



Finding Most Likely Haplotypes in General Pedigrees through Parallel Branch and Bound Search

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Outline

- Haplotype Inference as Bayes Net query.
- AND/OR Branch and Bound for Graphical Models.
 - State-of-the-art MPE solver. Won all three MPE tracks in PASCAL'11 Challenge.
 - Very complex instances necessitate parallelism. Run on grid of loosely coupled commodity hardware.
 - Pruning power causes significant job imbalance.
- Load Balancing through Complexity Estimation.
 - Learn linear regression models offline.
- Good parallel results on complex pedigree instances.



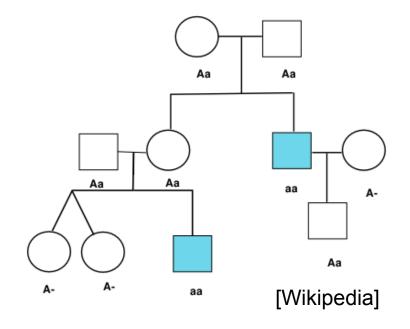
The Haplotype Configuration Problem

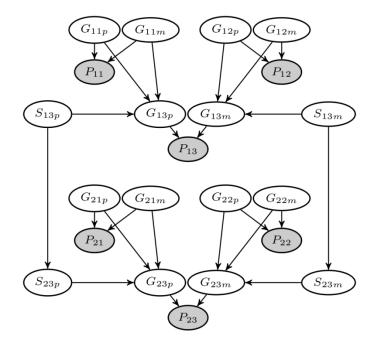
- Haplotype: the sequence of alleles at different loci inherited by an individual from one parent .
- Genotype: the two haplotypes of an individual constitute this individual's genotype. Measured genotypes results in a list of unordered pairs of alleles; one pair for each locus.
- A recombination occurrs between two loci, if an haplotype of an individual contains two alleles that resided in different haplotypes of the individual's parent.
- The Maximum Likelihood Haplotype Configuration problem, consists of finding a joint haplotype configuration for all members of the pedigree which maximizes the probability of the data.
- The haplotyping problem often does not have a unique solution.



Problem Statement

- Find most likely haplotype given partial genotypes.
 - *Pedigree* chart models ancestral relations.





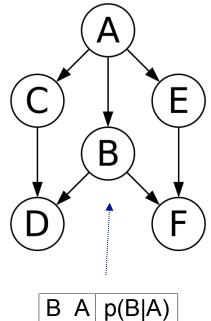
- Encode problems as Bayesian Network.
 - "Most Probable Explanation" (MPE) yields haplotype.



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Bayesian Networks

- Given is a graphical model and a query:
 - Bayesian Network:
 - Variables {X_i} and conditional probability tables { P(X_i | par_i) }.
 - Factorizes joint probability distribution.
 - MPE Query:
 - Most Probable Explanation: Find assignment that maximizes joint probability.
 - Problem is NP-hard in general.
 - Advanced algorithms exist, exponential in tree width *w** of graph.



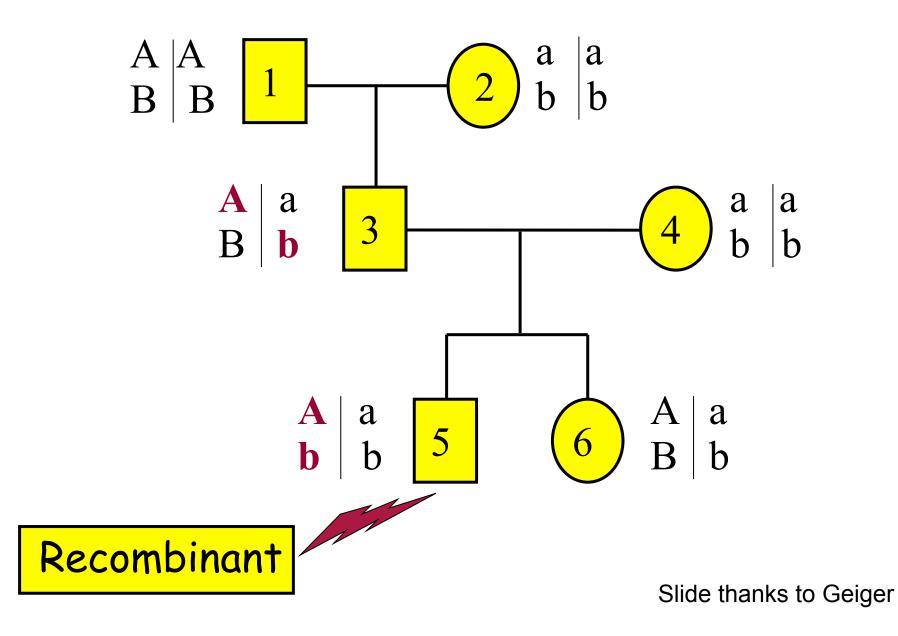
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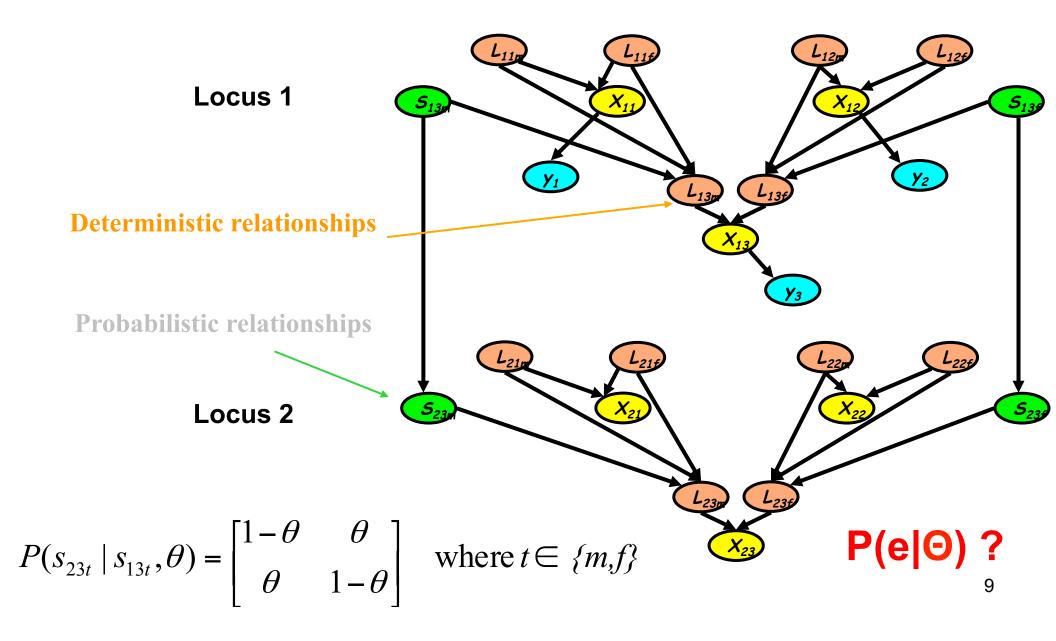
Two Loci Inheritance





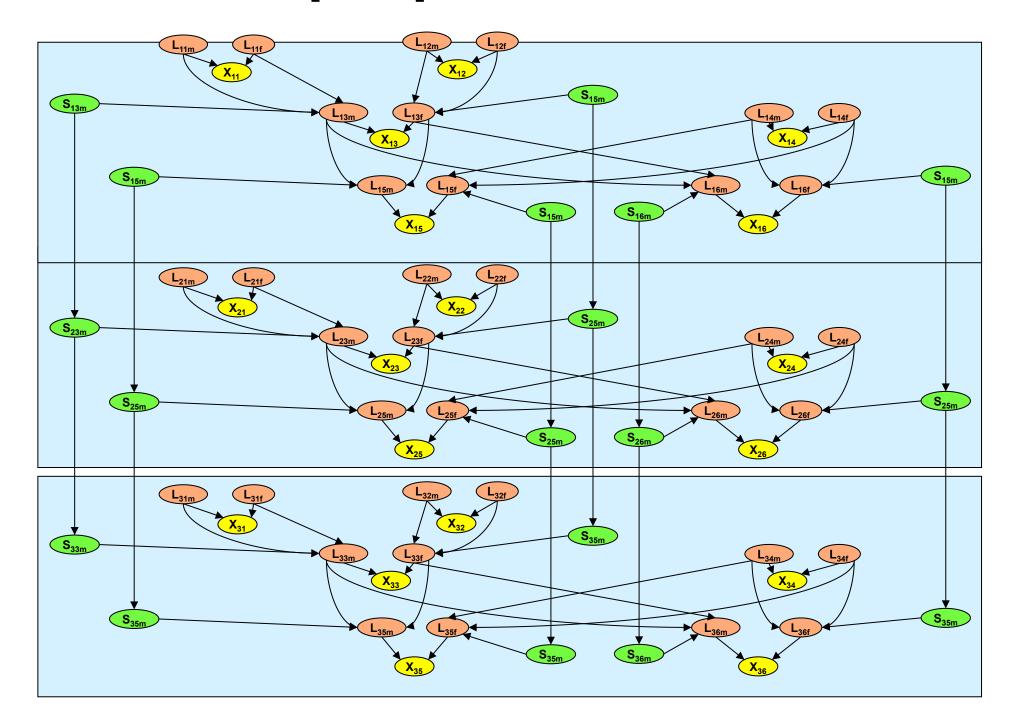
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Bayesian Network for Recombination





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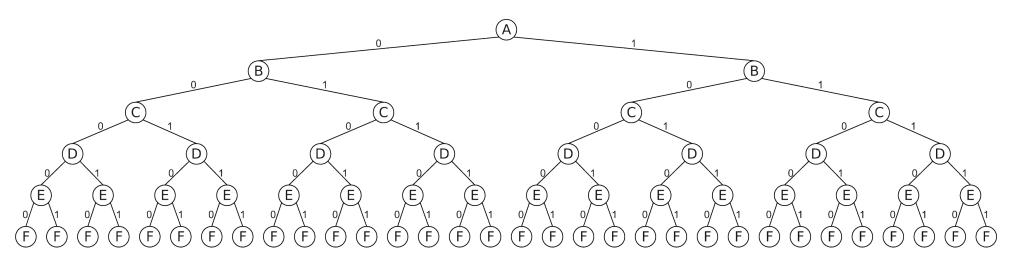






Searching the standard space (Depth-First Search)

- Standard depth-first search procedure:
 - Instantiate variables one at a time.
 - Backtrack in case of inconsistencies.
 - Time complexity: exp(n).
 - Linear space.



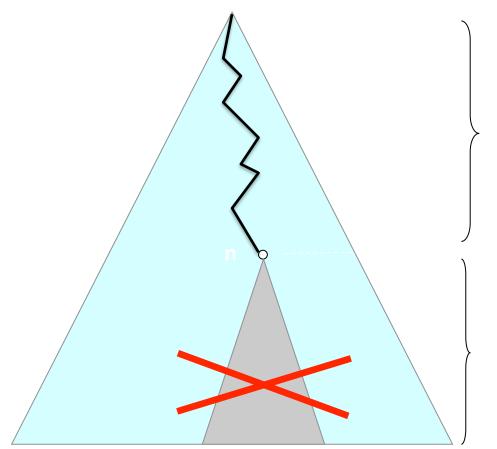
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Branch-and-Bound Search



Upper Bound UB

Lower Bound LB(n)

g(n)=cost of the search path to n

Prune if $LB(n) \ge UB$

H(n) = estimates the optimal cost below n

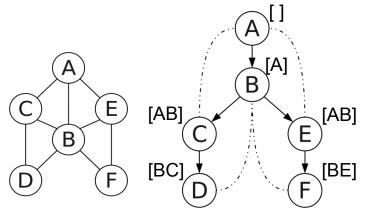
OR Search Tree

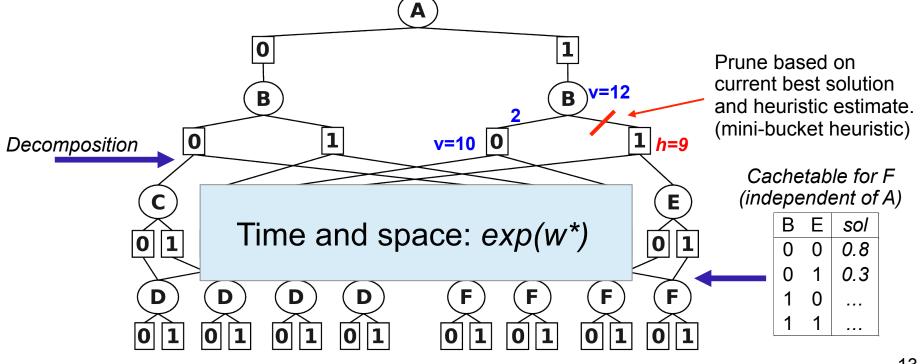
(Lawler & Wood66)



AND/OR Search Spaces Marinescu & Dechter

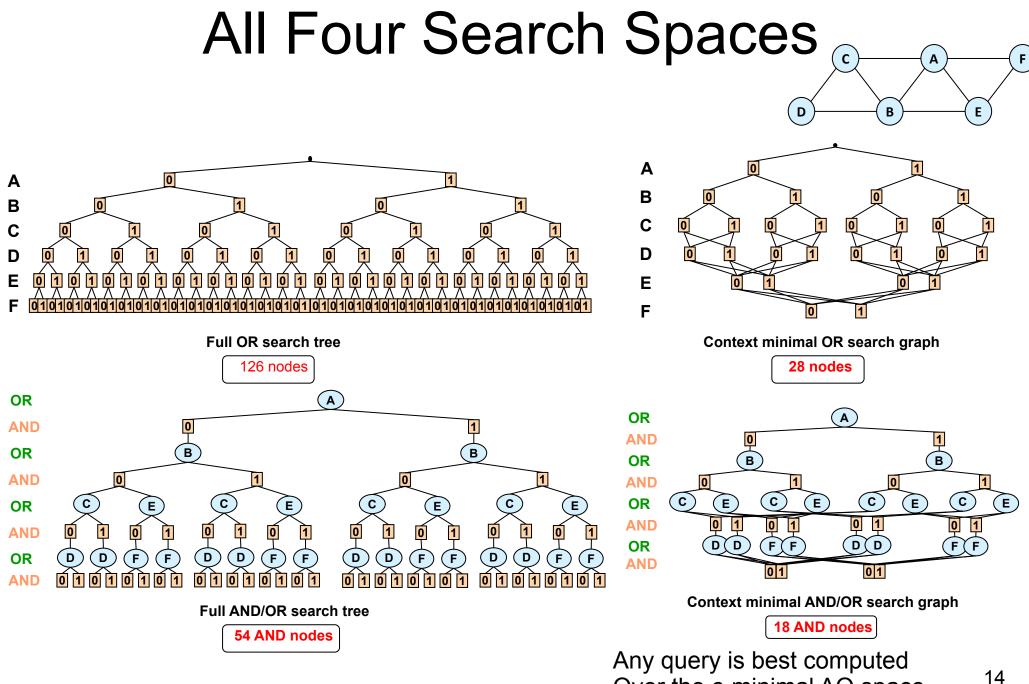
- Improves upon standard search:
 - Decompose independent subproblems.
 - Merge unifiable subproblems.







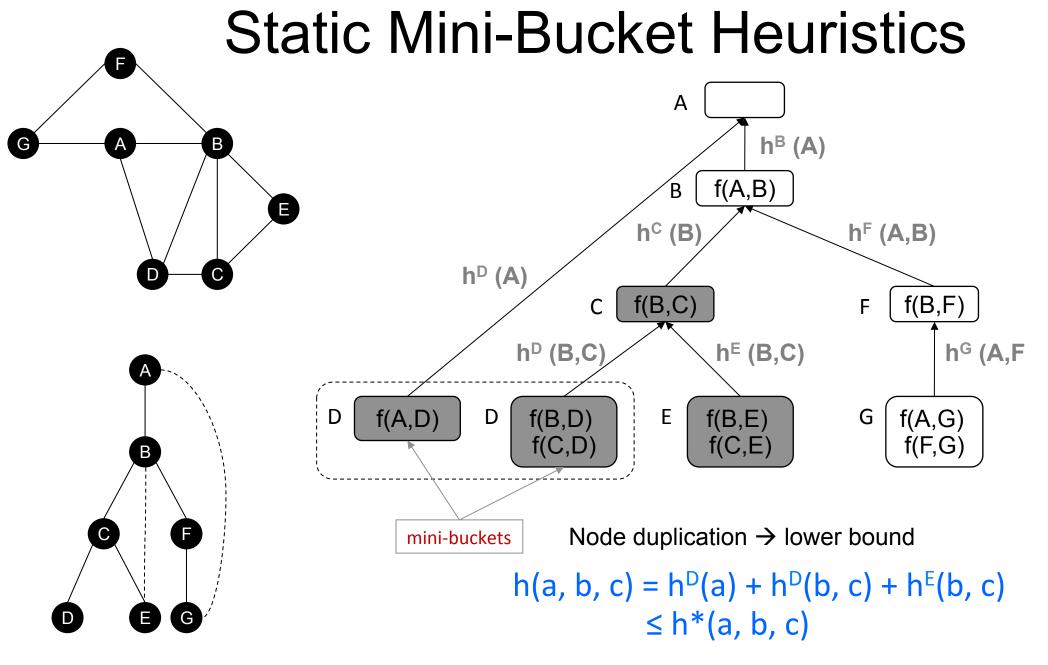




Over the c-minimal AO space

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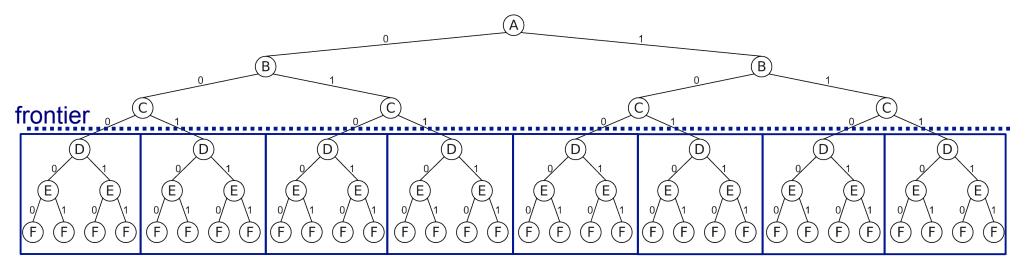
Ordering: (A, B, C, D, E, F, G)



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Searching in Parallel

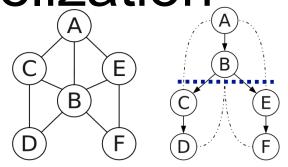
- Parallel tree search. [Kumar]
- Introduce *parallelization frontier* :
 - Condition on partial instantiations.
 - Solve subtrees in parallel and combine solutions.
 - Speedup at most linear.

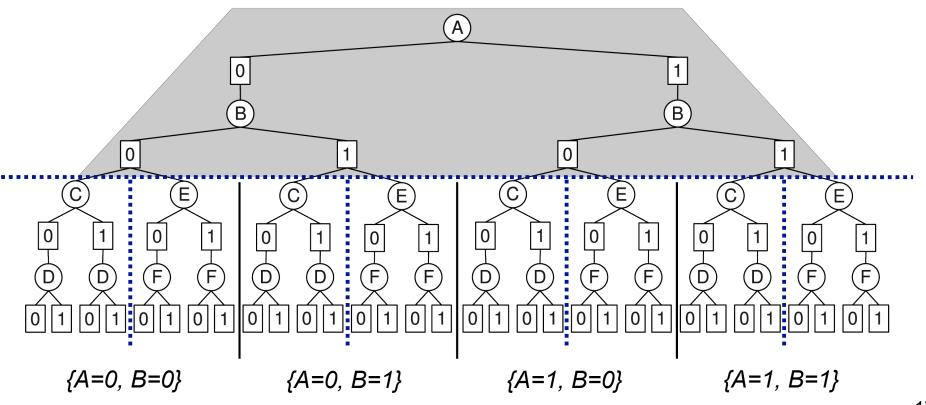




AND/OR Search Parallelization

- Depth 2 cutoff: 8 subproblems.
 - Conditioning and decomposition.
 - Full parallelization upfront (static).



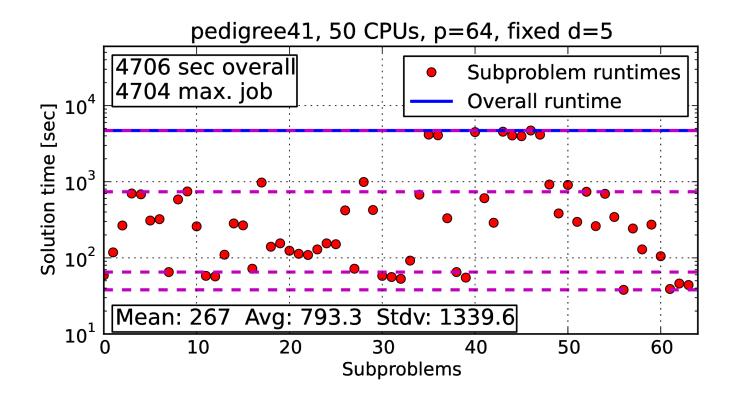






Subproblem Variance

- Fixed-depth cutoff:
 - Subproblems have identical structure.
 - But large variance in runtime complexity?

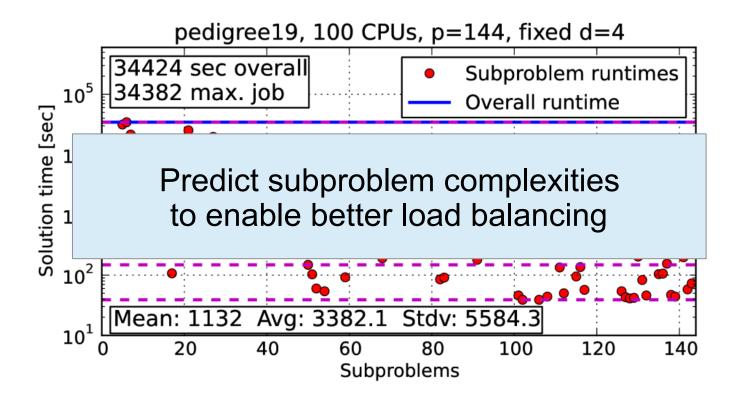




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Subproblem Variance

- In spite of identical structure:
 - Effect of bounds and pruning differs vastly.
 - Few subproblems dominate overall performance.





Subproblem Complexity Prediction

- Model number of nodes N(n) as exponential function of subproblem features $\varphi_i(n)$:

 $N(n) = b \uparrow \sum j \uparrow \square \lambda \downarrow j \varphi \downarrow j(n)$

• Then consider log number of nodes:

 $\log N(n) = \sum j \uparrow \mathbb{A} \downarrow j \varphi \downarrow j(n)$

- Thus, finding parameter values λ_j can be seen as a <u>linear</u> <u>regression</u> problem.
 - Given m sample subproblems n_k , minimize MSE:

 $1/m\sum k=1 \ \widehat{m} (\sum j \ \widehat{k}) \ j \ \varphi \downarrow j \ (n \downarrow k \) -\log N(n \downarrow k \) \) \ 12$



34 Subproblem Features

- Static, structural properties:
 - Number of variables.
 - Avg. and max. width.
 - Height of sub pseudo tree.
 - Etc.
- Dynamic, runtime properties:
 - Upper and lower bound.
 - Pruning ratio and depth of small AOBB probe.
 - Etc.

Subproblem variable statistics (static):

- 1: Number of variables in subproblem.
- 2-6: Min, Max, mean, average, and std. dev. of variable domain sizes in subproblem.

Pseudotree depth/leaf statistics (static):

- 7: Depth of subproblem root in overall search space.
- 8-12: Min, max, mean, average, and std. dev. of depth of subproblem pseudo tree leaf nodes, counted from sub-problem root.
 - 13: Number of leaf nodes in subproblem pseudo tree.

Pseudo tree width statistics (static):

- 14-18: Min, max, mean, average, and std. dev. of induced width of variables within subproblem.
- 19-23: Min, max, mean, average, and std. dev. of induced width of variables within subproblem, *when conditioning on subproblem root conditioning set*.

Subproblem cost bounds (dynamic):

- 24: Lower bound L on subproblem solution cost, derived from current best overall solution.
- 25: Upper bound U on subproblem solution cost, provided by mini bucket heuristics.
- 26: Difference U L between upper and lower bound, expressing "constrainedness" of the subproblem.

Pruning ratios (dynamic), based on running 5000 node expansion probe of AOBB:

- 27: Ratio of nodes pruned using the heuristic.
- 28: Ratio of nodes pruned due of determinism (zero probabilities, e.g.)
- 29: Ratio of nodes corresponding to pseudo tree leaf.

Sample statistics (dynamic), based on running 5000 node expansion probe of AOBB:

- 30: Average depth of terminal search nodes within probe.
- 31: Average node depth within probe (denoted \overline{d}).
- 32: Average branching degree, defined as $\sqrt[d]{5000}$.

Various:

- 33: Mini bucket *i*-bound parameter.
- 34: Max. subproblem variable context size minus mini bucket *i*-bound.





- Subproblem variable statistics (static):
 - N: Number of variables in subproblem.
 - Min, Max, mean, average, and std. dev. of variable domain sizes in subproblem.
- Pseudo tree depth/leaf statistics (static):
 - h: Depth of subproblem root in overall search space.
 - Min, max, mean, average, and std. dev. of depth of subproblem pseudo tree leaf nodes, counted from subproblem root.
 - L: Number of leaf nodes in subproblem pseudo tree.





- Pseudo tree width statistics (static):
 - Min, max, mean, average, and std. dev. of induced width of variables within subproblem.
 - Min, max, mean, average, and std. dev. of induced width of variables within subproblem, when conditioning on subproblem root conditioning set.
- Subproblem cost bounds (dynamic):
 - Lower bound *L* on subproblem solution cost, derived from current best overall solution.
 - Upper bound *U* on subproblem solution cost, provided by mini bucket heuristics.
 - Difference *U-L* between upper and lower bound, expressing "constrainedness" of the subproblem.





- Pruning ratios (dynamic), based on running 5000 node expansion probe of AOBB:
 - Ratio of nodes pruned using heuristic upper bound.
 - Ratio of nodes pruned due to determinism (zero probabilities, e.g.).
 - Ratio of nodes corresponding to pseudo tree leaf.
- Sample statistics (dynamic), based on running 5000 node expansion probe of AOBB:
 - Average depth of terminal search nodes within probe.
 - Average node depth within probe (denoted d).
 - Average branching degree, defined as $\sqrt[4]{5000}$





- Various:
 - Mini bucket *i*-bound parameter.
 - Max. subproblem variable context size minus mini bucket *i*-bound.
- In total 34 features.



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Specifics of Learning

- Lasso learning to avoid overfitting.
 - Add regularization term to MSE. $1/m \sum k = 1 \text{ fm} (\sum j \text{ fm} \lambda \downarrow j \varphi \downarrow j (n \downarrow k) - \log N(n \downarrow k)) \text{ f2} + \alpha$ $\|\lambda\||\downarrow 1$
 - Encourages sparsity, implicit feature selection.
 - α = 0.1 through cross validation.
- Measure:
 - MSE: Prediction error (MSE)
 - TER: Training error (MSE)
 - PCC: Pearson correlation coefficient (normalized cov.)





Regression Results

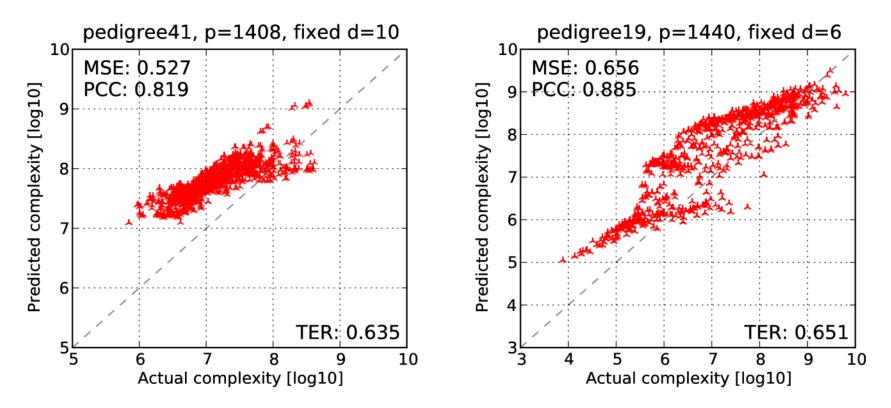
- 31 instances total (13 pedigrees) from 4 classes.
 - Run each with fixed-depth cutoff.
 - Choose up to 500 subproblem samples.
 - Yields 11,500 samples overall.
- Most general regression approach:
 - Train model on samples from 30 instances.
 - Test on samples from remaining instance.
- Other scopes of learning evaluated:
 - Per-instance and per-class, comparable results.



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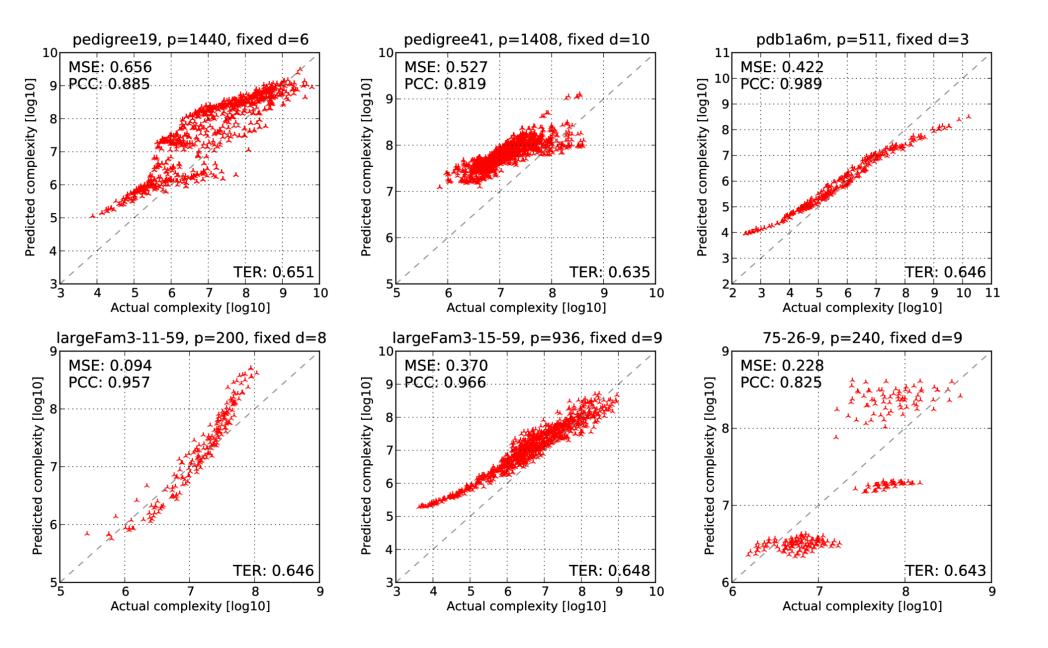
Regression Results

- Prediction on two pedigree examples:
 - Test error (MSE) close to training error (TER).
 - Fairly high correlation coefficient.





Across all Problems/Classes





Parallelization Scheme

- Iteratively split estimated largest subproblem.
 - Until desired number of subproblems is reached.

Algorithm 1 Finding the parallelization frontier

Input: Pseudo tree \mathcal{T} with root X_0 , subproblem count p, subproblem complexity estimator \hat{N} .

Output: Set F of subproblem root nodes with $|F| \ge p$.

1:
$$F \leftarrow \{\langle X_0 \rangle\}$$

2: while |F| < p:

3:
$$n' \leftarrow \arg \max_{n \in F} \hat{N}(n)$$

$$4: \quad F \leftarrow F \setminus \{n'\}$$

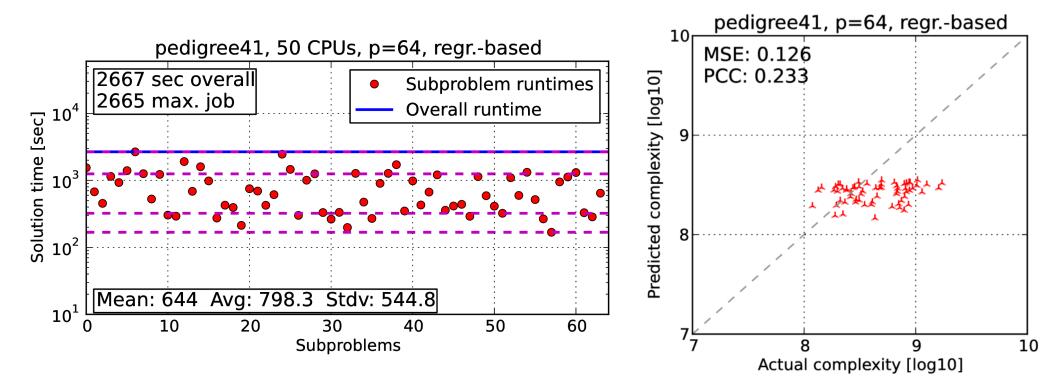
5: $F \leftarrow F \cup children(n')$





Detailed Parallel Results

- Pedigree41:
 - Left: detailed subproblem statistics
 - Right: actual vs. predicted complexity

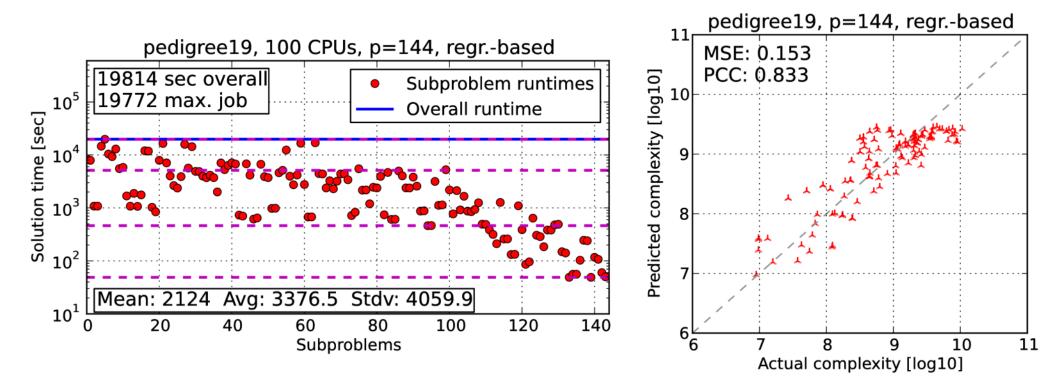






Detailed Parallel Results

- Pedigree19:
 - Left: detailed subproblem statistics.
 - Right: actual vs. predicted complexity.





Overall Parallel Results

- Pedigrees with 20-25 individuals and 20-25 loci.
 - *n* is number of variables, *k* max. domain size, *w* induced width, h pseudotree height. Runtime in *hh:mm*.

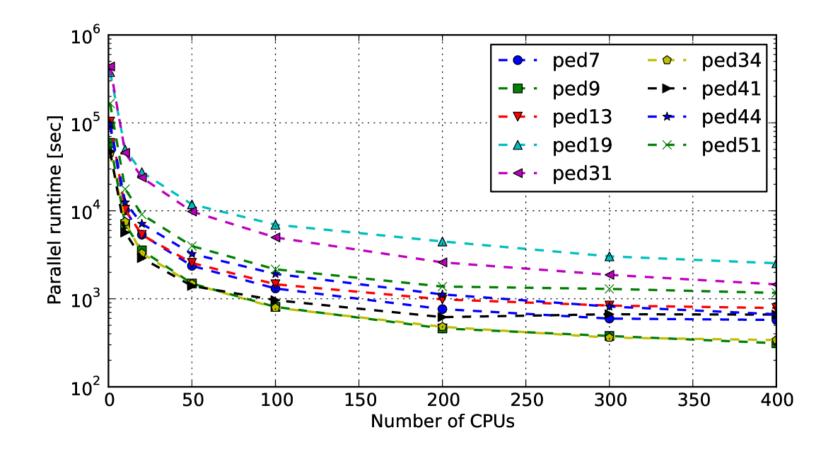
						Number of CPUs						
inst	n	k	w	h	seq	10	20	50	100	200	300	400
ped7	1068	4	32	90	26:11	02:49	01:29	00:39	00:21	00:12	00:09	00:09
ped9	1118	7	27	100	16:26	01:57	00:59	00:24	00:13	00:07	00:06	00:05
ped13	1077	3	32	102	28:42	02:51	01:28	00:42	00:24	00:16	00:13	00:13
ped19	793	5	25	98	105:11	13:48	07:38	03:17	01:56	01:14	00:50	00:42
ped31	1183	5	30	85	121:25	12:43	06:38	02:43	01:23	00:43	00:31	00:24
ped34	1160	5	31	102	12:34	02:05	00:54	00:24	00:13	00:08	00:06	00:05
ped41	1062	5	33	100	13:07	01:34	00:48	00:23	00:16	00:10	00:11	00:11
ped44	811	4	25	65	26:52	03:28	01:58	00:54	00:32	00:18	00:13	00:11
ped51	1152	5	39	98	46:13	04:54	02:31	01:06	00:36	00:22	00:21	00:19





Overall Parallel Results

• Parallel runtimes plotted.

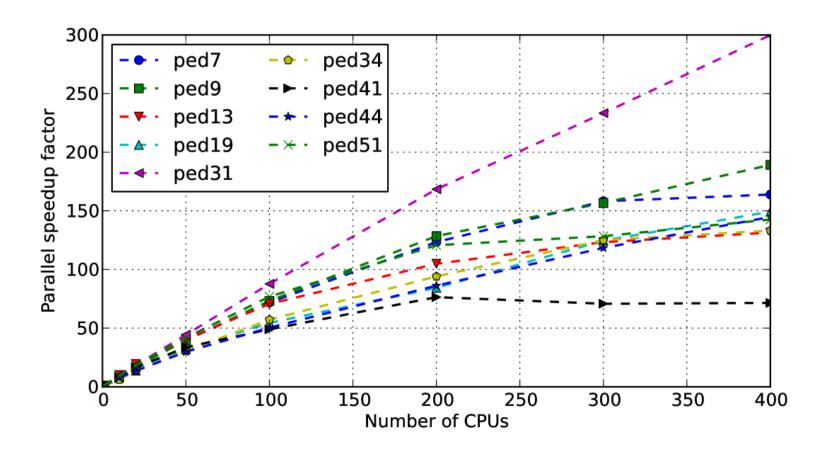






Parallel Speedup

- Speedup relative to sequential algorithm.
 - Highest potential with most complex problems.





Summary

- Express haplotype computation as MPE query.
 - Exploit graph structure and apply advanced AND/OR search algorithms (decomposition and caching and mini-bucket heuristics).
- Parallel AND/OR Branch and Bound:
 - Powerful pruning impedes load balancing.
 - Learn complexity regression model offline.
- Empirical results: Improved load balancing.
 - Good parallel performance and speedup on hard pedigree instances.
- Deployed in Superlink-Online SNP:
 - http://cbl-hap.cs.technion.ac.il/superlink-snp