

Learning with Partially Ordered Representations

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Thank you for the support!

Output in 2018-2019

- ▶ Journal Articles: 1 published, 1 in review
- ▶ Paper-Reviewed proceedings: 2
- ▶ Abstract-reviewed proceedings: 2
- ▶ Invited Talks: 6
- ▶ Conference Talks: 11
- ▶ Conference Posters: 1

The Main Idea

Learning is eased when shared properties of the domain structure
the space of hypotheses

Poverty of the Stimulus and Data Sparsity

Number of English words: $N \sim 10000$

Possible English 2-grams: $N^2 = 100000000$

Possible English 3-grams: $N^3 = 1000000000000$

Possible English 4-grams: $N^4 = 10000000000000000$

...

easy learning if normal distribution

Poverty of the Stimulus and Data Sparsity

BUT:

In the million-word Brown corpus of English:

45% of words,

80% of 2-grams

95% of 3-grams

appear EXACTLY ONCE

Bad for learning: Huge long-tailed distribution

How can a machine know that new sentences like

“nine and a half turtles yodeled” is good?

“turtles half nine a the yodeled” is bad?

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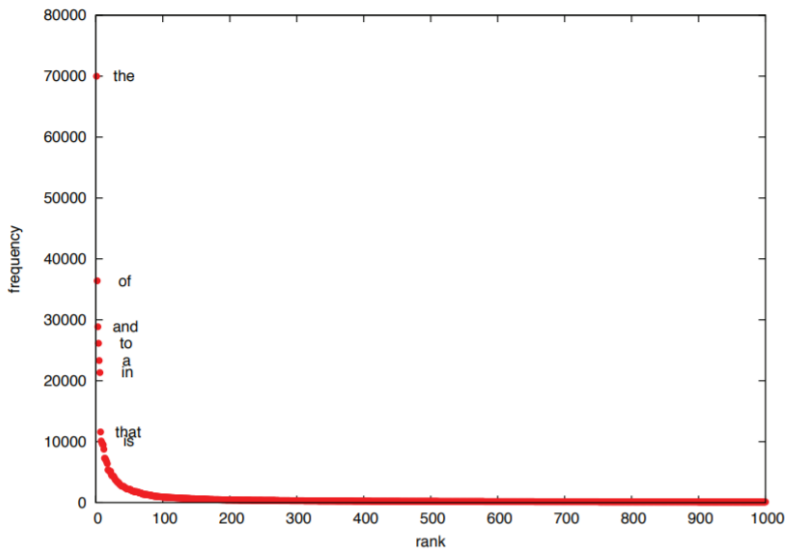
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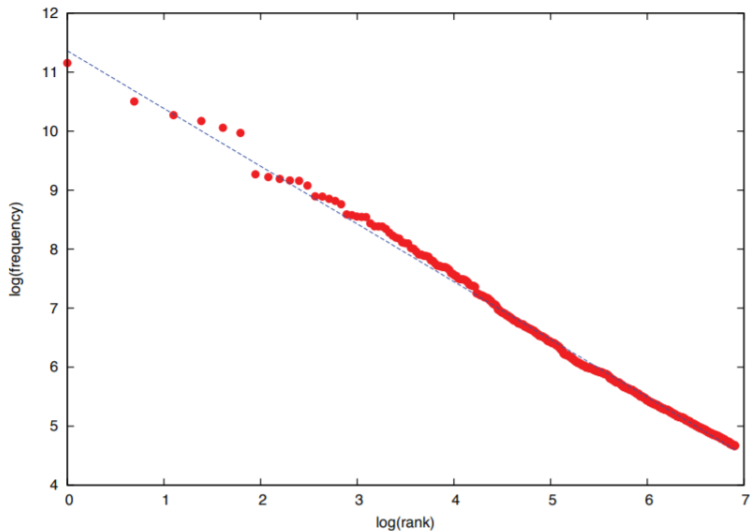
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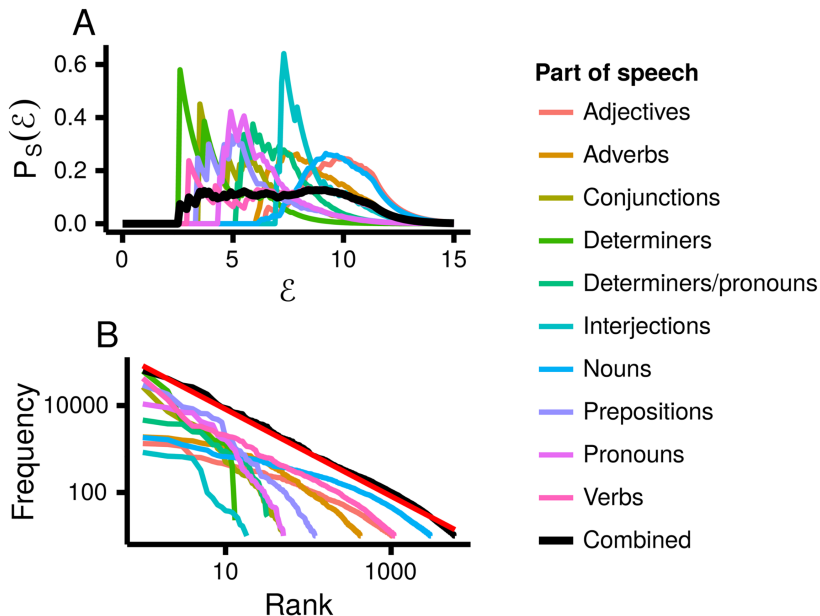
The Zipf Problem



The Zipf Problem



Zipf Emerges from Latent Features



NLP Example

In many NLP applications, text symbols are treated independently

Alphabet = $\{a, \dots, z, A, \dots, Z\}$ = 52 symbols

Forbidding maybe all capitals \rightarrow Explosion!

If we use feature `[capital]`, only 27! 26 letters + `[capital]`

Learning Algorithm (Chandlee et al 2018)

What have we done so far?

- ▶ Provably correct relational learning algorithm
- ▶ Prunes Hypothesis space according to ordering relation
- ▶ Provably identifies correct constraints for sequential data
- ▶ Uses data sparsity to its advantage!

Collaborative work with:



Jane Chandlee
(Haverford)

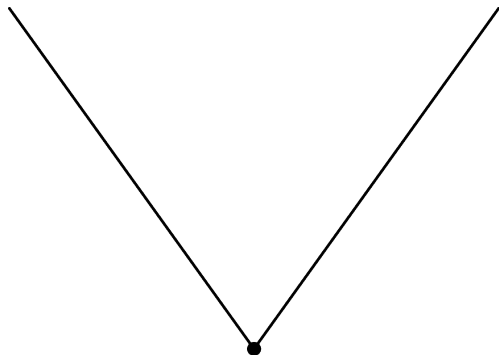


Jeff Heinz
(SBU)



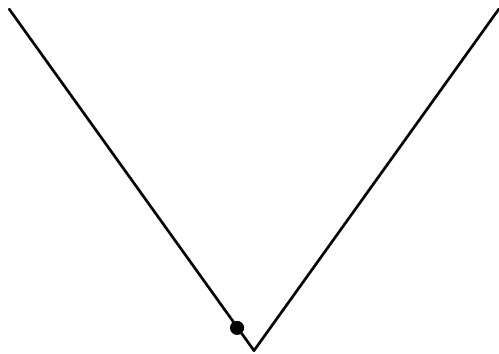
Adam Jardine
(Rutgers)

2D Schema of a Semilattice of Constraints



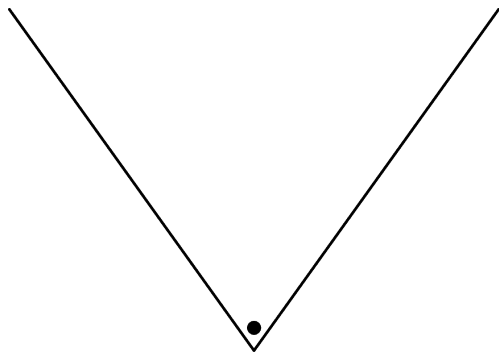
Is this sub-structure in the data sample?

2D Schema of a Semilattice of Constraints



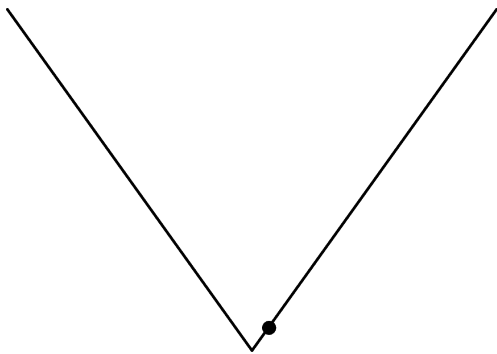
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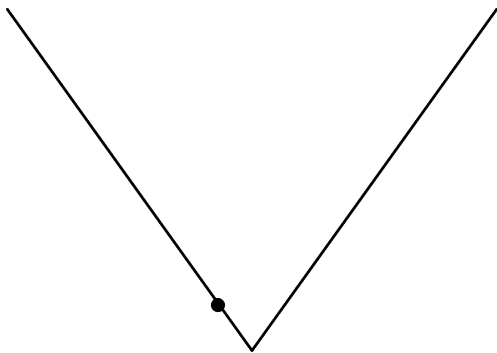
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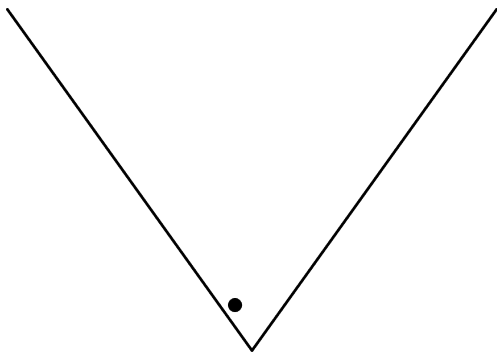
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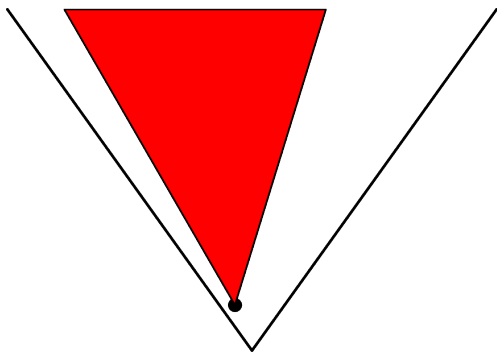
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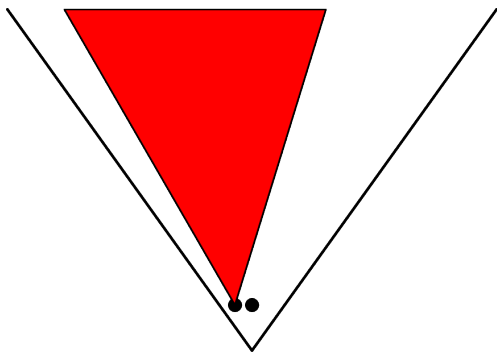
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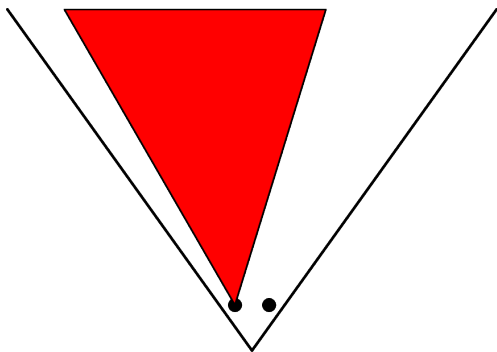
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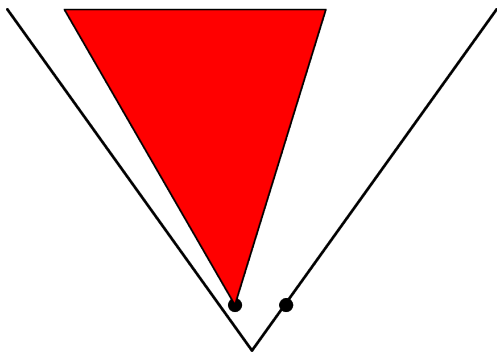
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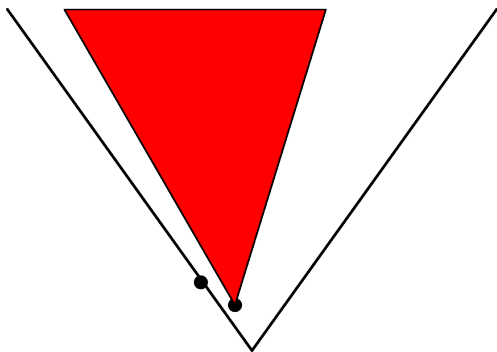
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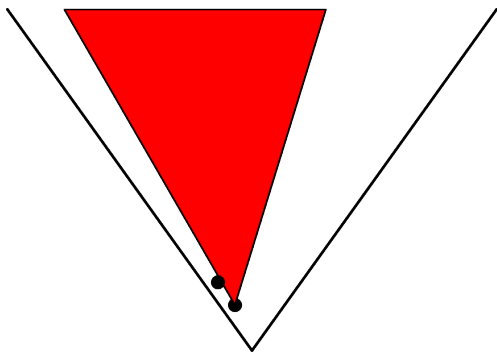
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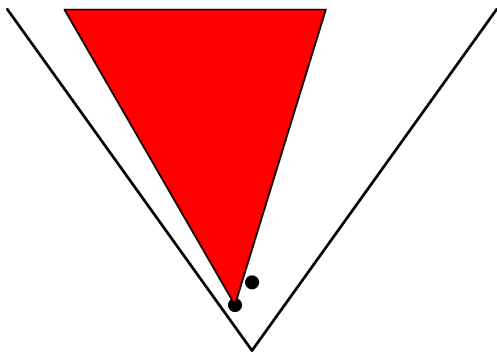
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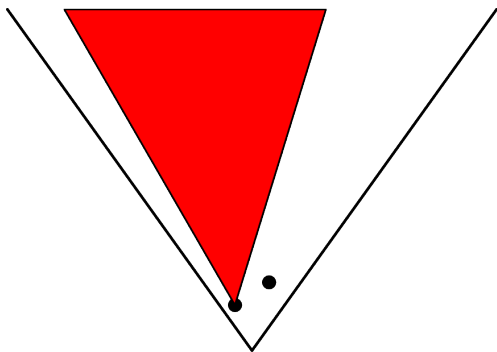
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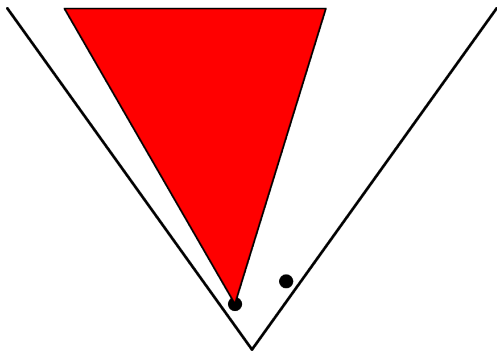
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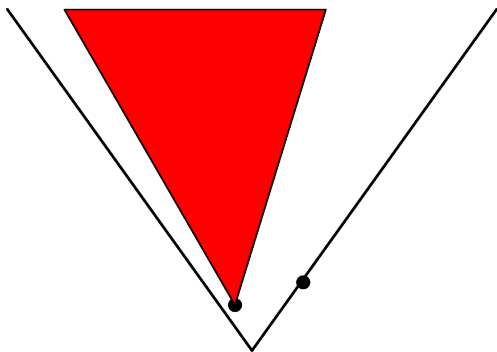
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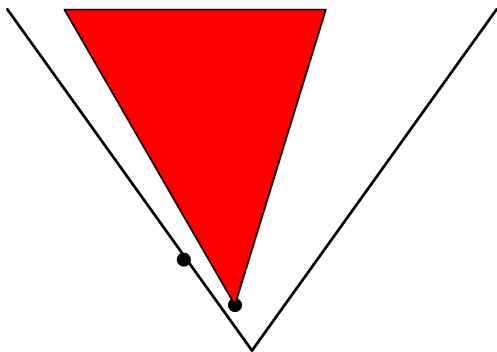
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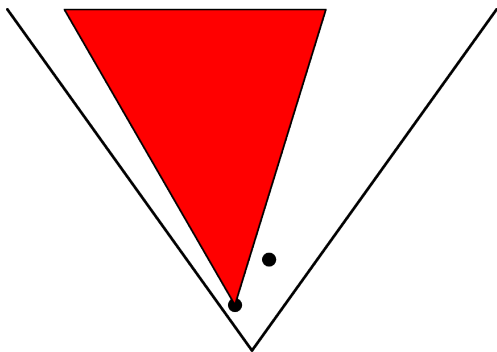
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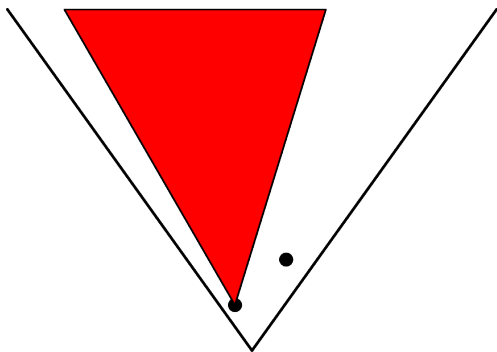
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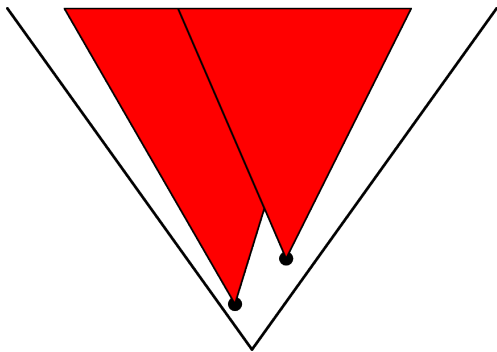
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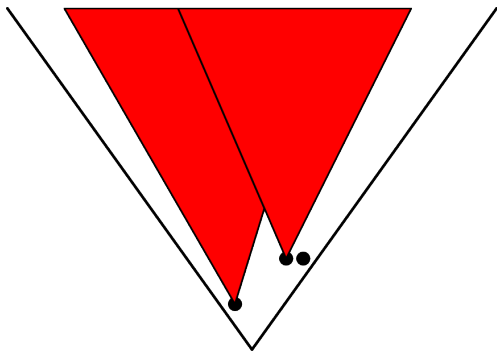
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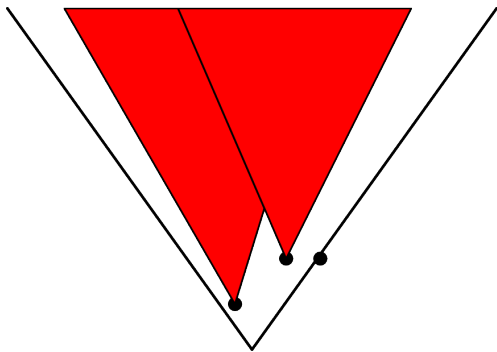
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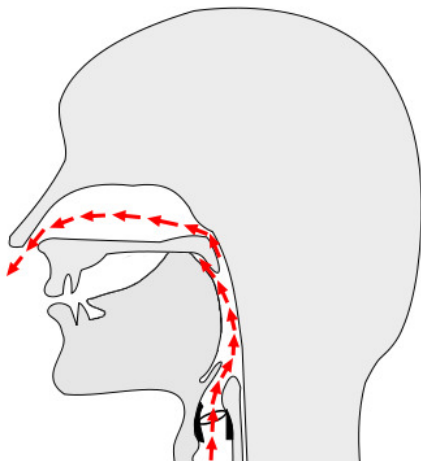
Example: Features in Linguistics

sing

ring

bling

ng = [+Nasal,+Voice,+Velar]



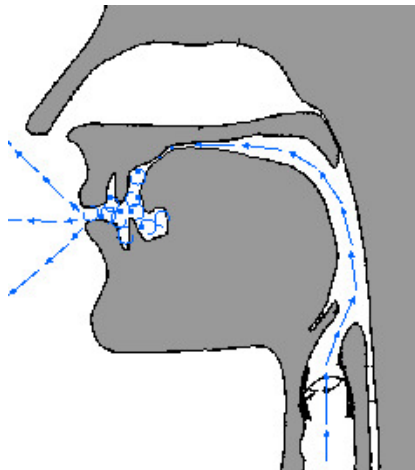
Example: Features in Linguistics

sand

sit

cats

s = [-Nasal, -**Voice**, - **Velar**]

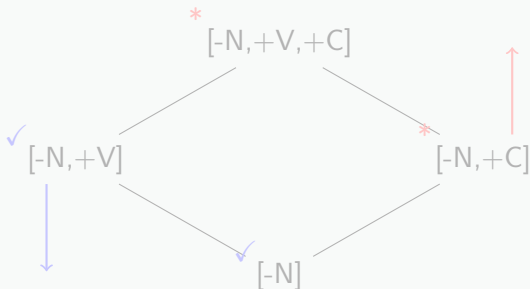


Structuring the Hypothesis Space: Feature Matrix Ideals

Feature Inventory

- ▶ $\pm N$ = Nasal
- ▶ $\pm V$ = Voiced
- ▶ $\pm C$ = Consonant

Example

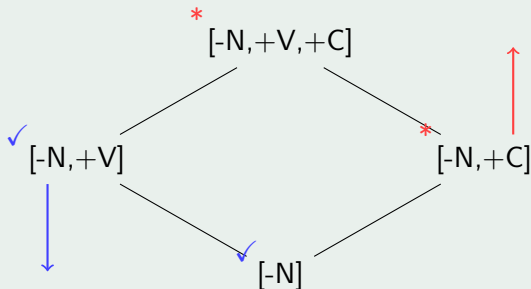


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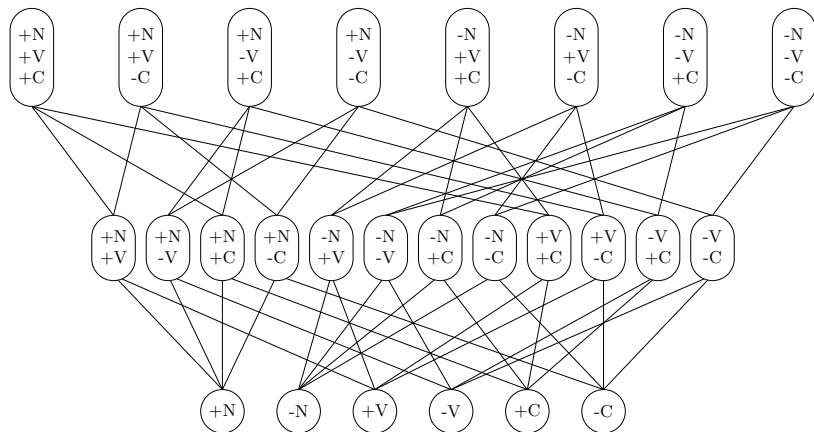
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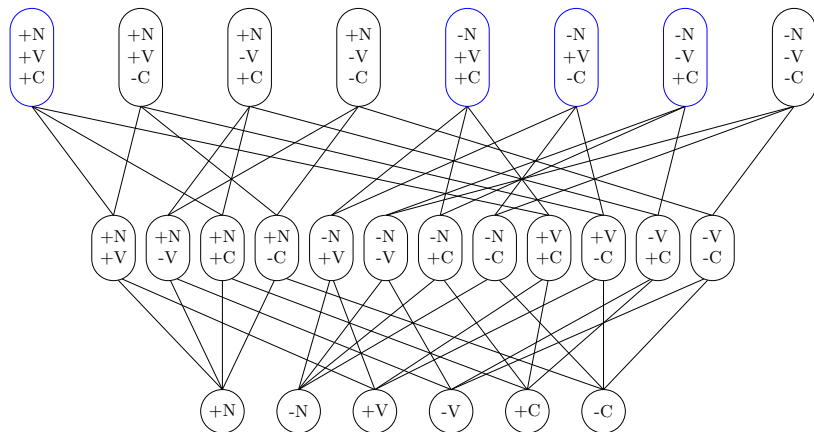
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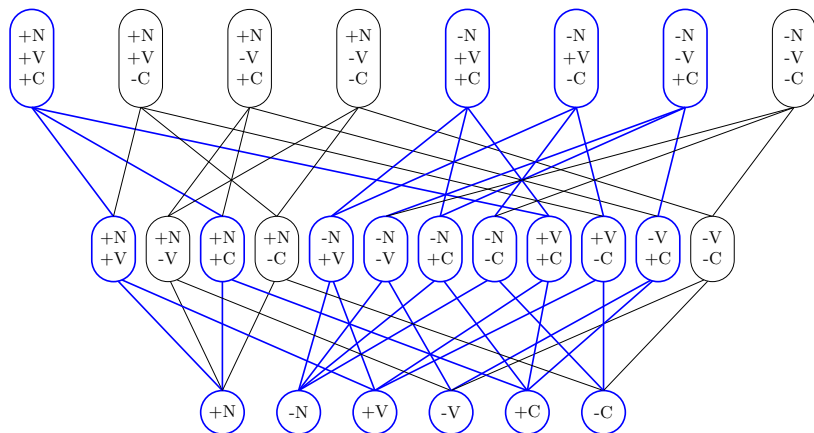
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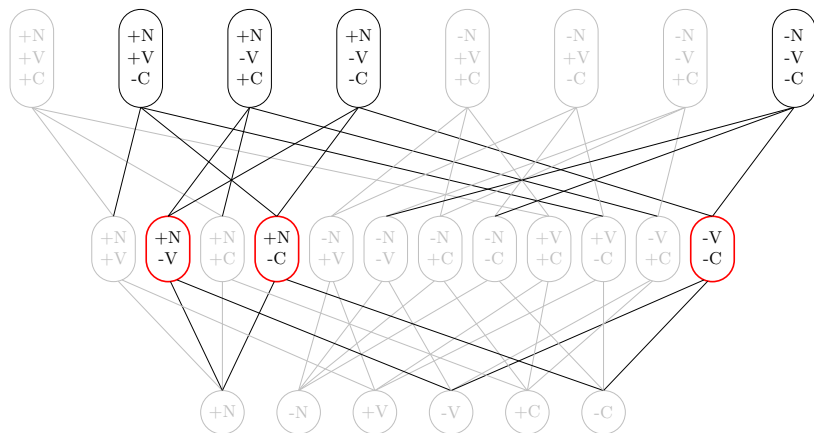
Example



Example



Example



Two Ways to Explore the Space

Top-Down Induction

- ▶ Start at the most specific points (highest) in the space
- ▶ Remove all the substructures that are present in the data.
- ▶ Collect the most general substructures remaining.

Bottom-Up Induction

- ▶ Beginning at the lowest element in the space,
- ▶ Check whether this structure is present in the input data.
- ▶ If so, move up the space, either to a point with an adjacent underspecified segment, or a feature extension of a current segment, and repeat.

Semilattice Explosion

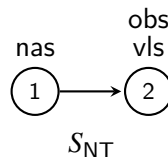
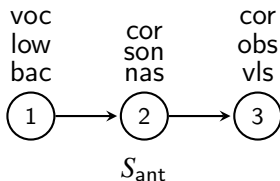


Table 2

Number of possible constraints for various values of $|C|$ and n

		$ C $			
		30	100	200	400
n	1	30	100	200	400
	2	900	10,000	40,000	160,000
	3	27,000	1,000,000	8 million	64 million
	4	810,000	100 million	1.6 billion	26 billion
	5	24 million	10 billion	320 billion	10 trillion

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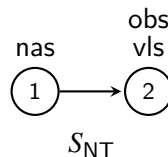
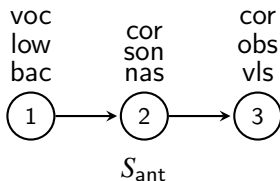


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Plan of the project

What has been done

Provably correct bottom-up learning algorithm

Goals of the Project

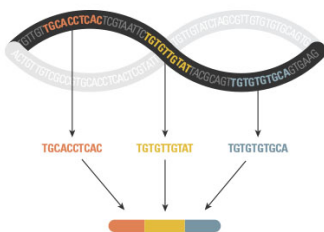
- ▶ Model Efficiency
- ▶ Model Implementation
- ▶ Model Testing - large linguistic datasets
- ▶ Model Comparison: UCLA Maximum Entropy Learner

Broader Impacts

- ▶ Learner that takes advantage of data sparsity
- ▶ applicable on any sequential data (language, genetics, robotic planning, etc.)
- ▶ implemented, open-source code

INSTRUCTIONS IN THE CODE

Healthy



DNA

Along with genes (shown here in **orange**, **yellow**, and **blue**), which produce the components for proteins, the genome contains non-coding instructions (**gray**) that direct how these components are assembled.

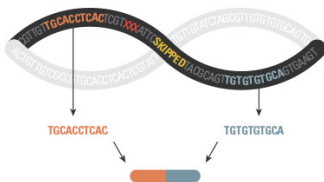
ASSEMBLY

The cell transcribes specific parts of the code according to the instructions.

PROTEIN

The parts are then assembled into a healthy protein.

Diseased



DNA

A mutation (**red**) in the non-coding instructions causes one gene segment to be ignored.

ASSEMBLY

This variation makes the cell skip over a protein-coding segment of the genome.

PROTEIN

The error in the instruction set leads to an altered protein, which may raise the risk for disease.