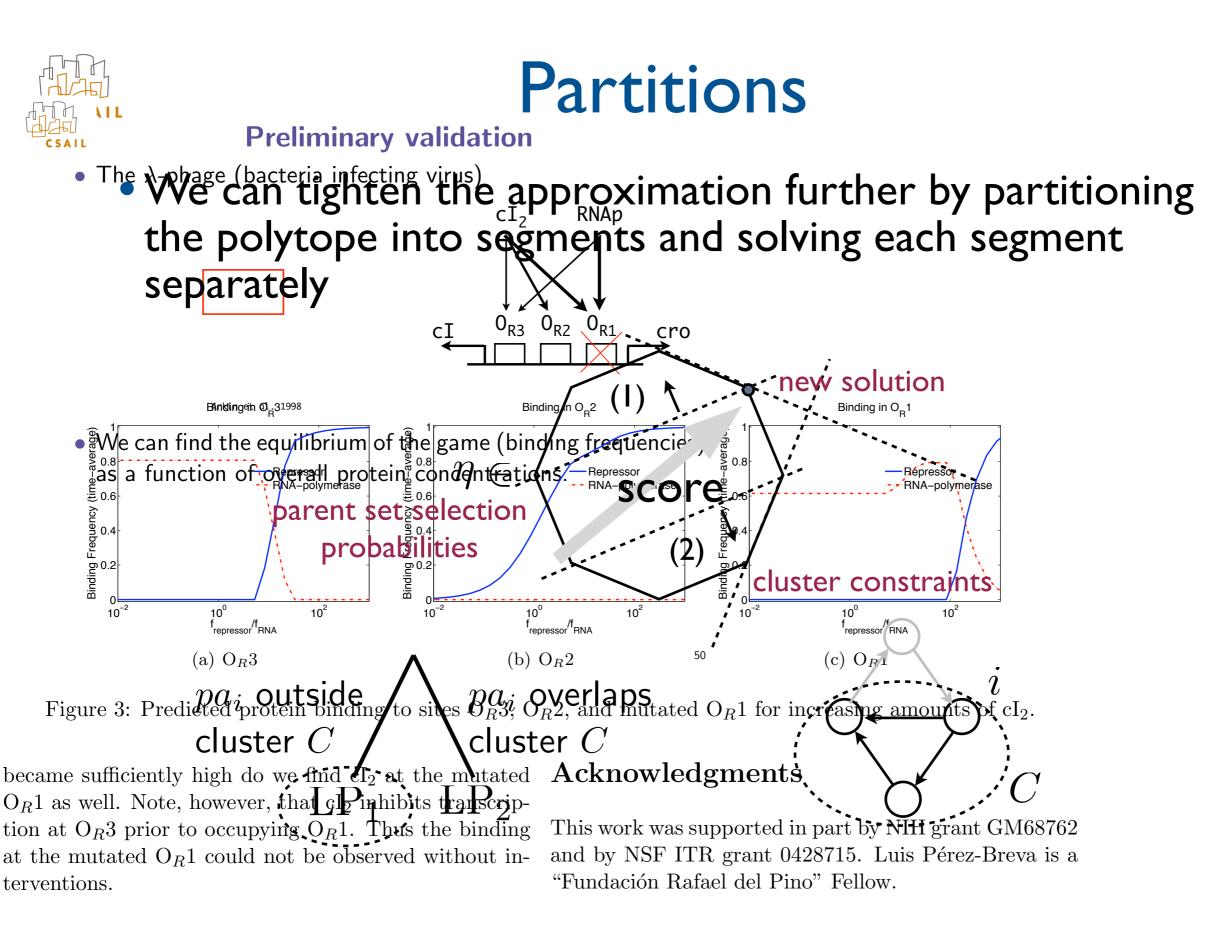
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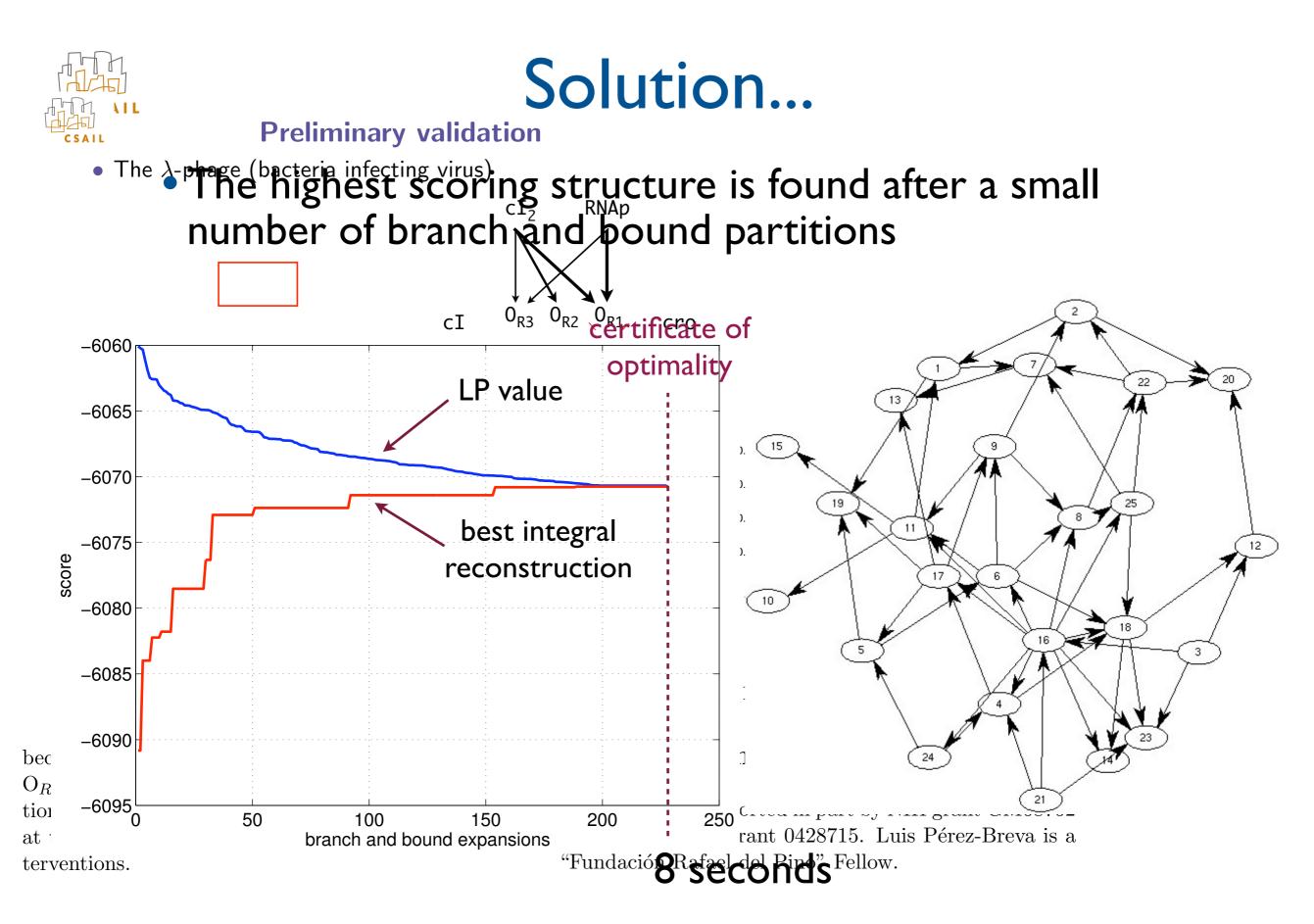
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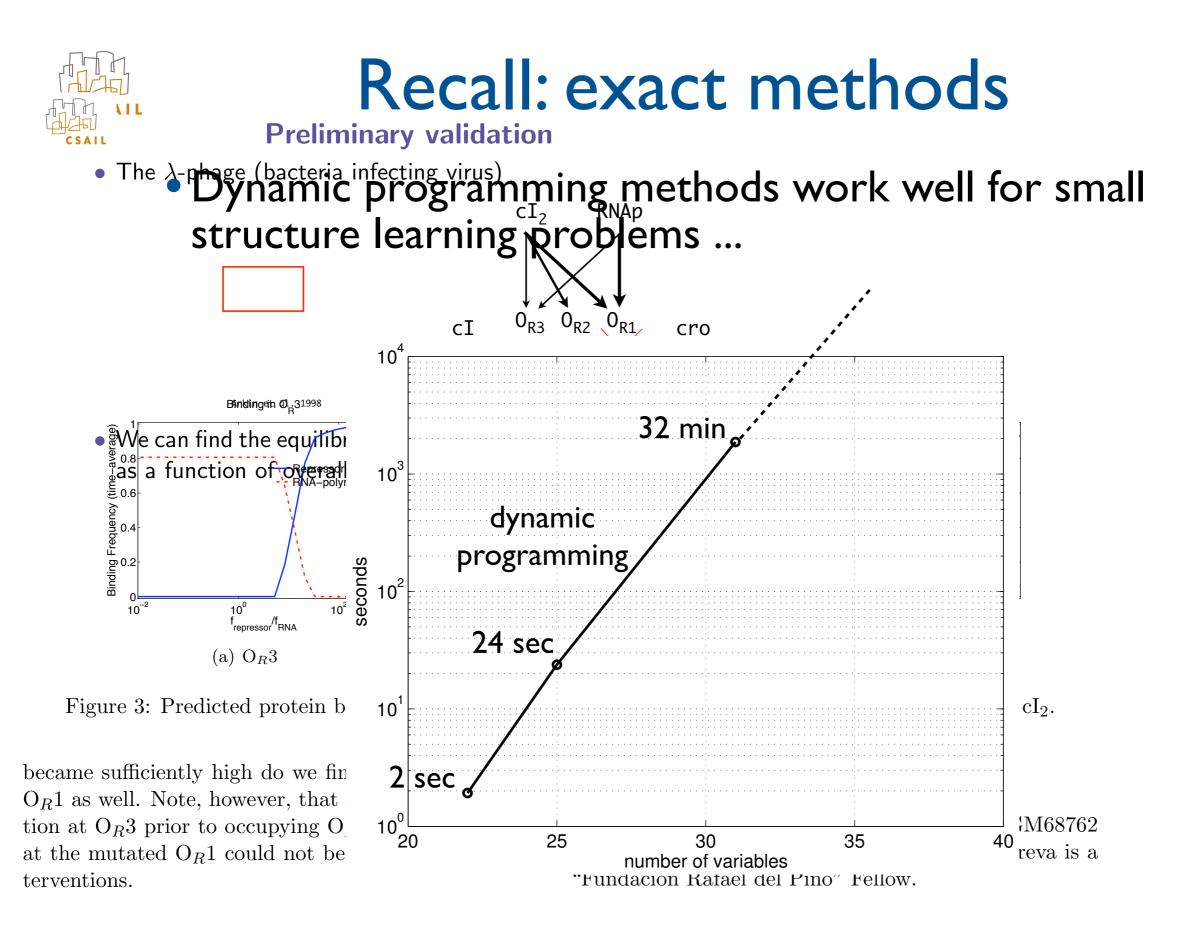
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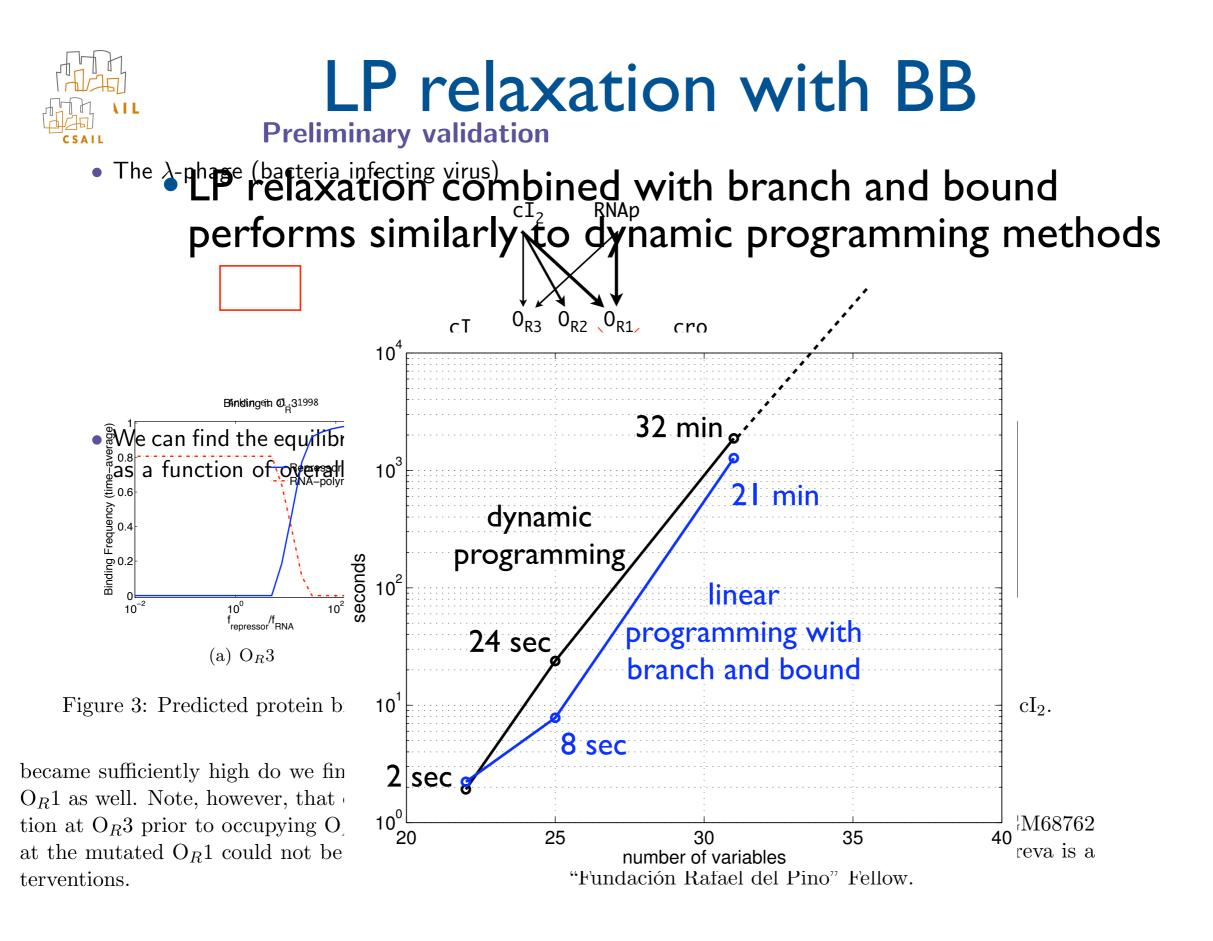
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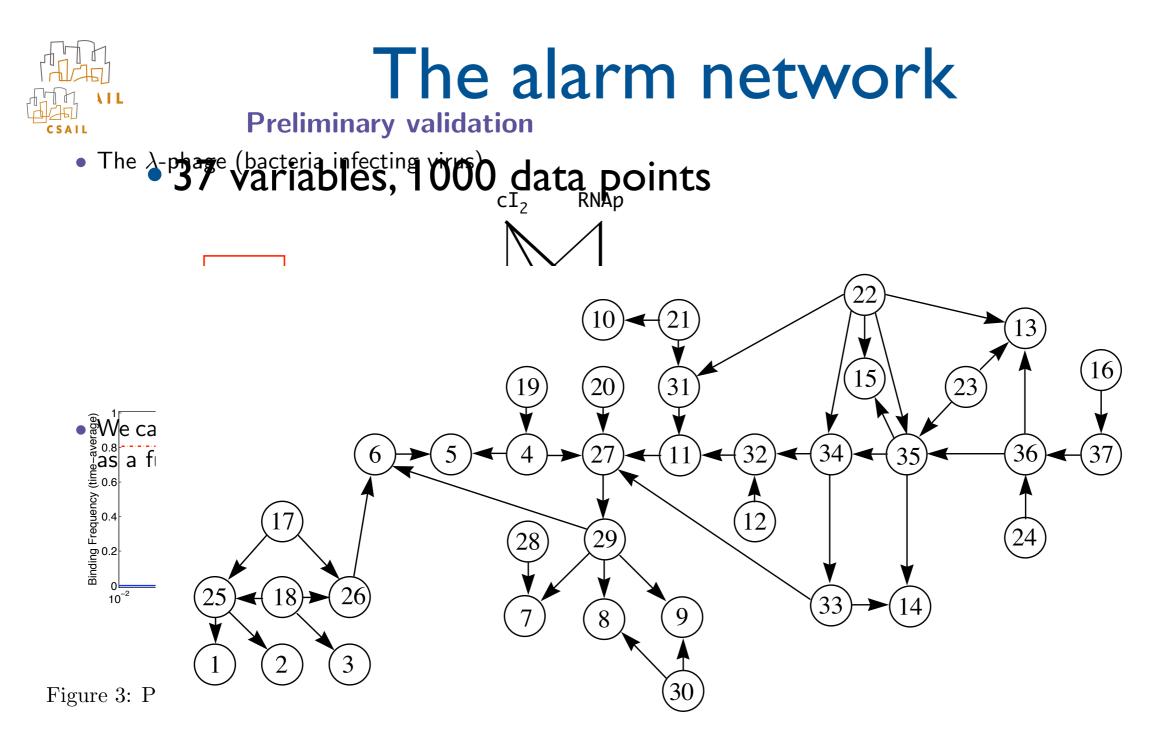
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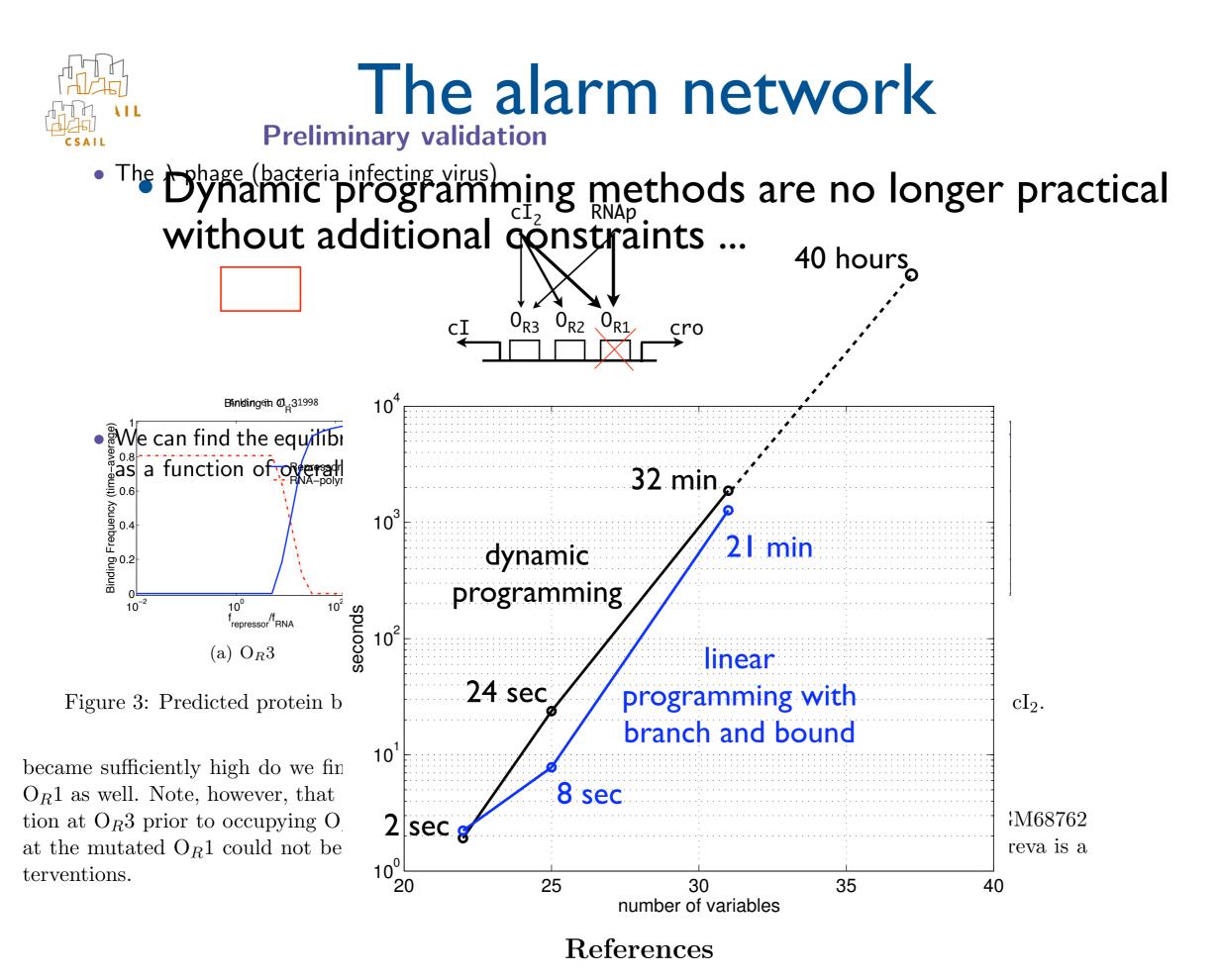


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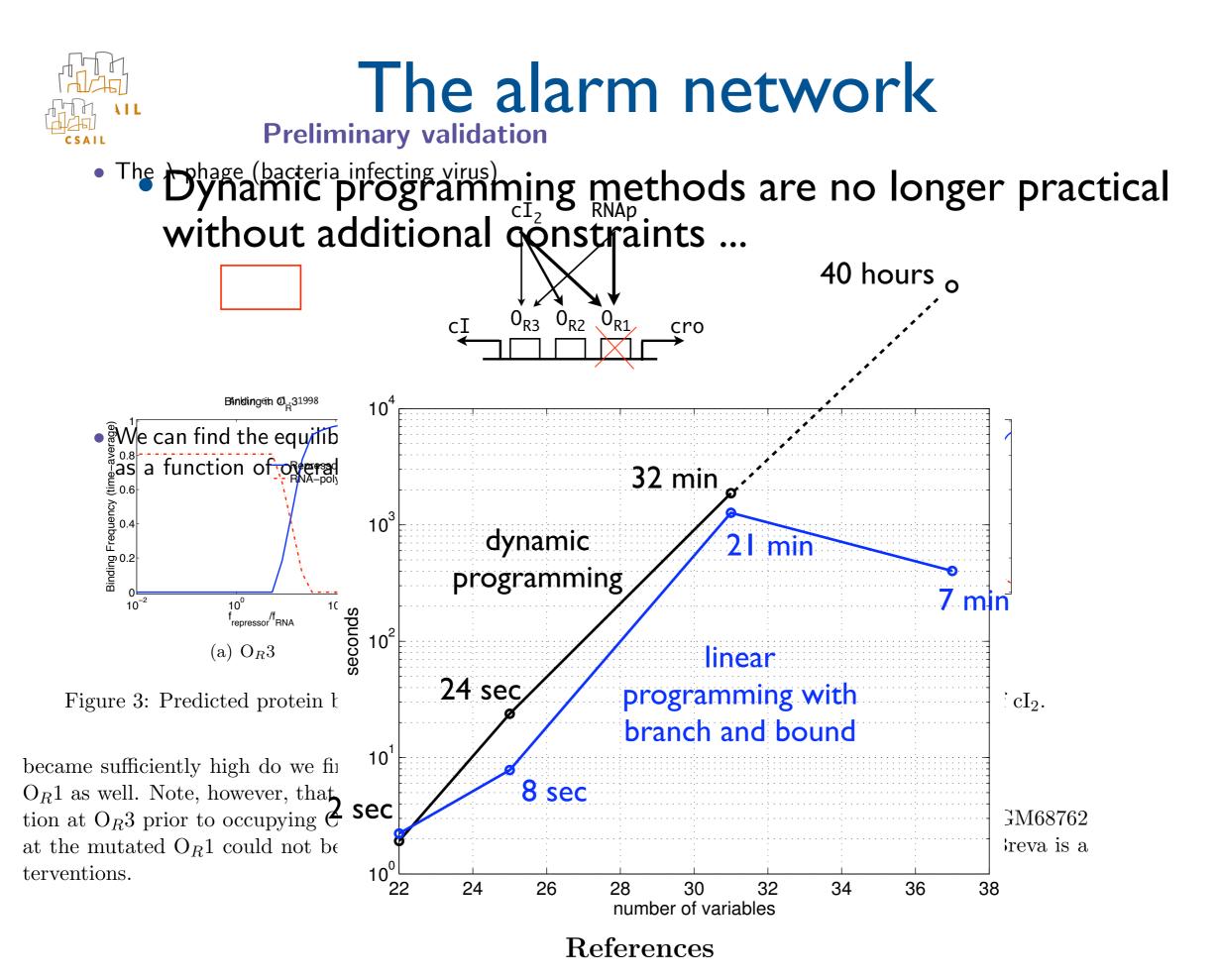
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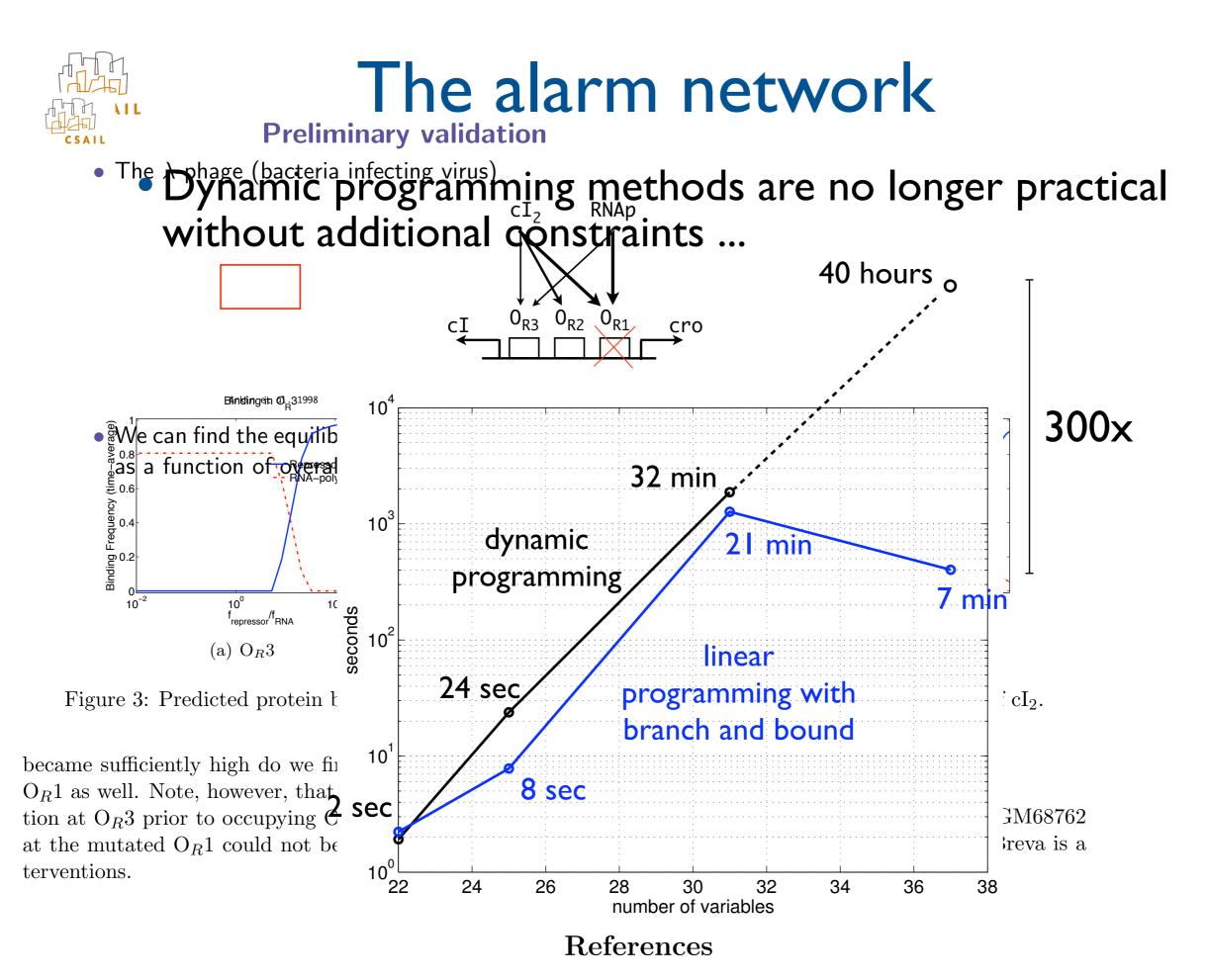
References









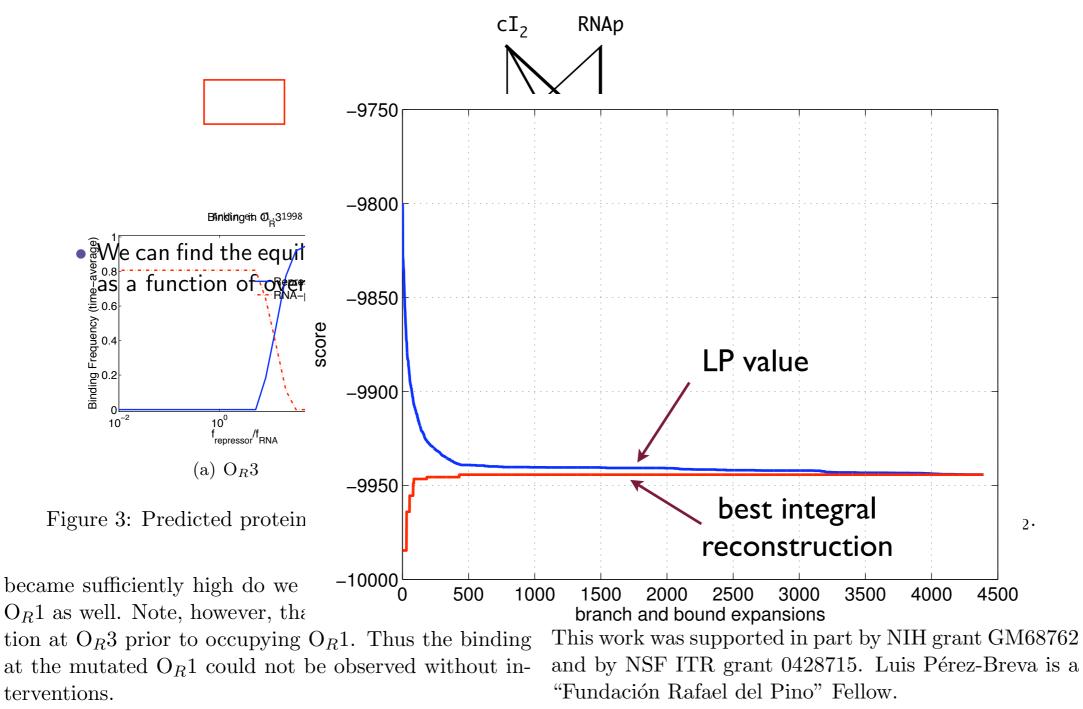




Anytime solution

Preliminary validation

• The λ -phage (bacteria infecting virus)



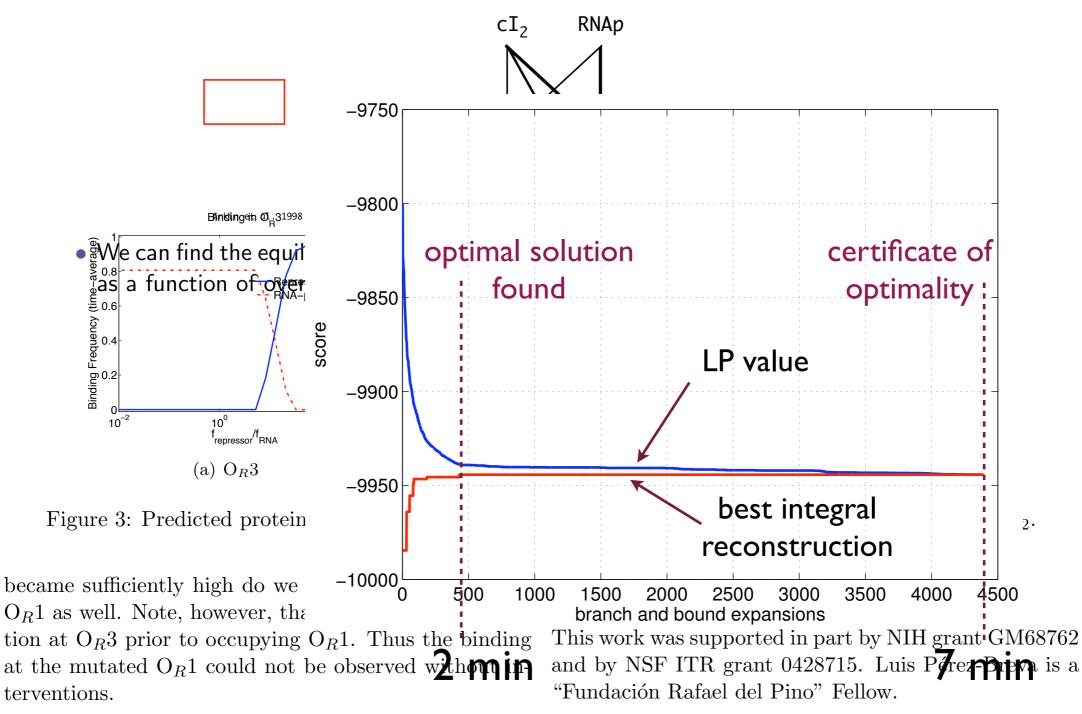
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References



Summary

Preliminary validation

- The Brinding the highest scoring Bayesian network structure from data is a hard combinatorial problem... but the "hard instances" may not be typical
- Our "anytime" approach to structure learning is based on linear programming relaxations that are iteratively • We can refine equipment of the sting iplane was high a function of operating protein concentrations. Repressor a function of operating protein concentrations. Repressor BNA-polymerase • The approach of the polymerase facets of the polymerase 0.4 -Répresso • The approach relies fundamentally on understanding the facets of the polytope corresponding to acyclic graphs 10^{-2} 10⁰ 10^{2} 10^{-2} 10^{2} 10^{-2} 10 10⁰ f /f repressor RNA /f RNA f /f repressor RNA (a) $O_R 3$ (b) $O_R 2$ 50 (c) $O_R 1$

Figure 3: Predicted protein binding to sites O_R3 , O_R2 , and mutated O_R1 for increasing amounts of cI_2 .

became sufficiently high do we find cI_2 at the mutated $O_R 1$ as well. Note, however, that cI_2 inhibits transcription at $O_R 3$ prior to occupying $O_R 1$. Thus the binding at the mutated $O_R 1$ could not be observed without interventions.

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References