

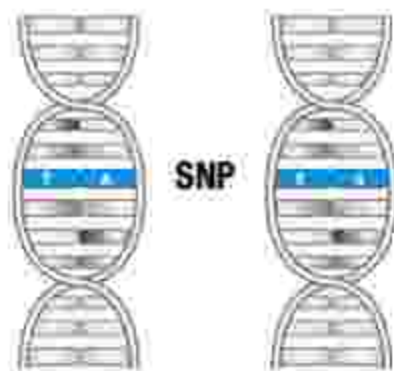
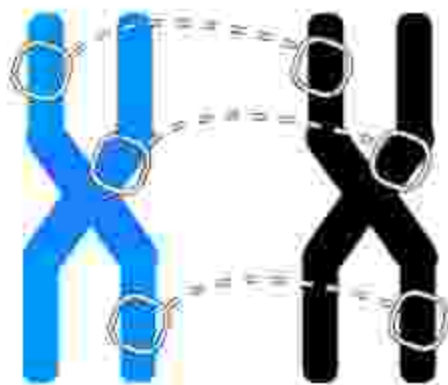


Accelerating epistasis detection on Intel CPUs and discrete GPUs with Intel® Advisor

Aleksandar Ilic, Diogo Marques, Rafael Campos and
Zakhar Matveev



Epistasis in a nutshell

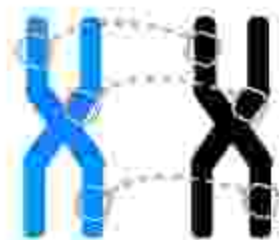
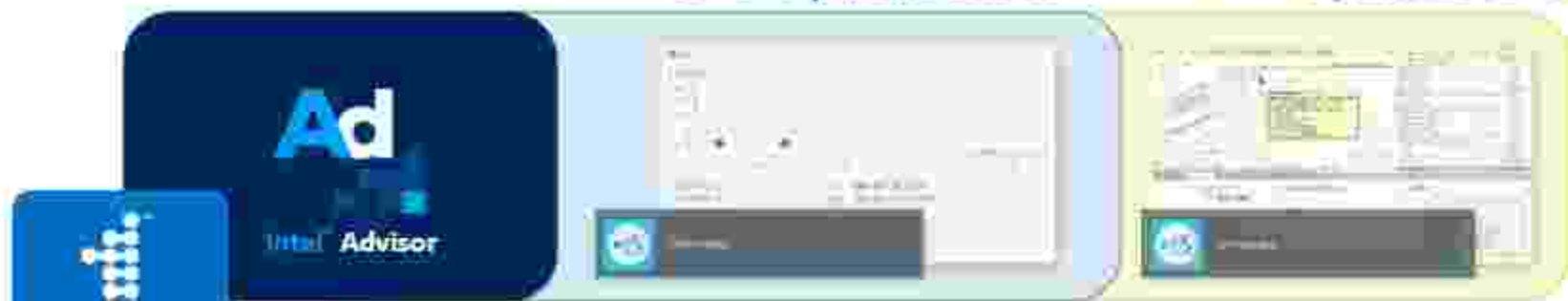


Some SNP interactions may cause life-threatening diseases (e.g., Alzheimer, breast cancer)
 Discovering which and how many is important, but challenging task!

Boosting Epistasis Detection with oneAPI

GPU Optimization

CPU Optimization



HiperBiooneAPI

SPAR
CITY

 EuroHPC
<http://sparcity.eu>



Hardware Heterogeneity



goals

OPTIMIZATION



demands

Application Diversity



Cache-aware Roofline





PERFORMANCE



POWER



ENERGY-EFFICIENCY



CASE-STUDY



Outline



PERFORMANCE



POWER



ENERGY EFFICIENCY



RELIABILITY

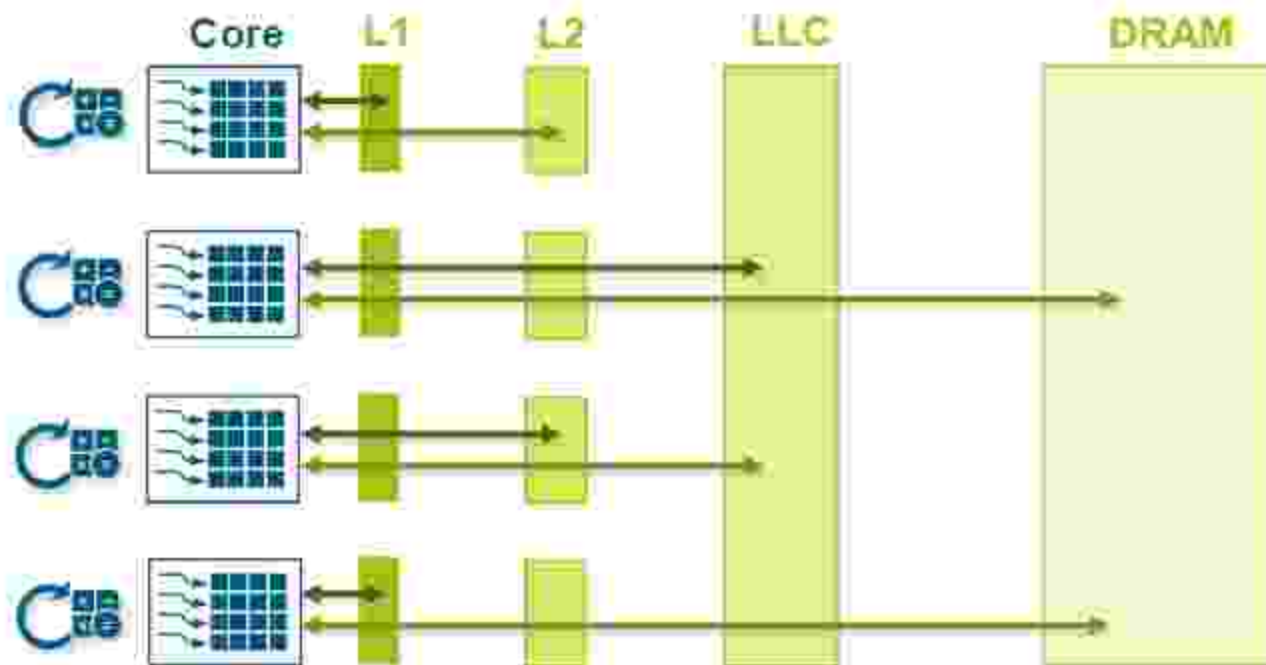


Cache-aware Roofline Model

A. Ilic, F. Pratas and L. Sousa, "Cache-aware Roofline Model: Upgrading the Loft", IEEE Computer Architecture Letters (2014)

D. Marques, A. Ilic, Z. Matveev and L. Sousa, "Application-driven Cache-Aware Roofline Model", Elsevier FGCS (2020)

Roofline in a nutshell



Communication overlapped with computation

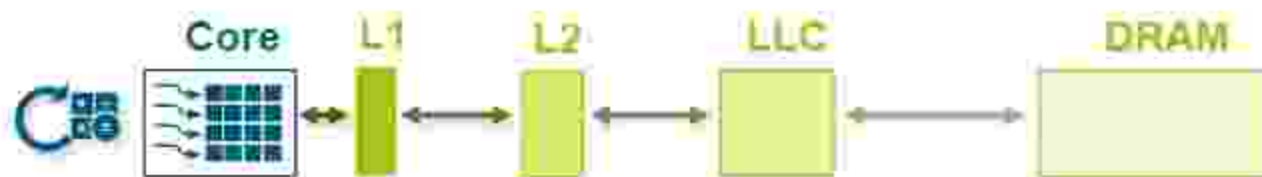
Max performance capped by peak compute throughput or available bandwidth (processor's view)

What is bandwidth?



Cache-aware Roofline Model (CARM)¹: Bandwidth as seen by the core

- Obtained via micro-benchmarking



Original Roofline Model (ORM)²: Bandwidth between memory levels

- Can be obtained from data-sheets

¹A. Illi, F. Pappas and L. Sousa, "Cache-aware Roofline Model: Upgrading the Loft", IEEE Computer Architecture Letters (2014)

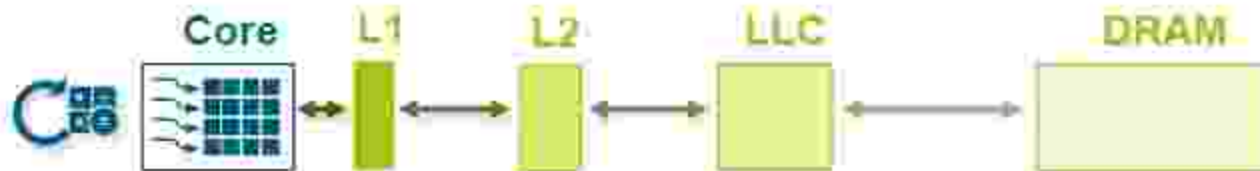
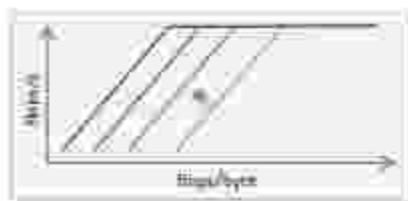
²J. S. Williams, A. Waterman, D. Patterson, "Roofline: An Insightful Visual Performance Model for Multicores Architectures", Commun. ACM (2009)

Implications ...



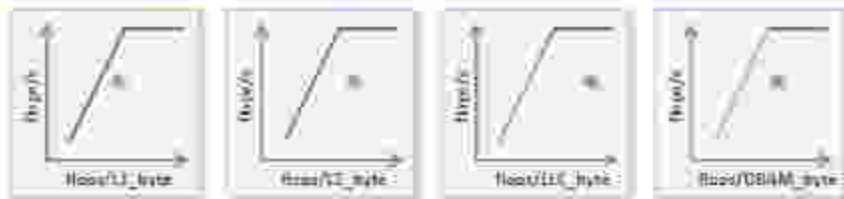
Cache-aware Roofline Model¹

- One model, one arithmetic intensity
- One application "point"



Original Roofline Model²

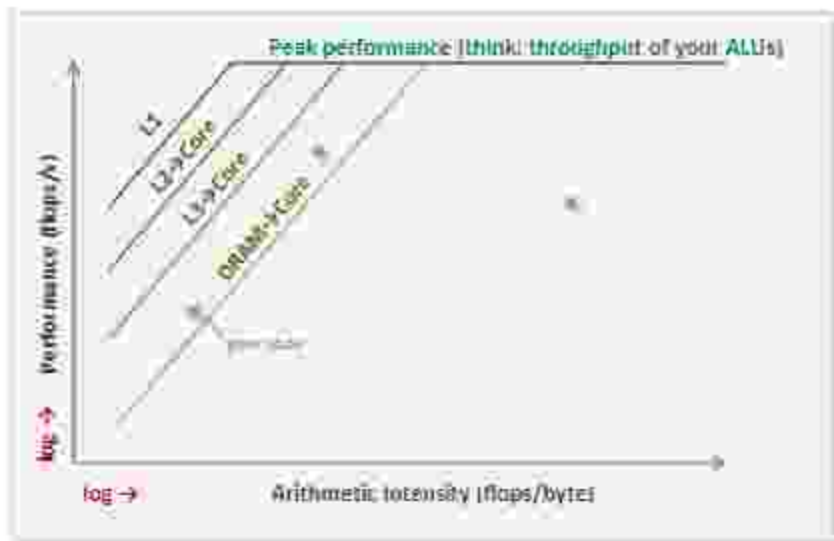
- Several models, several intensities
- Several application "points"



¹A. Illi, F. Pappas and L. Sousa, "Cache-aware Roofline Model: Upgrading the Loft", IEEE Computer Architecture Letters (2014)

²S. Williams, A. Waterman, D. Patterson, "Roofline: An Insightful Visual Performance Model for Multicores Architectures", Commun. ACM (2009)

Implications ... bring cool features

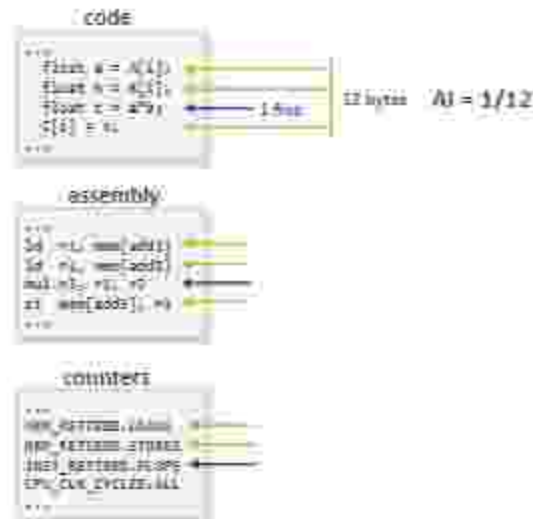


Cache-aware Roofline Model

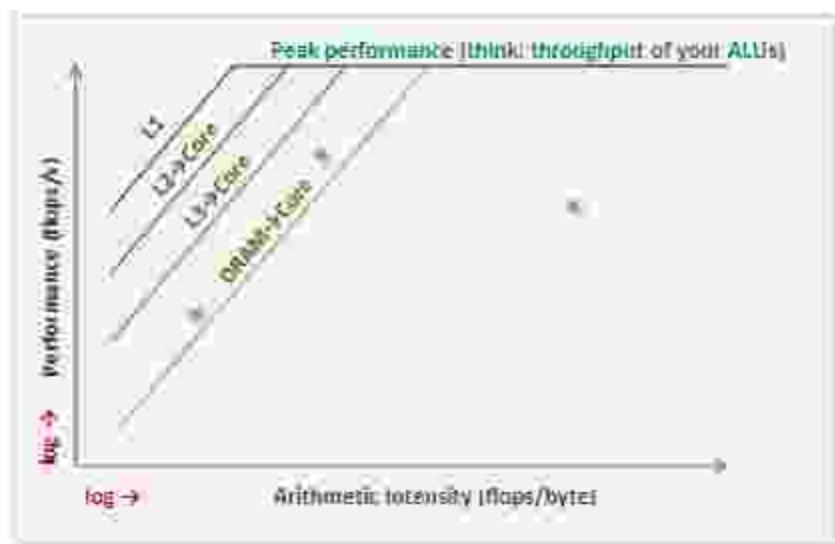
- Shows absolute architecture maximums* (You can't break them! Can your application exploit them?)

How to "plot" my code?

- CARM arithmetic intensity is exactly what you expect it to be!



Implications ... bring cool features



Cache-aware Roofline Model

- Shows absolute architecture maximums (You can't break them! Can your application exploit them?)

How to "plot" my code?

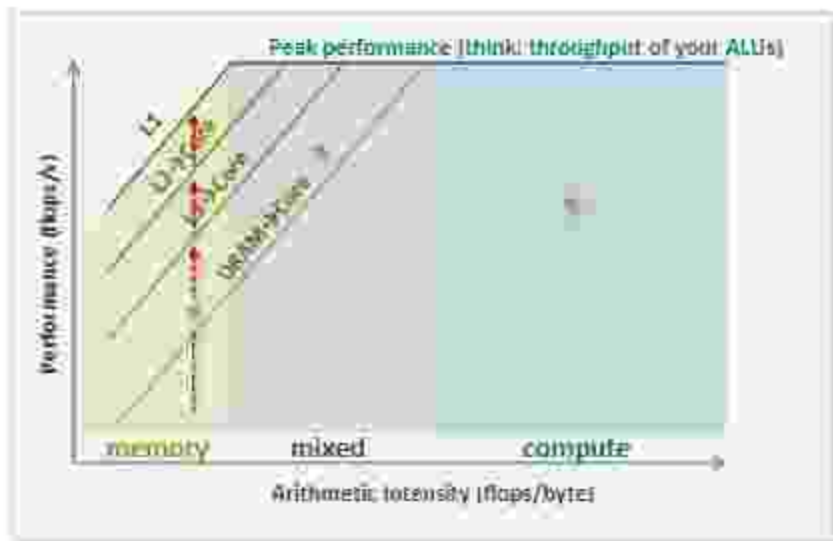
- CARM arithmetic intensity is exactly what you expect it to be!

Intel Advisor Roofline feature

- CARM is there since 2017



Implications ... bring cool features



memory bound

(improve access pattern, use of caches)

mixed

(all kinds of everything)

compute bound

(vectors, parallelize...)

Cache-aware Roofline Model

- Shows absolute architecture maximums
(You can't break them! Can your application exploit them?)

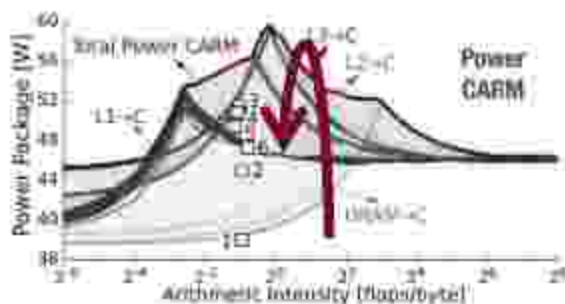
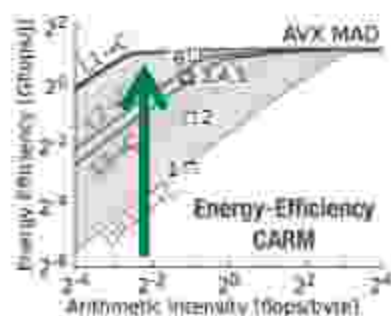
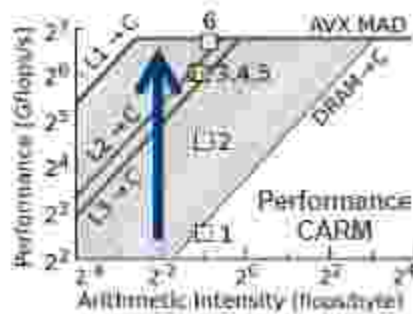
How to "plot" my code?

- CARM arithmetic intensity is exactly what you expect it to be!

How to use CARM?

- 1 **Detect the boundness region**
 - What are my expected maximums?
 - Provides first optimization hints
- 2 **Draw an imaginary vertical line**
 - What are my main bottlenecks? (observe intersected lines)
 - Focus your optimization (aim at surpassing the line above)
- 3 **Optimize your code: Break above roofs!**
 - You should move up (as your performance improves)
 - Unless you restructure the code, or your compiler decides so...

Matrix Multiplication



All codes AVX vectorized!

[1] Basic implementation (row major)

$$\begin{matrix} \rightarrow \\ \boxed{A} \end{matrix} \times \begin{matrix} \downarrow \\ \boxed{B} \end{matrix} = \begin{matrix} \rightarrow \\ \boxed{C} \end{matrix}$$

[2] Transposed B (improved mem. access)

$$\begin{matrix} \rightarrow \\ \boxed{A} \end{matrix} \times \begin{matrix} \rightarrow \\ \boxed{B} \end{matrix} = \begin{matrix} \rightarrow \\ \boxed{C} \end{matrix}$$

[3,4,5] Cache blocking: L3, L2, L1

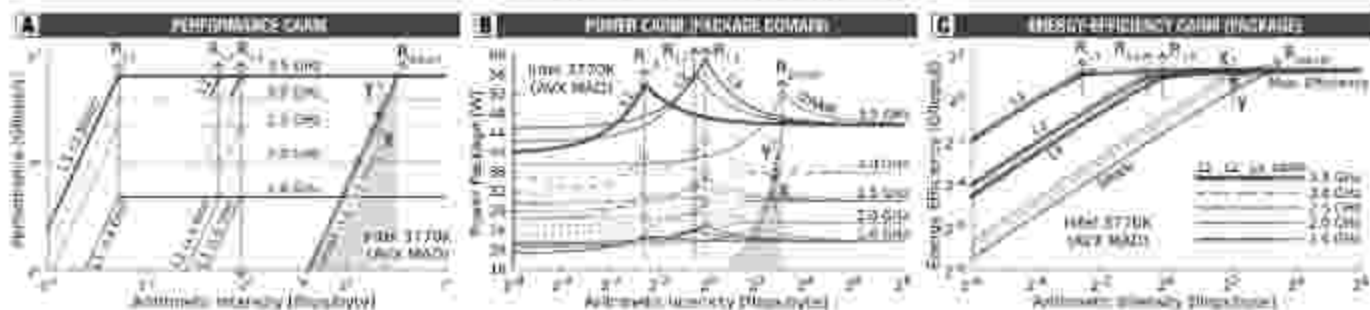
$$\begin{matrix} \rightarrow \\ \boxed{A} \end{matrix} \times \begin{matrix} \rightarrow \\ \boxed{B} \end{matrix} = \begin{matrix} \rightarrow \\ \boxed{C} \end{matrix}$$

[6] Intel MKL

$$\begin{matrix} \rightarrow \\ \boxed{A} \end{matrix} \times \begin{matrix} \rightarrow \\ \boxed{B} \end{matrix} = \begin{matrix} \rightarrow \\ \boxed{C} \end{matrix}$$

Cache-aware Roofline Model: Extensions

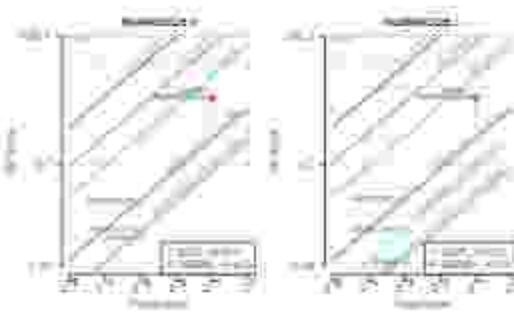
CARM-based DVFS analysis



GPU CARM: Performance, Power, DVFS



NUMA CARM: Multi-socket, KNL



A. Ilie, F. Prata, L. Sousa, "Beyond the Roofline: Cache-Aware Power and Energy-Efficiency Modeling for Multi-Cores", IEEE Trans. on Computers (2017)

A. Lopez, F. Prata, L. Sousa, A. Ilie, "Enabling GPU performance, power and energy-efficiency bounds with Cache-aware Roofline Modeling", ISPASS (2017)

N. Denoyelle, B. Goglin, A. Ilie, E. Jeannot, L. Sousa, "Modeling Non-Uniform Memory Access on Large Compute Nodes with the Cache-Aware Roofline Model", IEEETVDS (2018)



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CASE STUDY



Epistasis Detection

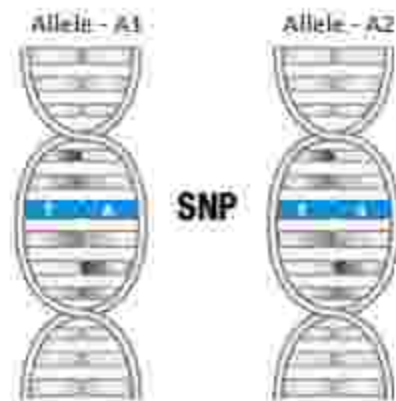
R. Nobre, A. Ilıc, S. Santander-Jiménez, L. Sousa, "Exploring the Binary Precision Capabilities of Tensor Cores for Epistasis Detection", IPDPS (2020)

R. Campos, D. Marques, S. Santander-Jiménez, L. Sousa, A. Ilıc, "Heterogeneous CPU+ iGPU Processing for Efficient Epistasis Detection", EuroPar (2020)

Binarizing your genotype

| SNP X | P0 | P1 | Genotype | A1 | A2 | |
|-----------|----|----|----------|---|---|------------------|
| X0 | 0 | 0 | 0 |  |  | Homozygous Major |
| X1 | 1 | 0 | 1 |  |  | Heterozygote |
| X2 | 0 | 1 | 2 |  |  | Homozygous Minor |
| phenotype | 0 | 1 | | | | |

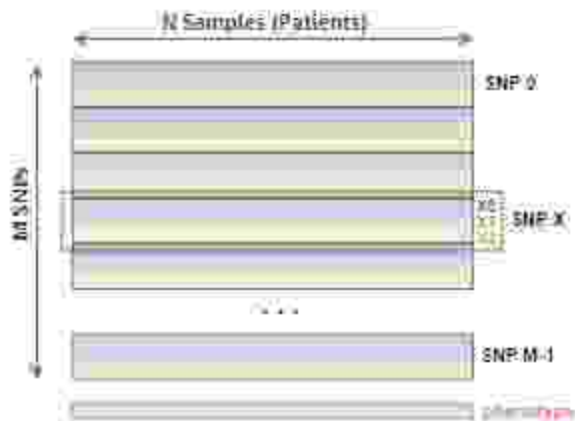
 dominant allele
 recessive allele



Think: Patient 1 (P1) with genotype 2 has disease (case)

Dataset structure

| SNP X | P0 | P1 | P2 | P3 | P4 | P5 | ... | PN |
|-----------|----|----|----|----|----|----|-----|----|
| X0 | 0 | 0 | 0 | 1 | 0 | 0 | ... | 1 |
| X1 | 1 | 0 | 1 | 0 | 0 | 1 | ... | 0 |
| X2 | 0 | 1 | 0 | 0 | 1 | 0 | ... | 0 |
| phenotype | 0 | 1 | 1 | 1 | 0 | 0 | ... | 1 |

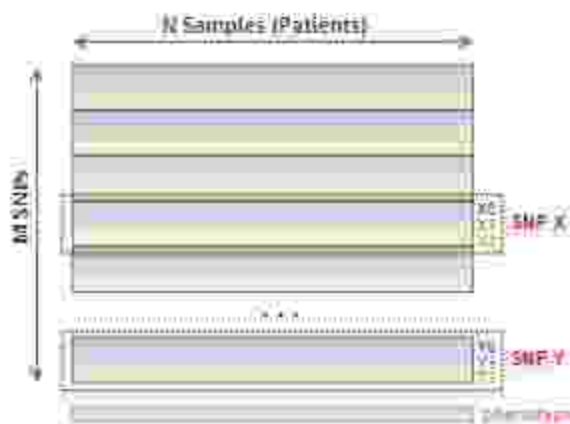
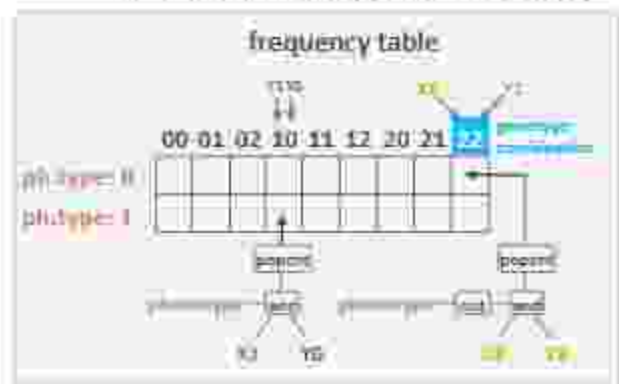


Dataset structure

Our dataset: 10 048 SNPs x 104 448 samples

2-way Epistasis Detection: Pair-wise interaction

Pair-wise Interaction: SNPs (X,Y)



Dataset structure

Our dataset: 10 048 SNPs x 104 448 samples

Search space: All SNP combinations

| | | | | | |
|-------|-------|-------|-------|---------|-----------|
| (0,1) | (0,2) | (0,3) | (0,4) | ... | (0,M-1) |
| (1,2) | (1,3) | (1,4) | ... | (1,M-1) | |
| | (2,3) | (2,4) | ... | (2,M-1) | |
| | | (3,4) | ... | (3,M-1) | |
| | | | ... | | |
| | | | | | (M-2,M-1) |

$M(M-1)/2$
combinations

Our dataset: 50 475 128 combinations

Each frequency table evaluated with Bayesian K2 score
Epistasis: Minimum K2 score among all combinations!



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CASE STUDY

Epistasis Detection: GPU Optimization

Host code

```

int dev_data = (int*) cl::buffer(device, context);
int dev_ptr = (int*) cl::buffer(device, context);
float dev_ptr2 = (float*) cl::buffer(device, context);

for(x = 0; x < N; x++) {
    dev_data[x] = host_ptr[x];
    dev_ptr[x] = host_ptr[x];
}

cl::range r(0, N);
cl::range r2(0, N);
queue.submit({cl::range(r), cl::range(r2)});

#pragma omp parallel for collapse(2)
for(x = 0; x < N; x++) {
    dev_ptr2[x] = dev_data[x] * dev_ptr[x];
}

```

Create USM
buffersTransfer data
from host to
deviceLaunch kernel
to execute on
device

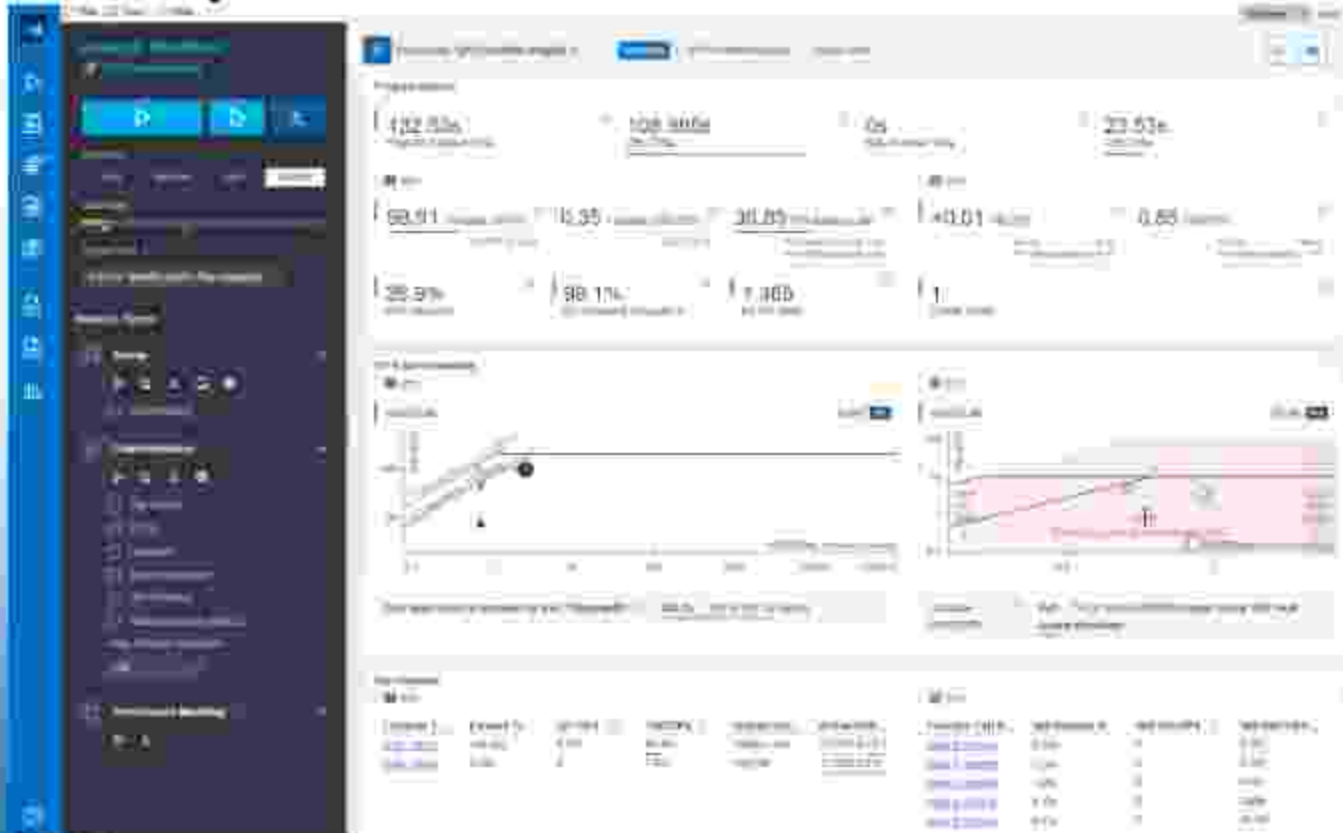
| | | | | | |
|-------|-------|-------|-------|-------|---------|
| (0,1) | (0,2) | (0,3) | (0,4) | ... | (M-3) |
| (1,1) | (1,2) | (1,3) | (1,4) | ... | (M-1) |
| ... | ... | (2,3) | (2,4) | ... | (2,M-1) |
| ... | (3,1) | (3,2) | (3,3) | (3,4) | (3,M-1) |
| ... | ... | ... | (4,3) | (4,4) | ... |
| ... | ... | ... | ... | (M-2) | (M-1) |

The kernel is launched for $M \times M$
work-items

Work-items without a valid combination
will not do work

GPU Roofline in Advisor

Summary View:



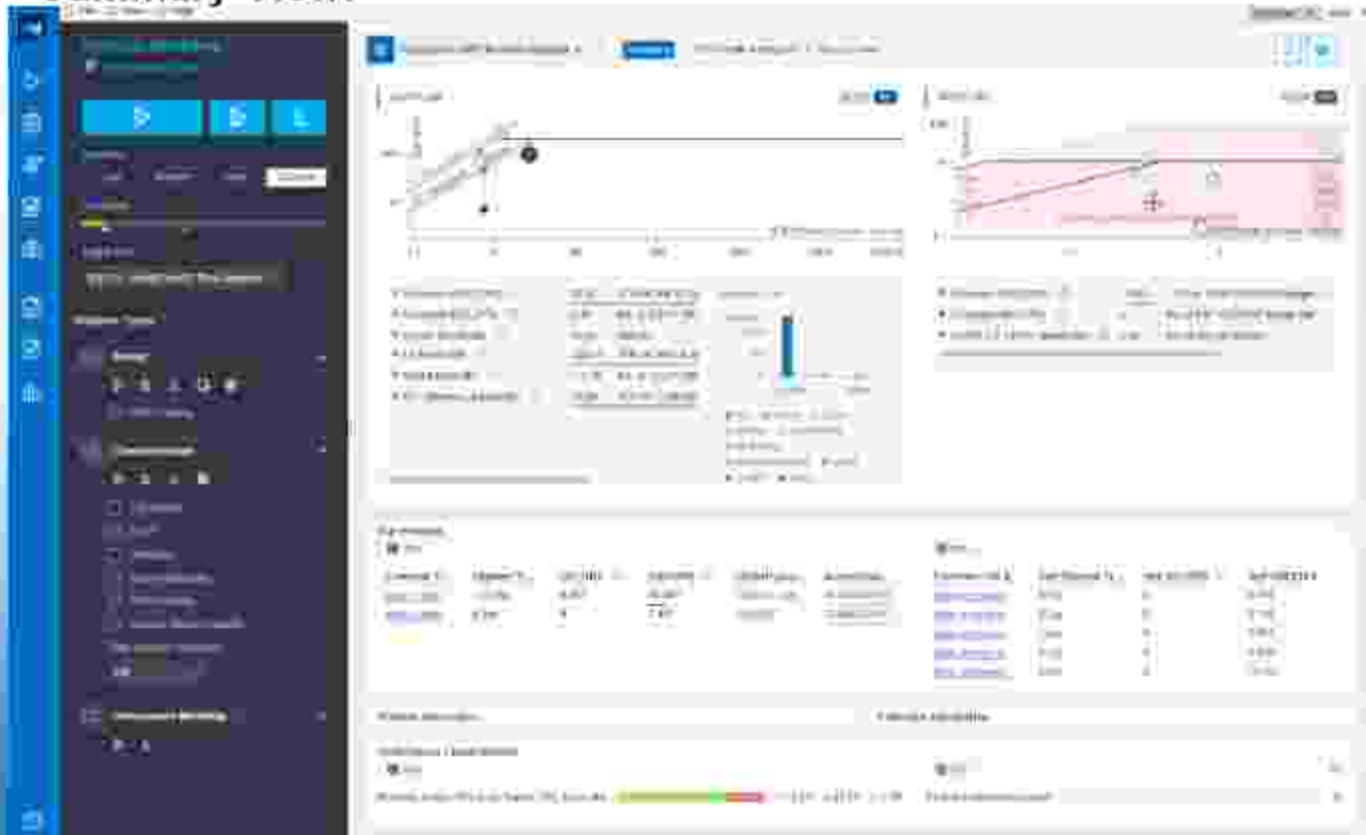
GPU Optimization

Three Genotypes → Phenotype



GPU Roofline in Advisor

Summary View:



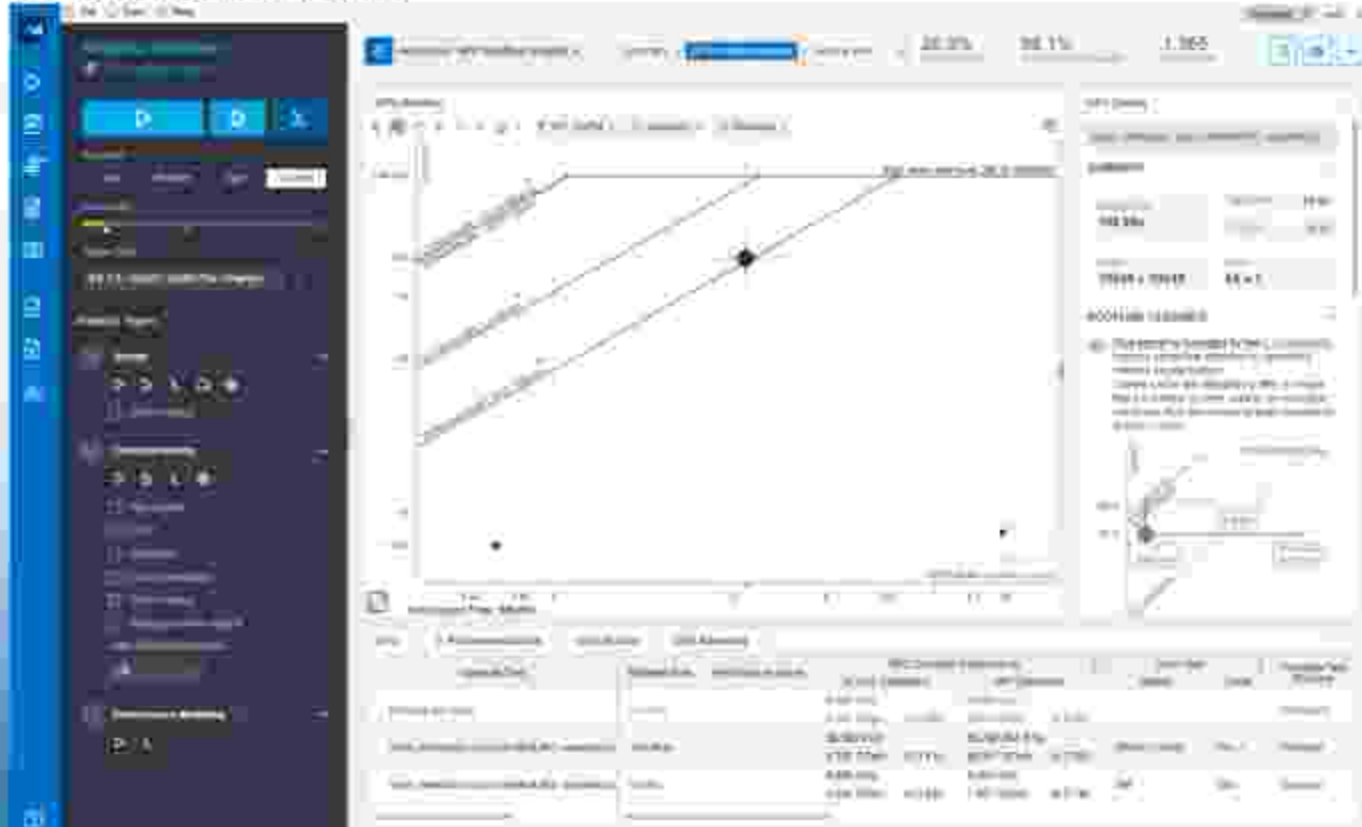
GPU Optimization

Three Genotypes → Phenotype



GPU Roofline in Advisor

GPU Roofline view:



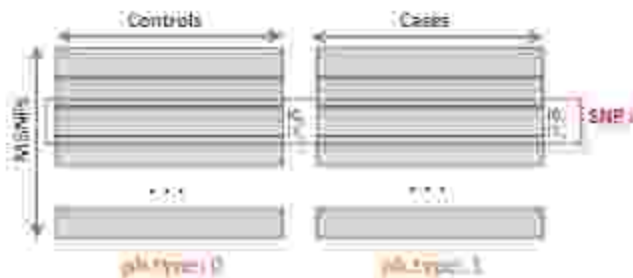
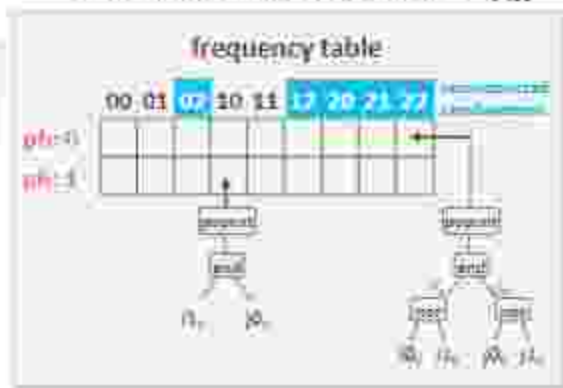
Three Genotypes → Phenotype





Restructuring our algorithm...

Pair-wise interaction: SNPs (i,j)



"New" Dataset structure
(removed: phenotype and genotype 2)

Reducing memory transfers!

GPU Optimization

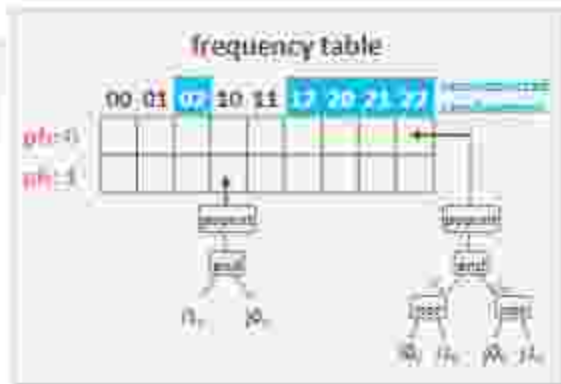
Three Genotypes \rightarrow Phenotype



Two Genotypes, No Phenotype



Pair-wise interaction: SNPs (i,j)



Device code

```

// genotype: int
SNP1 = SNPs_rows[1 + N_rows - 2];
SNP2 = SNPs_rows[0 + N_rows - 2];
int p = 0; while (2 * N_rows - 1 - p >= 0)
{
    int i = -(SNP1[p] | SNP2[p + 1]);
    int j = -(SNP1[p] | SNP2[p + 1]);

    r[i] += cl::sycl::popcount(SNP1[i] & SNP1[j]);
    r[j] += cl::sycl::popcount(SNP1[j] & SNP1[i + 1]);
    r[i] += cl::sycl::popcount(SNP1[i] & i2);
    r[j] += cl::sycl::popcount(SNP1[i + 1] & SNP1[j]);
    r[i] += cl::sycl::popcount(SNP1[i + 1] & SNP1[i + 1]);
    r[j] += cl::sycl::popcount(SNP1[i + 1] & i2);
    r[i] += cl::sycl::popcount(i2 & SNP1[j]);
    r[j] += cl::sycl::popcount(i2 & SNP1[i + 1]);
    r[i] += cl::sycl::popcount(i2 & i2);
}
// genotype: int

```

The frequency table is filled for SNPs i and j is filled separately for each phenotype

GPU Optimization

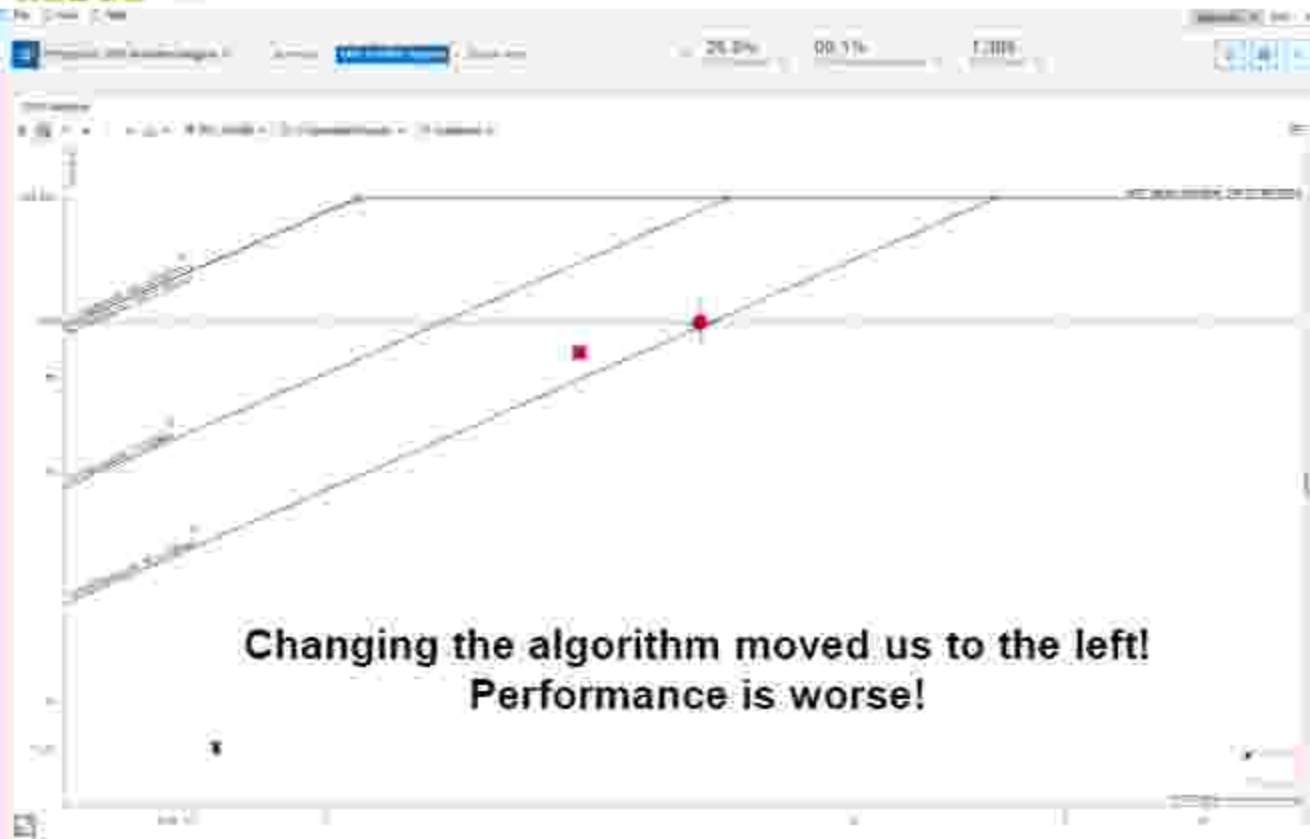
- Three Genotypes → Phenotype



- Two Genotypes, No Phenotype



Advisor in action...



Changing the algorithm moved us to the left!
Performance is worse!

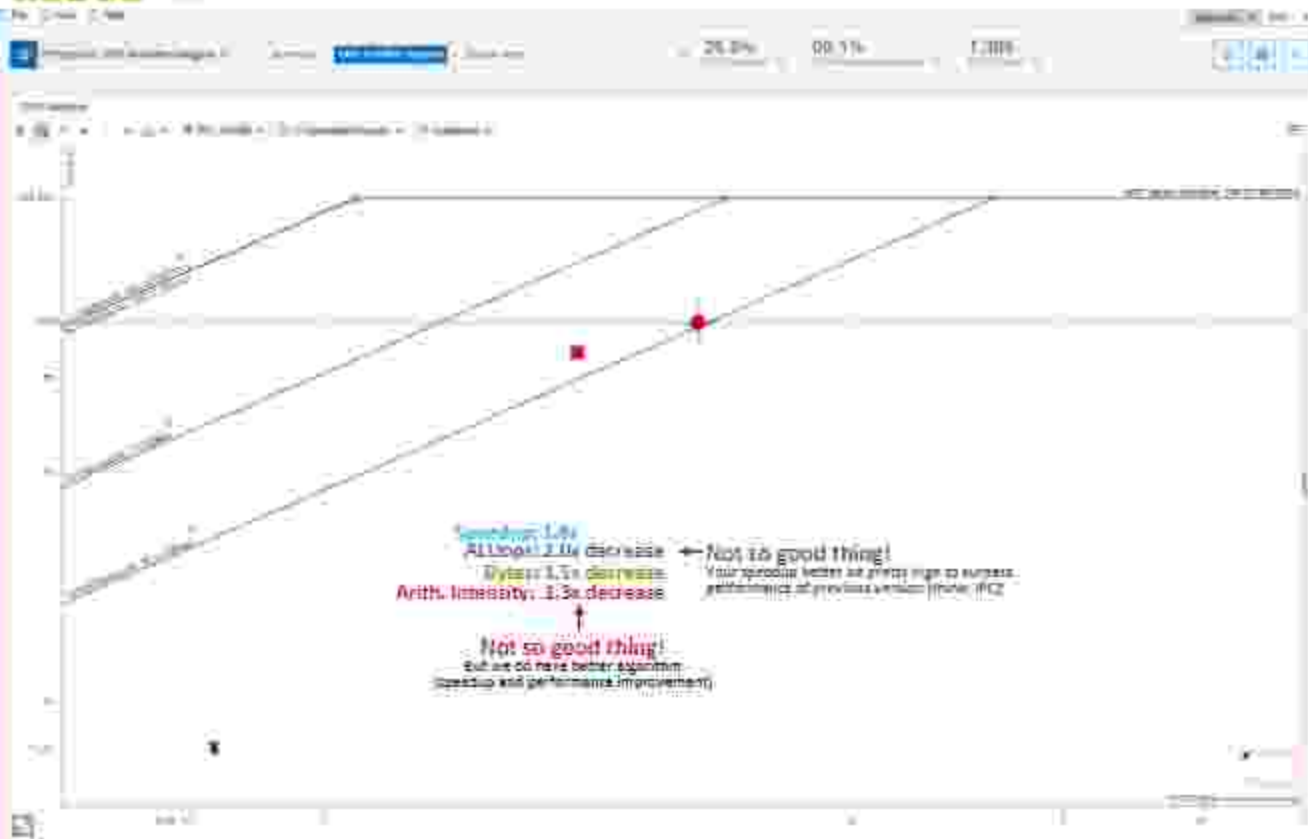
GPU Optimization

- Three Genotypes → Phenotype



- Two Genotypes, No Phenotype





GPU Optimization

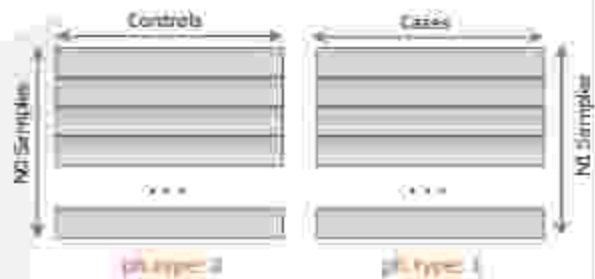
- Three Genotypes → Phenotype



- Two Genotypes, No Phenotype



Let's continue optimizing...



Transposed Dataset
(inverted SNPs and samples)

Device code

```

// genotype_t.h
SNP1 = (uint*) &data_genoc[0 * 2];
SNP2 = (uint*) &data_genoc[1 * 2];
for (p = 0; p < 2 * N_samps; p = 2 * N_samps + N_samps * 2 * N)
{
    u12 = ~(*SNP1[p] | *SNP1[p + 1]);
    u22 = ~(*SNP2[p] | *SNP2[p + 1]);

    r1[0] = 2 * (type1::popcount(SNP1[p] & SNP1[p + 1]));
    r1[1] = 2 * (type1::popcount(SNP1[p] & SNP1[p + 1]));
    r1[2] = 4 * (type1::popcount(SNP1[p] & u12));
    r1[3] = 4 * (type1::popcount(SNP1[p + 1] & SNP1[p + 1]));
    r1[4] = 4 * (type1::popcount(SNP1[p + 1] & SNP1[p + 1]));
    r1[5] = 2 * (type1::popcount(SNP1[p + 1] & u12));
    r1[6] = 2 * (type1::popcount(u12 & SNP1[p + 1]);
    r1[7] = 4 * (type1::popcount(u12 & SNP1[p + 1]));
    r1[8] = 4 * (type1::popcount(u12 & u12));
}
// genotype_t.h

```

Improving memory accesses by dataset transposition
Coalescing of memory accesses by the work-items

GPU Optimization

- Three Genotypes → Phenotype

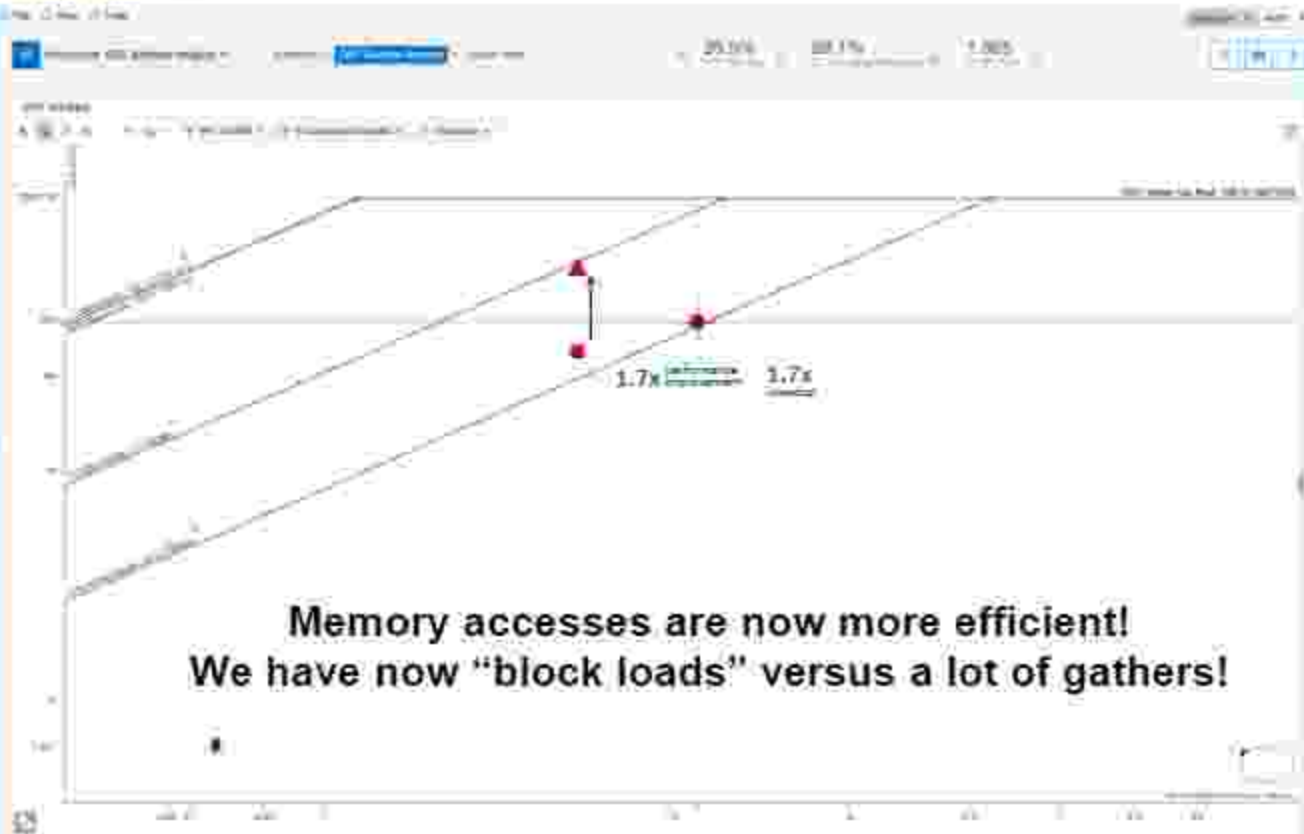


- Two Genotypes, No Phenotype



- Transposed Dataset





GPU Optimization

- Three Genotypes → Phenotype

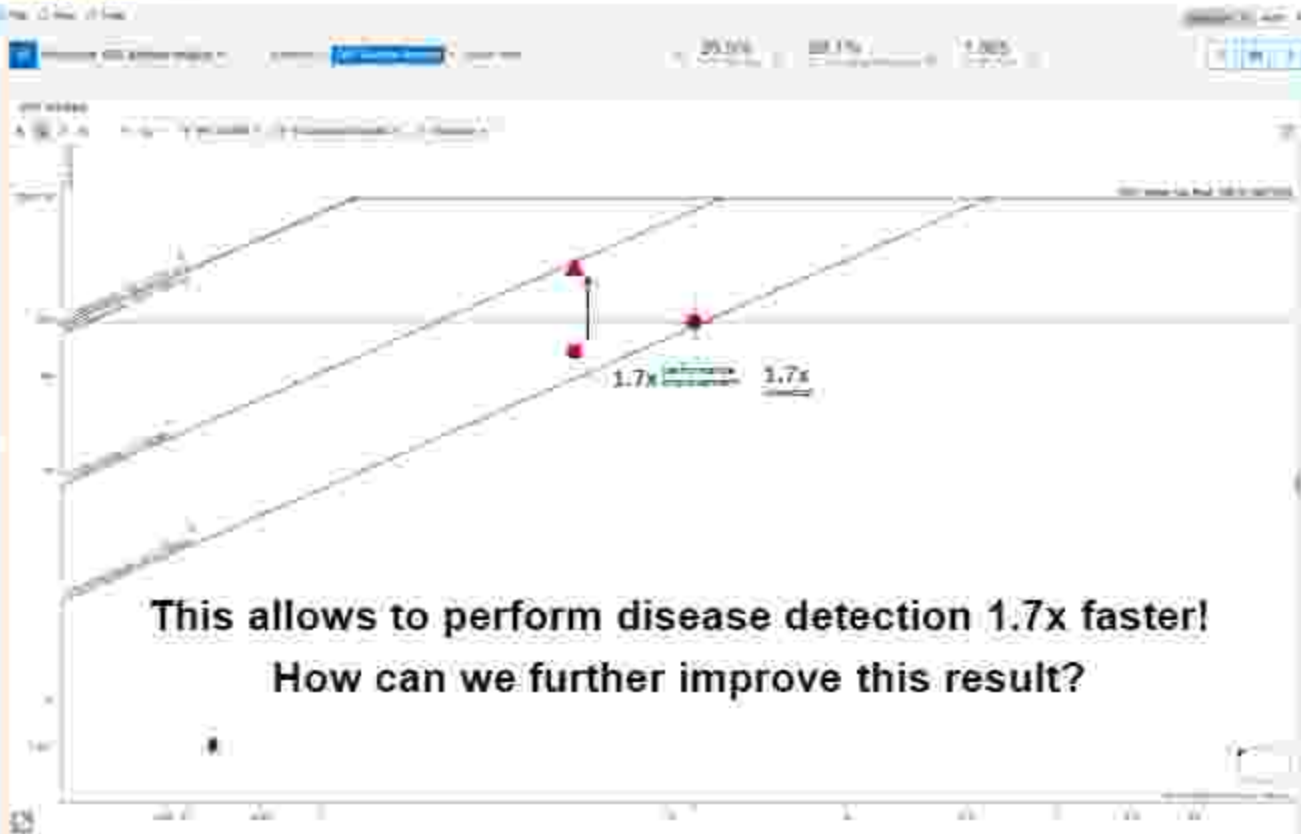


- Two Genotypes, No Phenotype



- Transposed Dataset





This allows to perform disease detection 1.7x faster!

How can we further improve this result?

GPU Optimization

- Three Genotypes → Phenotype



- Two Genotypes, No Phenotype



- ▲ Transposed Dataset



Data set tiling

Device code

```

// genotypes.cu
SNP1 = Adata_zeros[(1_block * N_zeros + (1 - 1_block)) * 2];
SNP2 = Adata_zeros[(2_block * N_zeros + (2 - 2_block)) * 2];
for (p = 0; p < 2 * block_snp * N_zeros; p += 2 * B_SNP)
{
    d12 = -(SNP1[p] | SNP1[p + 1]);
    d12 = -(SNP1[p] | SNP1[p + 1]);

    F1[0] += d12 * y1 * popcount(SNP1[p] & SNP1[p]);
    F1[1] += d12 * y1 * popcount(SNP1[p] & SNP1[p + 1]);
    F1[2] += d12 * y1 * popcount(SNP1[p] & d12);
    F1[3] += d12 * y1 * popcount(SNP1[p + 1] & SNP1[p]);
    F1[4] += d12 * y1 * popcount(SNP1[p + 1] & SNP1[p + 1]);
    F1[5] += d12 * y1 * popcount(SNP1[p + 1] & d12);
    d12 = d12 * y2 * popcount(d12 & SNP1[p]);
    F1[6] += d12 * y2 * popcount(d12 & SNP1[p + 1]);
    F1[7] += d12 * y2 * popcount(d12 & SNP1[p + 1]);
    F1[8] += d12 * y2 * popcount(d12 & d12);
}
// genotypes.cu
}

```

The data set is filtered
by rows of size $2 * B_{SNP}$

The 2nd genotype is
constructed

The frequency table is
filled using 2 genotypes

Tiling our dataset to squeeze the maximums!
Using a tile size of B_{SNP} we can maintain constant
access stride

GPU Optimization

- Three Genotypes → Phenotype



- Two Genotypes, No Phenotype

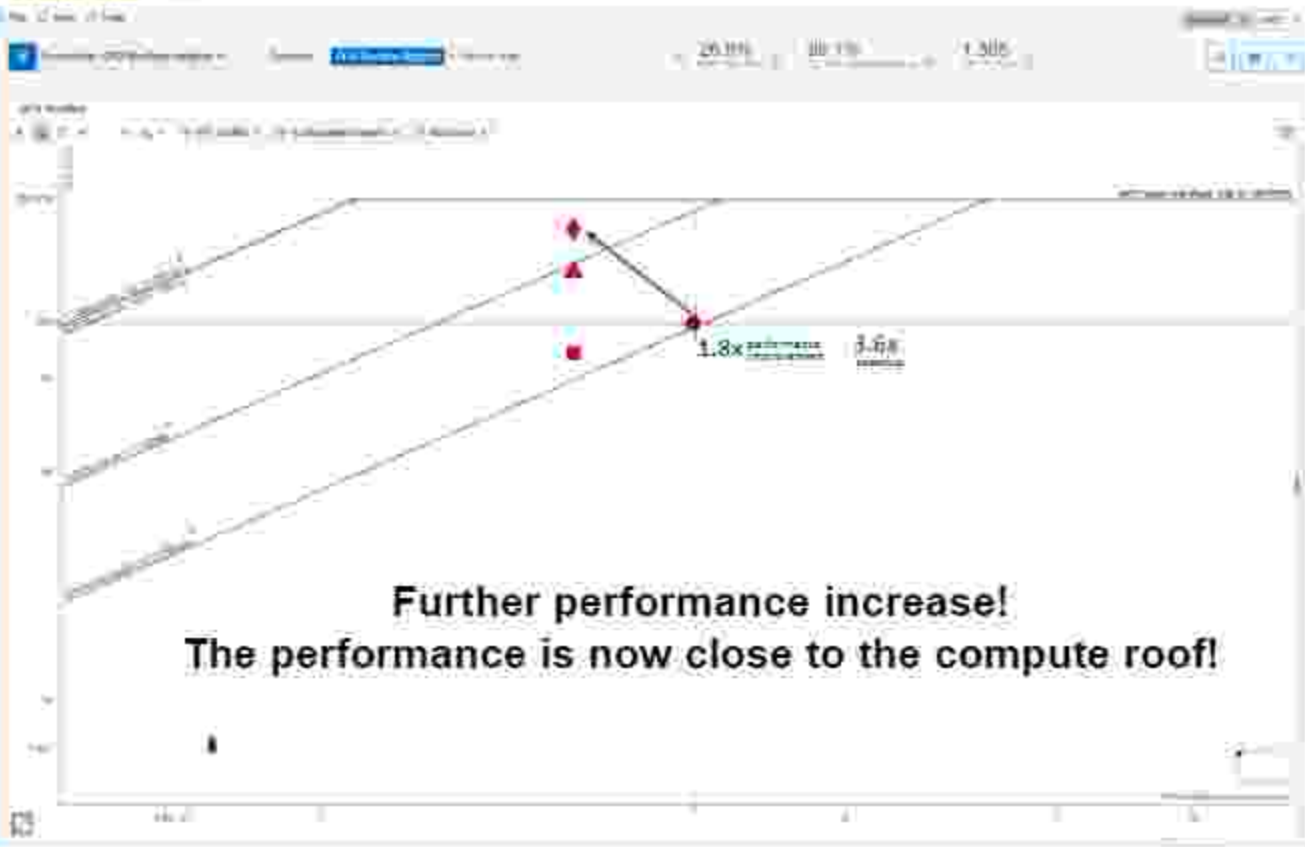


- Transposed Dataset



- Dataset Tiling





GPU Optimization

- Three Genotypes → Phenotype



- Two Genotypes, No Phenotype



- Transposed Dataset



- Dataset Tiling





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CASE STUDY

Conclusions

Conclusions



The insights of Intel Advisor can allow to vastly improve performance

This allows to perform epistasis detection 3.6x faster!

These techniques can be applied to applications in CPU or GPU



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CASE STUDY

Acknowledgements

Special thanks to Sugata Tibrewala, the Intel Advisor team, and Igor Vorobitsov

Intel DevMesh Project – <https://www.intel.com/content/www/us/en/devmesh/>

HPerBio Repository – <https://github.com/HPerBio>

D. Marques, A. Ilic, Z. Matveev and L. Sousa, "Application-driven Cache-Aware Roofline Model", Elsevier FGCS (2020)

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A. Ilic, F. Pratas, L. Sousa, "Beyond the Roofline: Cache-Aware Power and Energy-Efficiency Modeling for Multi-Cores", IEEE Trans. on Computers (2017)

A. Lopes, F. Pratas, L. Sousa, A. Ilic, "Exploring GPU performance, power and energy-efficiency bounds with Cache-aware Roofline Modeling", ISPASS (2017)

A. Ilic, F. Pratas and L. Sousa, "Cache-aware Roofline Model: Upgrading the Loft", IEEE Computer Architecture Letters (2014)



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Supported by Intel Corporation, Portuguese FCT national funds and EuroHPC Joint Undertaking under projects UIDB/50021/2020, PTDC/CCI-COM/31901/2017 (HIPErBio), and grant agreement no. 956213 (Sparsity)

Thank you!