Comparing Benchmarks Using Key Microarchitecture-Independent Characteristics

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Comparing benchmarks is easy... or is it?

Hardware performance counters are a popular tool to compare emerging workloads with established benchmark suites.

examples:

- BioInfoMark (vs. SPECint CPU2000)
  Workload Characterization of Bioinformatics Applications
  (Li et.al, MASCOTS 2005)
- BioMetricsWorkload (vs. SPECint CPU2000)
  Workload Characterzation of Biometrics Applications on Pentium4 Microarcitecture
  (Cho et.al., IISWC 2005)
- ...

How reliable are these metrics?

How can we catch true inherent program behavior?

Beware of the pitfall!

hardware performance counters

instruction per cycle (IPC)

branch misprediction rate

L1 D-cache and I-cache miss rate

L2 cache miss rate

D-TLB miss rate

- measure native execution of benchmarks ⇒ fast
- no need to instrument code or implement analysis
- expose performance bottlenecks

BUT:

- true inherent program behavior may be hidden, which can be misleading

How to avoid the pitfall

microarchitecture-independent characteristics

instruction mix

instruction-level parallelism (ILP)

register traffic

(data and instr.) working set size

data stream strides

branch predictability (PPM)

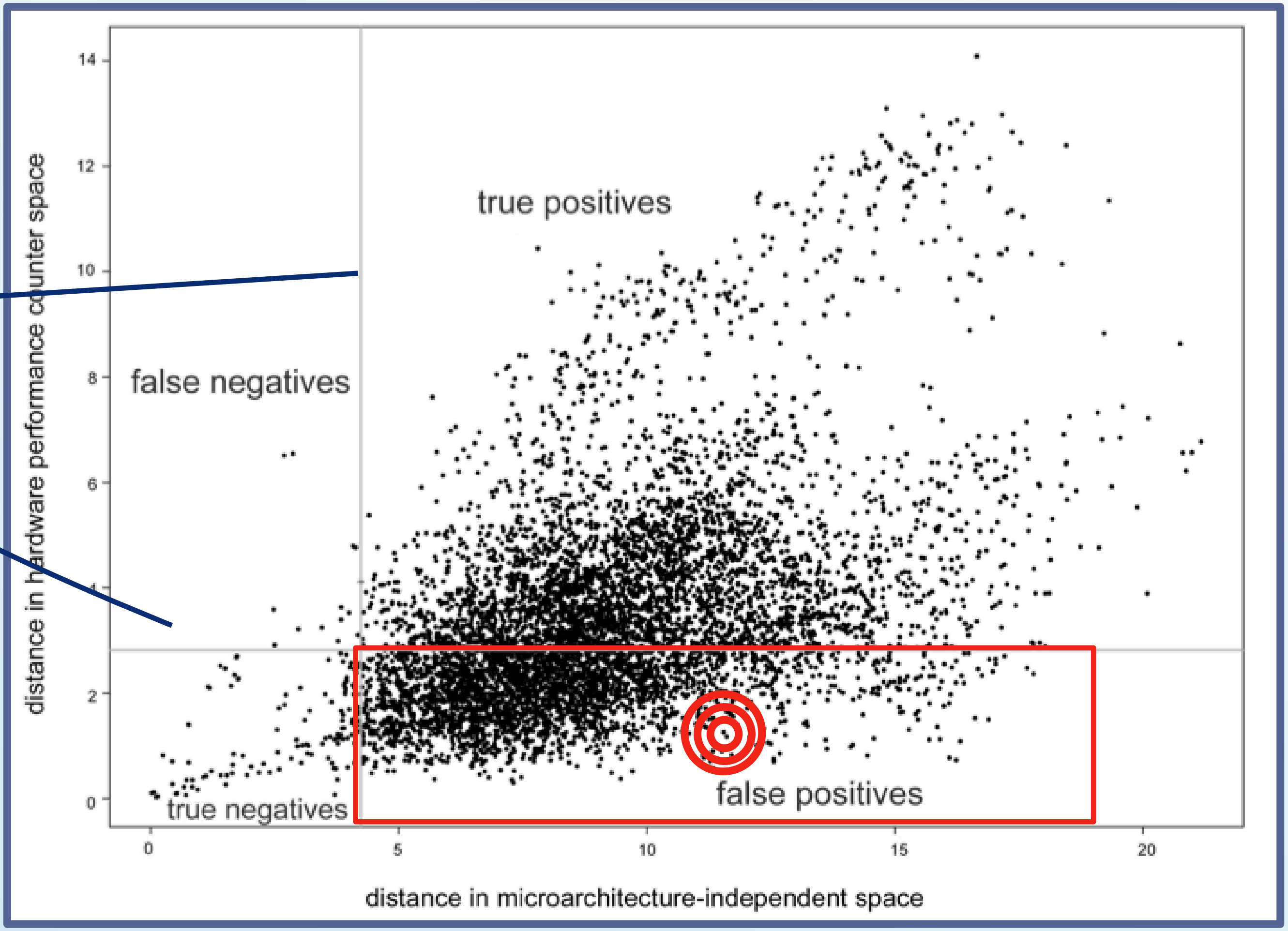
- are able to catch true inherent program behavior
- independent of the microarchitecture
  (cache configuration, issue width, # functional units, ...)

BUT:

- more time needed to measure them (time-consuming profiling)

Quantifying the pitfall

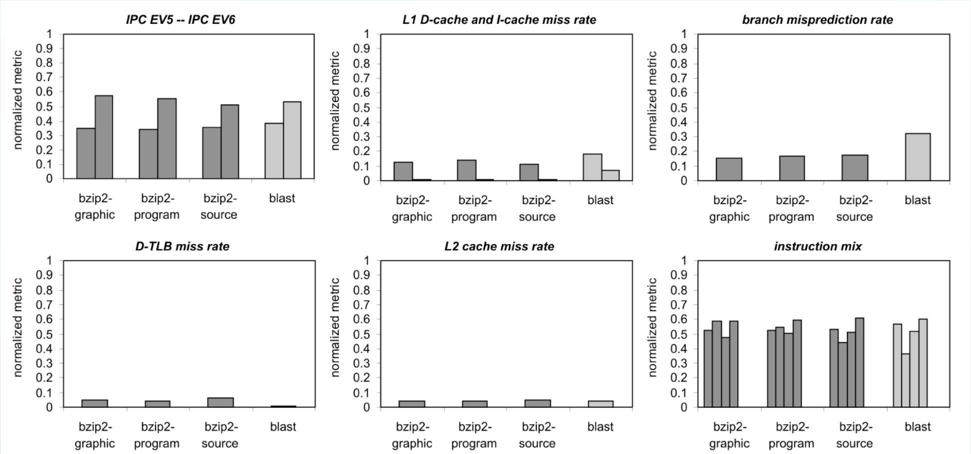
20% of maximum distance



41.1% of all benchmark pairs

Comparing benchmarks: a case study

comparing bzip2 (SPEC CPU2000) with blast (BioInfoMark)



hardware performance counters

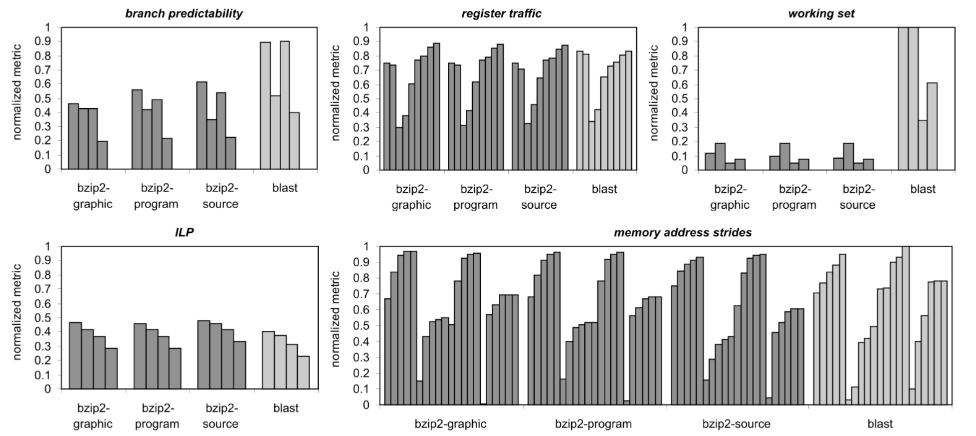
minor difference in branch mispred. rate

⇒ **these benchmarks are quite similar**

microarchitecture-independent characteristics

various differences noticable (working set sizes!)

⇒ **these benchmarks are quite different**



Efficiently comparing benchmarks

measuring microarchitecture-independent characteristics takes more time

on Alpha:

110 machine-days (instrumentation using ATOM)

vs

4 machine-days (dcpi on Alpha 21164/21264A)

Problem

How can we limit the time needed to characterize benchmarks?

Solution

limit the number of characteristics without losing too much information

How?

exploit correlation between characteristics (2 techniques)

Eliminating correlation between characteristics

identify the pair of characteristics with
the highest correlation, and drop one characteristic

for example:

data work.set (block level)
& ~~data work. set (page level~~)
=> 97.96% correlation

instr. work.set (block level)
& ~~instr. work. set (page level~~)
=> 97.70% correlation

ILP (win.size=256)
& ~~ILP (win.size=128~~)
=> 97.40% correlation

ILP (win.size=64)
& ~~ILP (win.size=32)~~
=> 96.75% correlation

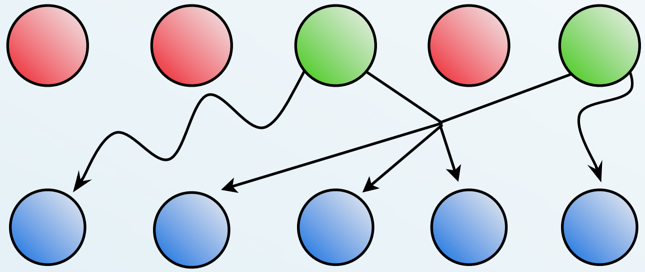
global store stride (prob. < 4096)
& ~~global store stride (prob. < 512~~)
=> 96.73% correlation

ILP (win.size=128)
& ILP (win.size=32)
=> 96.60% correlation

Finding the optimal set of characteristics

learn how to retain maximum correlation with the full set of characteristics with as few characteristics as possible

using a **genetic algorithm**:



1) start with a random population of subsets of characteristics
2) score each subset with a fitness score

$$f = \rho(1 - \frac{n}{N})$$

ρ: correlation with full set
n: number of characteristics in subset
N: total number of characteristics

3) fittest subsets produce offsprings (using crossover and mutation)
4) repeat step 2 and 3 for subsequent generations

*) search stops when solutions converge, or when a maximum number of generations is reached

What about PCA?

Principal Components Analysis (PCA) is often used to obtain uncorrelated characteristics from a given set

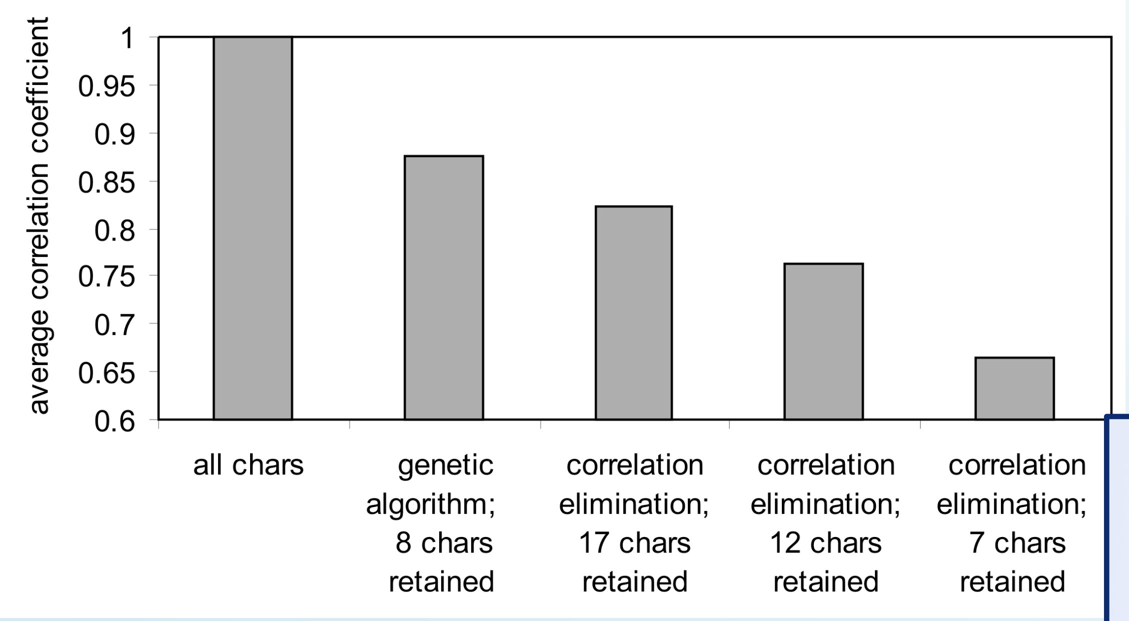
each Principal Component = linear combination of characteristics

$$PC_i = \sum_j w_{ij} c_j$$

hence, we still need to *measure all* characteristics in order to obtain uncorrelated principal components

PCs are hard to interpret in terms of original program characteristics

Which subset of characteristics is optimal?



47 characteristics → 8 characteristics

110 machine-days → 37 machine-days

1) percentage loads
2) average number of input operands
3) prob. register dependency distance ≤ 8
4) prob. local load stride ≤ 64
5) prob. global load stride ≤ 512
6) prob. local store stride ≤ 4096
7) D-stream working set size (4KB page level)
8) ILP (256-entry window)

Comparing existing benchmark suites

using this optimal subset of characteristics,
we compare:

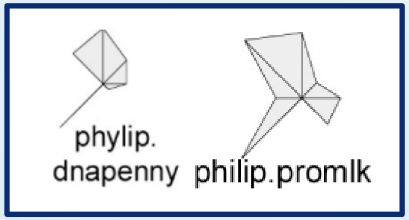
- 6 benchmark suites

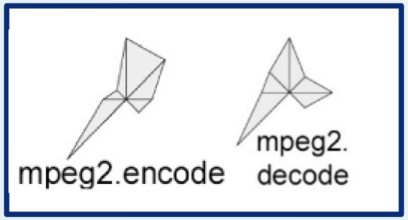
  BioInfoMark, BioMetricsWorkload, CommBench, MediaBench, MiBench, SPEC CPU2000

- 122 benchmarks

clustering of the benchmarks based on the subset of characteristics is done using k-means clustering

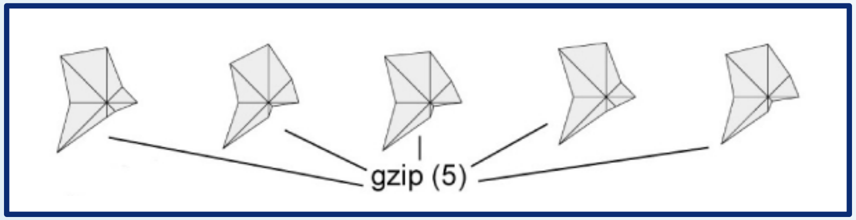
Different inputs yield different behavior... or not

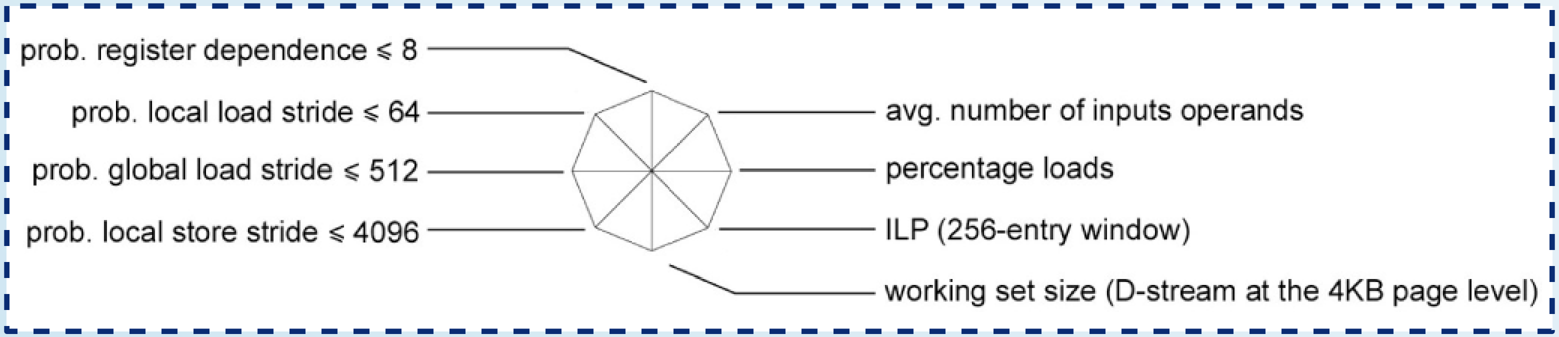




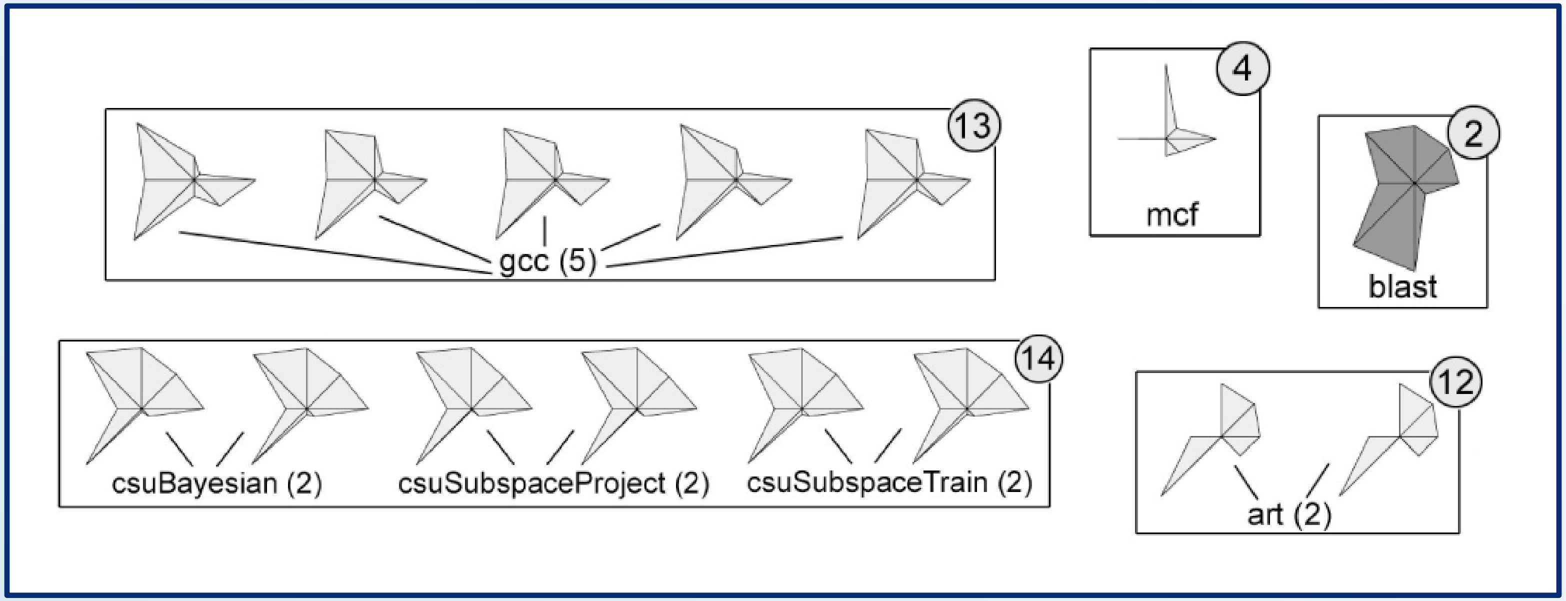
different inputs for phylip (BioInfoMark) & mpeg2 (MediaBench) yield quite *different* behavior

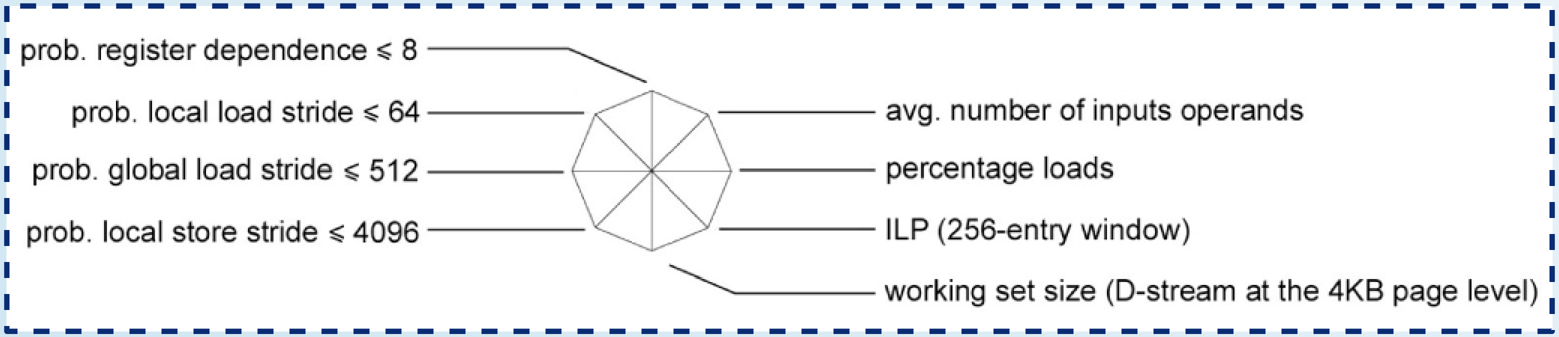
different inputs for gzip (SPEC CPU2000) yield quite *similar* behavior




prob. register dependence ≤ 8
prob. local load stride ≤ 64
prob. global load stride ≤ 512
prob. local store stride ≤ 4096
avg. number of inputs operands
percentage loads
ILP (256-entry window)
working set size (D-stream at the 4KB page level)

Some benchmarks are quite unique

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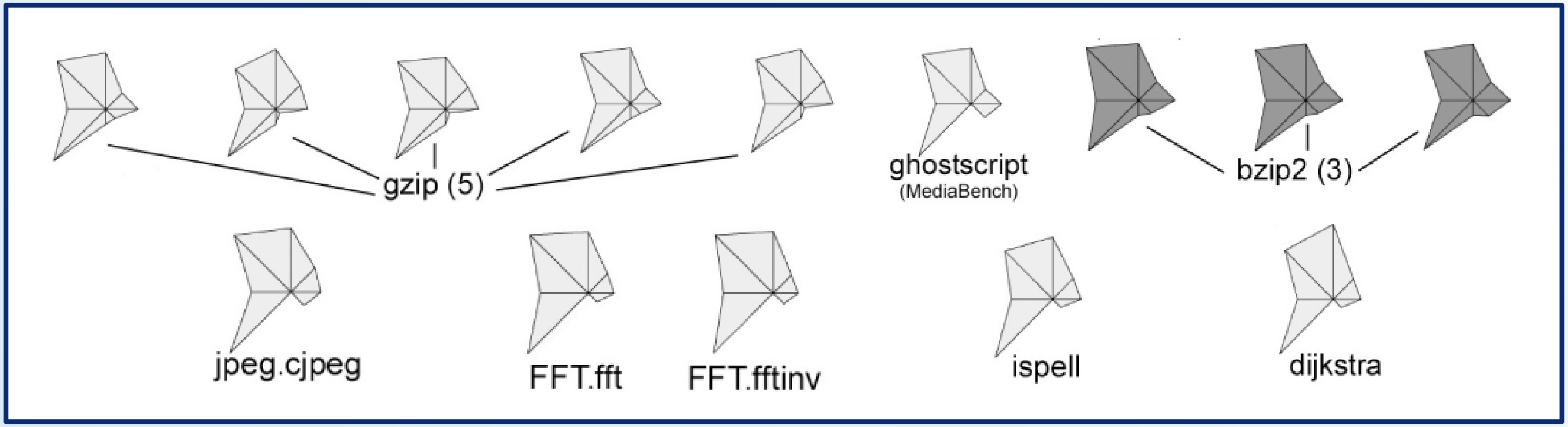
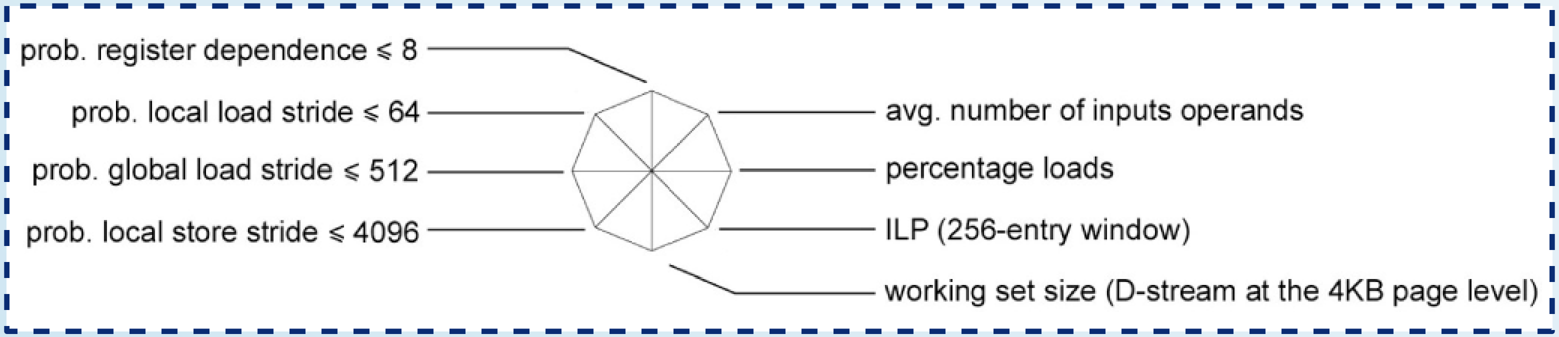
Others are very similar to each other

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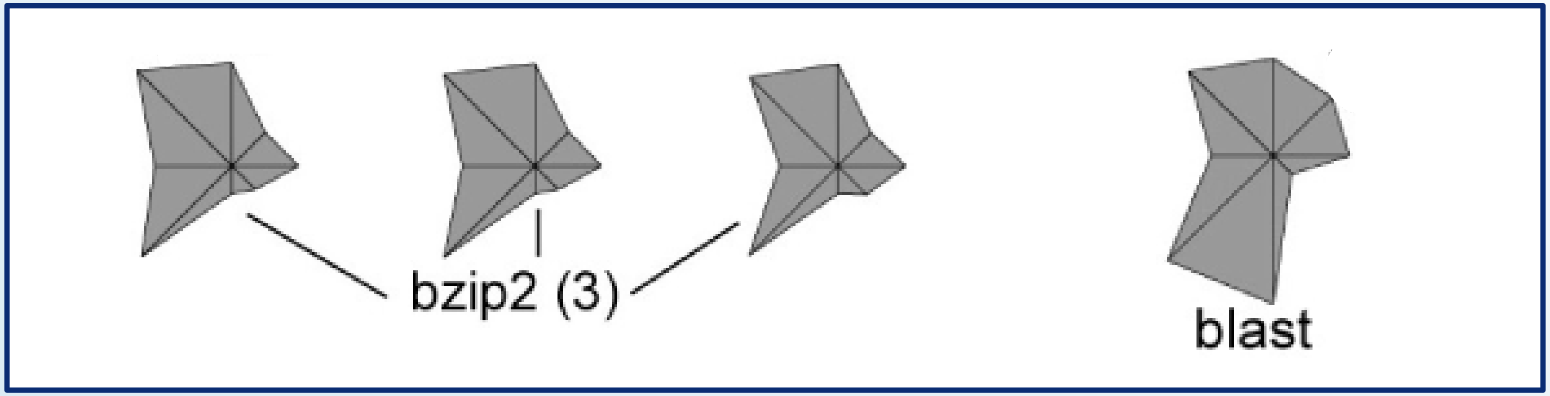
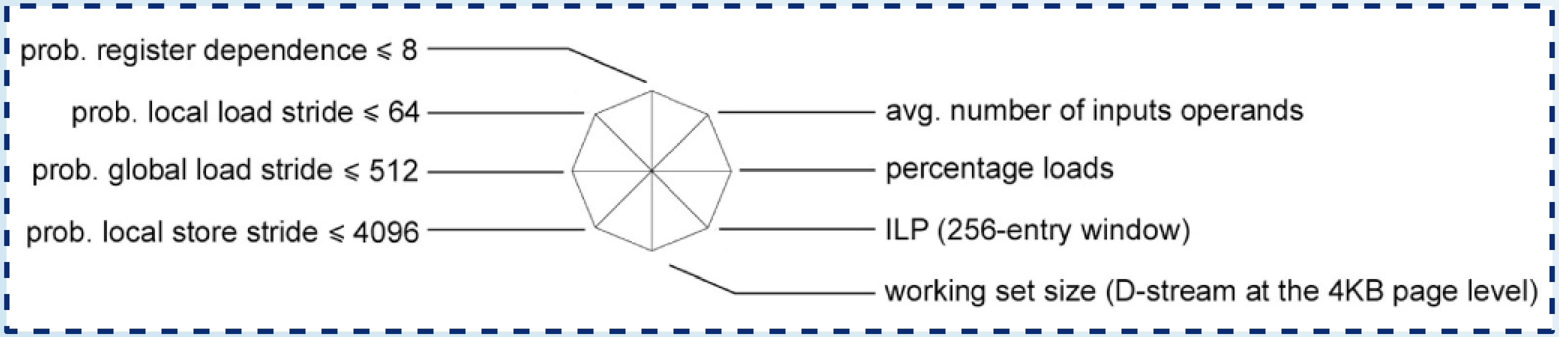
working set size (D-stream at the 4KB page level)

Don’t be fooled: bzip2 vs blast

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avg. number of inputs operands
percentage loads
ILP (256-entry window)
working set size (D-stream at the 4KB page level)

Interesting observations on benchmark suites

- 9 SPECfp benchmarks are isolated in a single cluster

- various recently introduced benchmarks exhibit dissimilar behavior compared to SPEC CPU2000

  blast, fasta, hmmer, phylip.promlk *(BioInfoMark)*
  csu *(BioMetricsWorkload)*

  ⇒ important to take into account!

- most MediaBench and MiBench benchmarks are similar to SPEC CPU2000 benchmarks

Conclusions

- using microarchitecture-dependent metrics might be misleading
- microarchitecture-independent metrics are a solution, but take longer to measure
- using a genetic algorithm, we limited the number of characteristics to measure from 47 to 8
- comparison of 122 workloads from 6 benchmark suites yields various interesting results

Questions?