

#### The Computational Stumbling Blocks Fault-Tolerance and Reproducibility · 20th of May 2023

Lukas Hübner





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KIT – The Research University in the Helmholtz Association Heidelberg Institute of Theoretical Studies

#### **Fault-Tolerance**





1 20th of May 2023

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#### **Fault-Tolerance**



- Some existing supercomputers average over 2 hardware failures/day
- Increasing number of CPUs in supercomputers  $\rightarrow$  increased failure probability
- More CPU s  $\rightarrow$  more faults  $\rightarrow$  more recoveries
- Lowering operational voltage of CPUs conserves energy  $\rightarrow$  more faults
- Compute Node failure  $\rightarrow$  reload *dynamic* program state and *static* (e.g., input) data





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#### **Shrinking Recovery**



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#### **Shrinking Recovery**



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#### **Shrinking Recovery**



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![](_page_10_Picture_1.jpeg)

#### **Substituting Recovery**

#### Shrinking Recovery

![](_page_10_Figure_4.jpeg)

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**Substituting Recovery** 

![](_page_11_Picture_1.jpeg)

#### 

#### Shrinking Recovery

![](_page_11_Figure_4.jpeg)

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![](_page_12_Picture_1.jpeg)

#### **Substituting Recovery**

#### Shrinking Recovery

![](_page_12_Figure_4.jpeg)

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5

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![](_page_13_Picture_1.jpeg)

#### **Substituting Recovery** = E Up to 5% of nodes idling Limited number of failures supported

Recovery time does not scale

#### Shrinking Recovery

![](_page_13_Figure_5.jpeg)

- Unlimited number of failures supported
- Recovery time scales with 1/p

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![](_page_14_Picture_1.jpeg)

![](_page_14_Figure_2.jpeg)

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### **Design Goals**

![](_page_15_Picture_1.jpeg)

![](_page_15_Picture_2.jpeg)

- **in-memory** access to the parallel file system is a bottleneck
- **no spare nodes required** spare nodes are wasted resources
- **no checkpointing nodes required** checkpoint nodes are wasted resources
- **scalable recovery**  $\in O(1/p)$  time per failure
- arbitrary replication level more flexibility and robustness
- **rapid recovery** because recovery cannot be asynchronous

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![](_page_16_Picture_1.jpeg)

![](_page_16_Picture_2.jpeg)

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![](_page_17_Picture_1.jpeg)

![](_page_17_Picture_2.jpeg)

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![](_page_18_Picture_1.jpeg)

![](_page_18_Picture_2.jpeg)

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![](_page_19_Picture_1.jpeg)

![](_page_19_Figure_2.jpeg)

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## **Data Distribution for Faster Recovery**

![](_page_20_Picture_1.jpeg)

![](_page_20_Picture_2.jpeg)

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## **Data Distribution for Faster Recovery**

![](_page_21_Picture_1.jpeg)

![](_page_21_Picture_2.jpeg)

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# **Data Distribution for Faster Recovery**

![](_page_22_Picture_1.jpeg)

![](_page_22_Picture_2.jpeg)

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## **Recovering Replicas After a Node Failure**

![](_page_23_Picture_1.jpeg)

- **Goal:** Restore lost replicas after a failure; copying only the lost data
- **Idea:** For each block x, draw pseudorandom permutation  $\rho_x$  on [0, p 1]
- Place copies on  $\rho_x(0), \rho_x(1), \ldots$

![](_page_23_Figure_5.jpeg)

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## **Recovering Replicas After a Node Failure**

![](_page_24_Picture_1.jpeg)

- **Goal:** Restore lost replicas after a failure; copying only the lost data
- **Idea:** For each block x, draw pseudorandom permutation  $\rho_x$  on [0, p-1]
- Place copies on  $\rho_x(0), \rho_x(1), \ldots$

![](_page_24_Figure_5.jpeg)

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## **Recovering Replicas After a Node Failure**

![](_page_25_Picture_1.jpeg)

- **Goal:** Restore lost replicas after a failure; copying only the lost data
- **Idea:** For each block x, draw pseudorandom permutation  $\rho_x$  on [0, p 1]
- Place copies on  $\rho_x(0), \rho_x(1), \ldots$

![](_page_25_Figure_5.jpeg)

#### No need to redistribute any block that did not lose a replica!

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![](_page_26_Picture_1.jpeg)

![](_page_26_Picture_2.jpeg)

OpenClipart

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![](_page_27_Picture_1.jpeg)

Computational Reproducibility: Run program with the same parameters n times  $\rightarrow$  same result?!

Archiving, storing, and sharing the data, as well as providing scripts for reproducing results and figures are not enough.

![](_page_27_Picture_4.jpeg)

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![](_page_28_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_28_Picture_3.jpeg)

algorithm

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![](_page_29_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_29_Picture_3.jpeg)

algorithm

![](_page_29_Picture_5.jpeg)

source code

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![](_page_30_Picture_1.jpeg)

![](_page_30_Figure_2.jpeg)

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![](_page_31_Picture_1.jpeg)

![](_page_31_Figure_2.jpeg)

#### 15 to 17 decimal digits

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![](_page_32_Picture_1.jpeg)

Floating-Point numbers are an imperfect mapping of the infinite real numbers to a finite number of machine values!

![](_page_32_Figure_3.jpeg)

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15

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![](_page_33_Picture_1.jpeg)

![](_page_33_Figure_2.jpeg)

2<sup>52</sup> + 0.2 =  $2^{52}$  (next number after  $2^{52}$  is  $2^{52}$  + 1)

**1** +  $1/2^{54} = 1$  (next number is  $1 + 1/2^{52}$ )

Between  $2^n$  and  $2^{n+1}$  there are always  $2^{52}$  evenly spaced values

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![](_page_34_Picture_1.jpeg)

- Likelihood of a tree: multiply probabilities ( $\in [0, 1]$ ) along a tree
- $\blacksquare$   $\rightarrow$  values get smaller and smaller as we approach the root of the tree

![](_page_34_Figure_4.jpeg)

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![](_page_35_Picture_1.jpeg)

![](_page_35_Figure_2.jpeg)

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![](_page_36_Picture_1.jpeg)

![](_page_36_Figure_2.jpeg)

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![](_page_37_Picture_1.jpeg)

![](_page_37_Figure_2.jpeg)

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## How to Avoid Underflow?

![](_page_38_Picture_1.jpeg)

![](_page_38_Figure_2.jpeg)

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# What Went Wrong?

![](_page_39_Picture_1.jpeg)

- DNA models without rate heterogeneity: Scaling approach worked fine → check if all 4 conditional likelihoods at a given CLV and site are smaller than a minimum and multiply with large number
- DNA models with rate heterogeneity: doesn't always work
  - Range of values is too large because of distinct rate categories
  - Solution: Scale rate categories individually
  - Slower :-/

20

> BMC Bioinformatics. 2011 Dec 13;12:470. doi: 10.1186/1471-2105-12-470.

Algorithms, data structures, and numerics for likelihood-based phylogenetic inference of huge trees

Fernando Izquierdo-Carrasco <sup>1</sup>, Stephen A Smith, Alexandros Stamatakis

Affiliations + expand

PMID: 22165866 PMCID: PMC3267785 DOI: 10.1186/1471-2105-12-470 Paperple Free PMC article

![](_page_40_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_40_Picture_3.jpeg)

algorithm

![](_page_40_Picture_5.jpeg)

source code

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![](_page_41_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_41_Picture_3.jpeg)

algorithm

![](_page_41_Picture_5.jpeg)

source code

![](_page_41_Picture_7.jpeg)

binary

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## **Floating-Point Math is Non-Associative**

![](_page_42_Picture_1.jpeg)

![](_page_42_Picture_2.jpeg)

different round-off errors

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# **Floating-Point Math is Non-Associative**

![](_page_43_Picture_1.jpeg)

- We reorder code
  - Manually
  - Compiler optimizes code
  - CPUs reorder instructions
  - Number of threads/processes change reduction algorithm
- We round values at different points in time
  - 80-bit floating-point registers get flushed to 64-bit memory or regular registers
  - Different SIMD instruction sets

![](_page_43_Figure_10.jpeg)

## **Floating-Point Math is Non-Associative**

![](_page_44_Picture_1.jpeg)

![](_page_44_Figure_2.jpeg)

#### Small differences in the Likelihood computation can lead the tree searches to diverge.

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## **Compiler Optimizations**

![](_page_45_Picture_1.jpeg)

- In RAxML uses matrix exponential function from the book Numerical Recipes in C
- Especially the Intel icc compiler was very aggressive when optimizing this function  $\rightarrow$  numerical breakdown
- Solution: Disable compiler optimization for respective subroutine

![](_page_45_Picture_5.jpeg)

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![](_page_46_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_46_Picture_3.jpeg)

algorithm

![](_page_46_Picture_5.jpeg)

source code

![](_page_46_Picture_7.jpeg)

binary

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![](_page_47_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_47_Picture_3.jpeg)

algorithm

![](_page_47_Picture_5.jpeg)

source code

![](_page_47_Picture_7.jpeg)

binary

![](_page_47_Picture_9.jpeg)

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#### **SIMD Instructions**

![](_page_48_Picture_1.jpeg)

![](_page_48_Picture_2.jpeg)

- Single Instruction Multiple Data
- Parallelism inside a single CPU
- Different versions: SSE3, AVX, AVX2

![](_page_48_Figure_6.jpeg)

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### **SIMD Instructions: Horizontal Add**

![](_page_49_Picture_1.jpeg)

SIMD register

![](_page_49_Picture_3.jpeg)

- Sum over the values in this vector
- E.g. per-site log likelihoods

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## **SIMD Instructions: Horizontal Add**

![](_page_50_Picture_1.jpeg)

![](_page_50_Figure_2.jpeg)

- Different SIMD versions have different register widths
- Leads to different round-off errors
- Effects even visible on easy datasets

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![](_page_51_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_51_Picture_3.jpeg)

algorithm

![](_page_51_Picture_5.jpeg)

source code

![](_page_51_Picture_7.jpeg)

binary

![](_page_51_Picture_9.jpeg)

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![](_page_52_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_52_Picture_3.jpeg)

algorithm

![](_page_52_Picture_5.jpeg)

source code

![](_page_52_Picture_7.jpeg)

binary

![](_page_52_Picture_9.jpeg)

![](_page_52_Picture_10.jpeg)

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#### **Pseudorandom Number Generators**

![](_page_53_Picture_1.jpeg)

- Example: Linear Congruential Generator  $X_{n+1} = (a \cdot X_n) + c \mod m$
- Generates sequence of number deterministically
- $\blacksquare \rightarrow$  Same seed leads to same sequence of numbers
- Sequence "looks" random

![](_page_53_Figure_6.jpeg)

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### **Pseudorandom Number Generators**

![](_page_54_Picture_1.jpeg)

A Critical Assessment of Storytelling: Gene Ontology Categories and the Importance of Validating Genomic Scans

Pavlos Pavlidis,\*1 Jeffrey D. Jensen,2 Wolfgang Stephan,3 and Alexandros Stamatakis1

Results not reproducible on different machine; even with same random-number generator seed

#### $\rightarrow$ different Random Number Generator library lead to different sequence of numbers

Take-home message: Version control for external libraries, too.

![](_page_55_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_55_Picture_3.jpeg)

algorithm

![](_page_55_Picture_5.jpeg)

source code

![](_page_55_Picture_7.jpeg)

binary

![](_page_55_Picture_9.jpeg)

![](_page_55_Picture_10.jpeg)

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![](_page_56_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_56_Picture_3.jpeg)

![](_page_56_Picture_4.jpeg)

binary

![](_page_56_Picture_6.jpeg)

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#### Multi-Thread and Multi-Processor Reduce

![](_page_57_Picture_1.jpeg)

- Running the same binary on the same cluster with different number of processes can lead to different results
- We observed this on real data
- We have to sum numbers stored across multiple CPUs

![](_page_57_Figure_5.jpeg)

#### $\rightarrow$ different number of CPUs results in different round-off errors

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#### Multi-Thread and Multi-Processor Reduce

![](_page_58_Picture_1.jpeg)

- Idea: Do local summation as a tree, too. Send intermediate results over network
- Same order of summation  $\rightarrow$  same round-off error
- Slower than local summation + reduce
- We verified reproducibility under different number of CPUs with RAxML-NG

![](_page_58_Figure_6.jpeg)

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![](_page_59_Picture_1.jpeg)

#### For reproducible results, fix

![](_page_59_Picture_3.jpeg)

![](_page_59_Picture_4.jpeg)

![](_page_59_Picture_5.jpeg)

source code

![](_page_59_Picture_7.jpeg)

binary

#### **Bonus: Measurement of Runtime**

![](_page_59_Picture_10.jpeg)

![](_page_59_Picture_11.jpeg)

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## **Strange Runtime-Measurements**

![](_page_60_Picture_1.jpeg)

- Phylogenetic placement methods: Inexplicable run time deviations of about 50 %
- with the same number and type of operations just on different input data?

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#### **Strange Runtime-Measurements**

![](_page_61_Picture_1.jpeg)

Phylogenetic placement methods: Inexplicable run time deviations of about 50 %

with the same number and type of operations just on different input data?

#### **De-normalized floating-point number**

![](_page_61_Figure_5.jpeg)

## **Strange Runtime-Measurements**

![](_page_62_Picture_1.jpeg)

Phylogenetic placement methods: Inexplicable run time deviations of about 50 %

with the same number and type of operations just on different input data?

#### **De-normalized floating-point number**

![](_page_62_Figure_5.jpeg)

- Values too close to zero  $\rightarrow$  slower multiplications and additions
- Benchmarks data dependent

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#### Conclusion

![](_page_63_Picture_1.jpeg)

- Node-failures in supercomputers will get more frequent
- We need to be able to handle node failures (FT-RAxML-NG, ReStore)
- Compiler optimization, SIMD version, and number of CPUs hinder reproducibility
- Version control is essential (RNG)

![](_page_63_Picture_6.jpeg)

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