Automatic Algorithm Configuration based on Local Search

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Real-world example for algorithm configuration: Tree search for SAT-encoded software verification

- New DPLL-type SAT solver (Spear)
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- Minimize expected run-time

- Problems:
  - Huge variation in runtime (with default setting):
    <1 second for some instances
    >1 day for others
  - Good performance on a few instances does not generalise well
  - Many possible configurations (8.34×10^{17} after discretization)

Standard algorithm configuration approach

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- Perform iterative manual tuning:

  start with some parameter configuration
  repeat
      modify a single parameter
      if *results on tuning set improve* **then**
          keep new configuration
  until *no more improvement possible (or "good enough")*

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Solution:

- Automate process
- Use more powerful search method

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- Search approaches
  [Minton 1993, 1996], [Hutter 2004], [Cavazos & O'Boyle 2005], [Adenso-Diaz & Laguna 2006], [Audet & Orban 2006]

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- Lots of work on per-instance tuning / reactive search
  $\rightsquigarrow$ orthogonal to the approach followed here

Outline

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with probability $p_{restart}$ randomly pick new θ

$\rightsquigarrow$ Performs **biased random walk over local optima**

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  (user-defined: *e.g.* empirical mean, median, ...)

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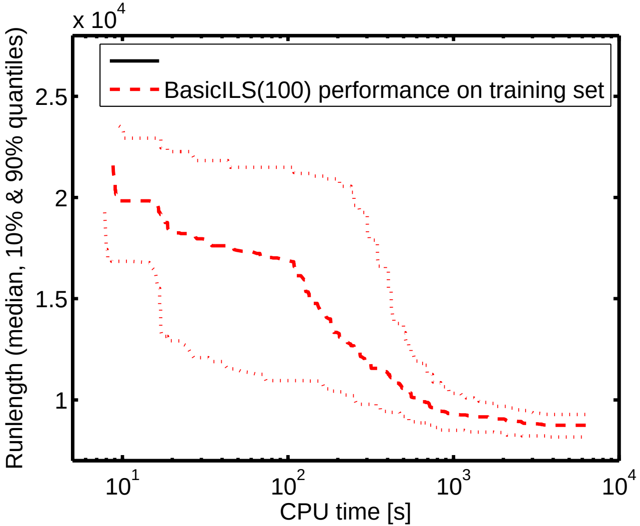
- Too few
  - $\rightsquigarrow$ very noisy approximations $\hat{c}_N(\theta)$
  - $\rightsquigarrow$ poor generalisation to independent test runs

Generalisation to independent test set,large N (N=100)

(SAPS on quasigroups with holes)



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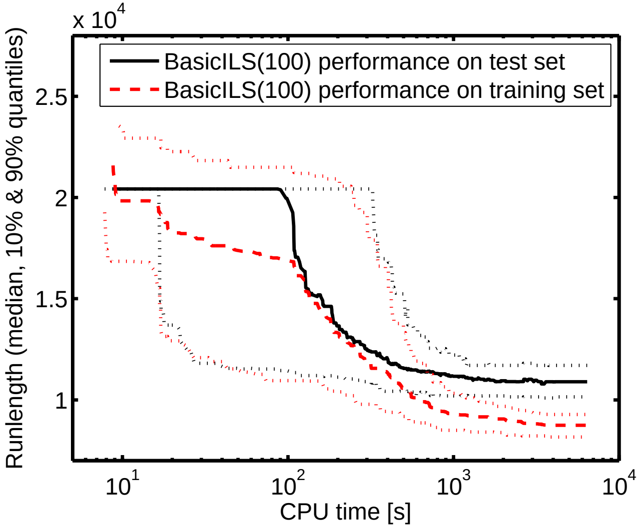

Generalisation to independent test set, small N (N=1)

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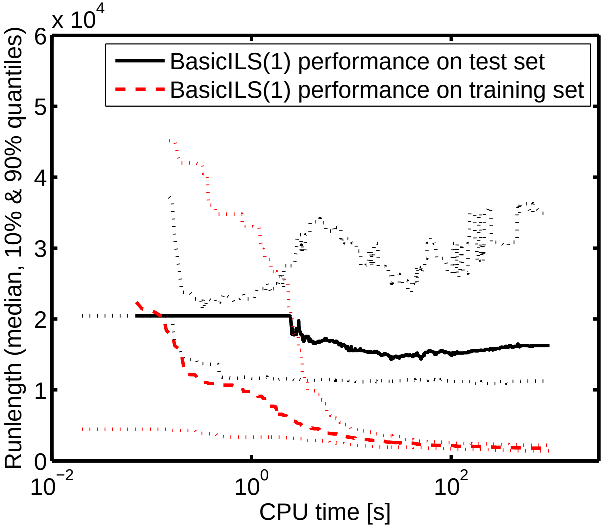

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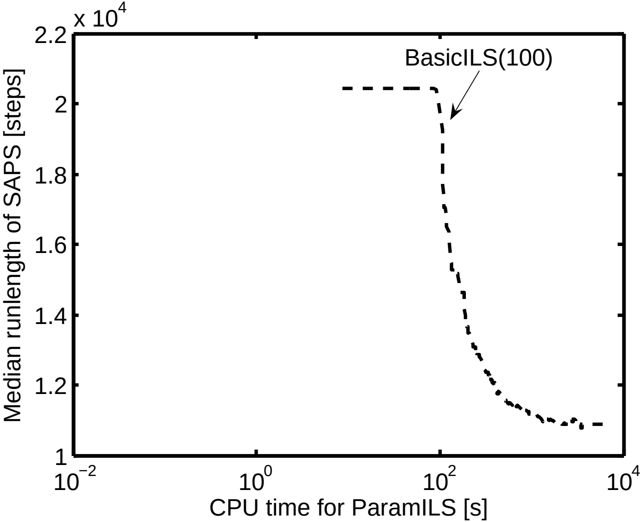

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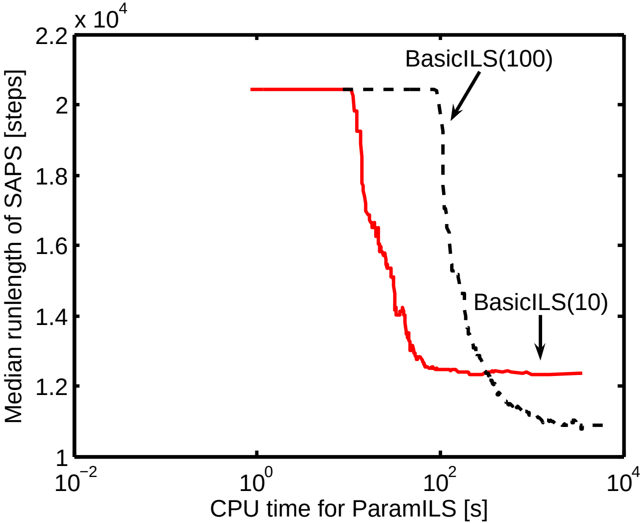

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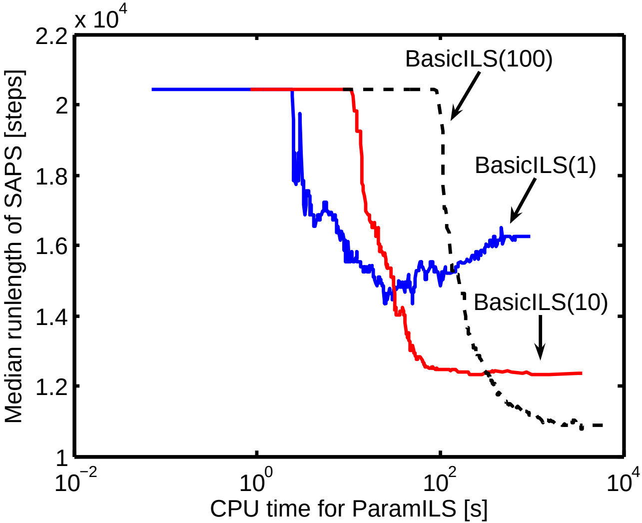

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- Key ideas in proof
  1. For $N(\theta) \rightarrow \infty$, $\hat{c}_N(\theta) \rightarrow c(\theta)$
  2. Underlying ILS eventually reaches any configuration θ.

Performance of FocusedILS vs BasicILS

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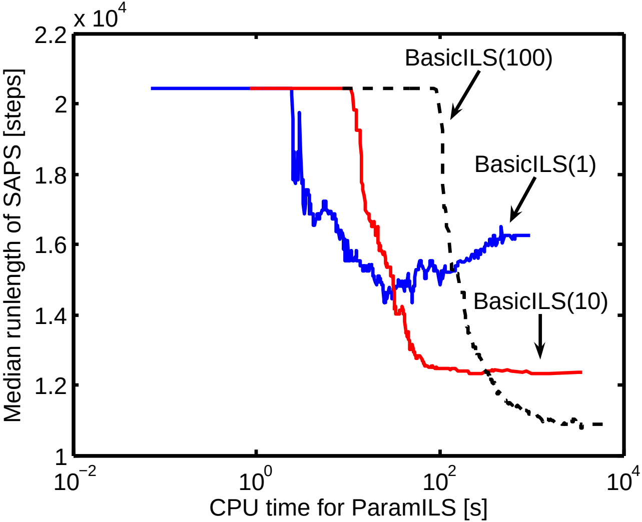

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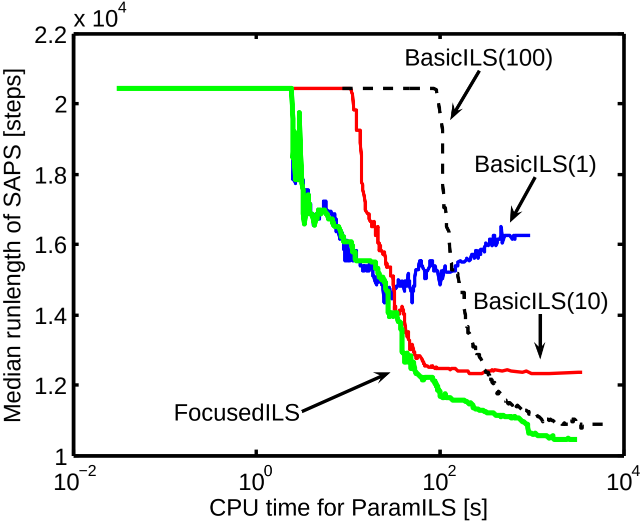

Sample applications and performance results

Comparison against CALIBRA [Adenso-Diaz & Laguna 2006]

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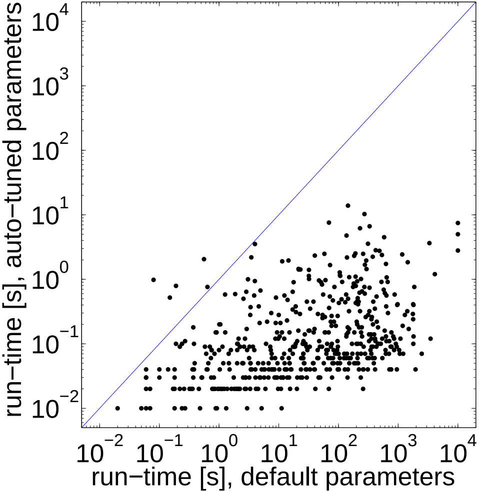
SAT4J on GC	Runtime	7.02 s	$\mathbf{0.65 \pm 0.2}$	1.19 ± 0.58	(too many param.)

Speedup obtained by automated tuning

(SAPS default *vs* tuned on graph colouring, test set performance)



Two "real-world" applications

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  - 26 parameters
  - Software verification: 500-fold speedup (won QB_FQ category in SMT'07 competition)
  - Hardware verification: 4.5-fold speedup
  - ⇝ New state of the art for those instances
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- New replica exchange Monte Carlo algorithm for protein structure prediction
  - 3 parameters
  - 2-fold improvement
  - $\rightsquigarrow$ New state of the art for 2D/3D protein structure prediction
  - $\rightsquigarrow$ [Thachuk, Shmygelska & Hoos: BMC Bioinformatics '07 (to appear)]

Conclusions

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