

# GPU Computing at the Netherlands eScience Center

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netherlands

eScience center

by SURF & NWO





# GPU Applications

- Climate Modeling
- Radio Astronomy
- Super-resolution Microscopy
- Astro-particle Physics
- Life Sciences
- Computational Linguistics
- Digital Forensics





## How we work

**Yearly calls for proposals**

**Accepted projects receive:**

- **250K to hire Postdoc or PhD student**
- **2.5FTE eScience Research Engineers**

# Projects started in 2017



**Data mining  
tools for abrupt  
climate change**



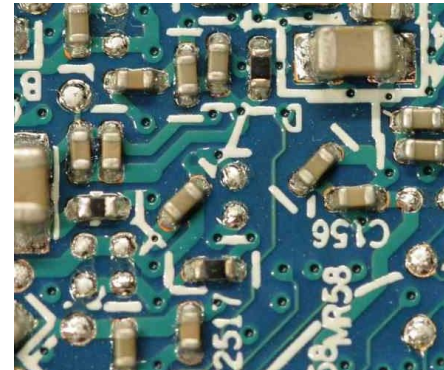
**DIRAC -  
Distributed Radio  
Astronomical  
Computing**

**ASTRON**



**Accelerating  
Astronomical  
Applications 2**

**ASTRON**



**Methodology and  
ecosystem for  
many-core  
programming**



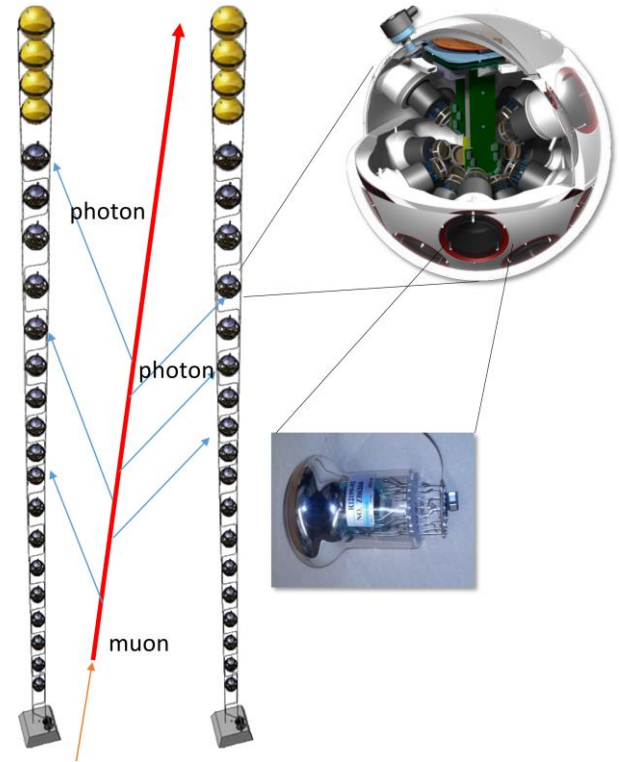


A row of spherical photomultiplier tubes (PMTs) is arranged on a wooden table. Each sphere is covered in numerous small, circular photomultiplier tubes. The spheres are connected to a network of red and black cables. The background shows a laboratory setting with a white wall and a metal frame.

# Real-time detection of neutrinos from the distant Universe

# KM3NeT – Neutrino Telescope

- Huge instrument at the bottom of the Mediterranean Sea
- Pretty high data rate due to background noise from bioluminescence and Potassium-40 decay
- Current event detection / reconstruction happens on pre-filtered data (so called L1 hits)
- Our goal: Work towards event detection based on unfiltered data (so called L0 hits)



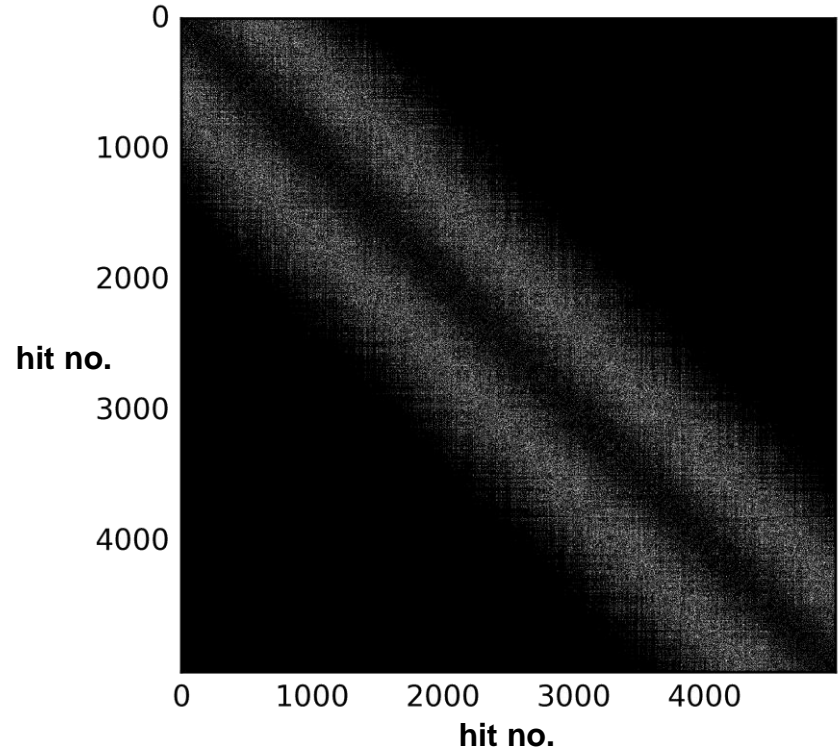
# Correlating hits

- Hits are correlated based on their time and location
- Correlations can only occur in a small window of time
- Density of the narrow band depends on correlation criterion in use

Try-out two designs:

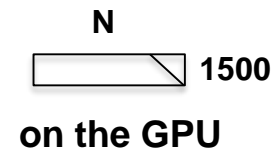
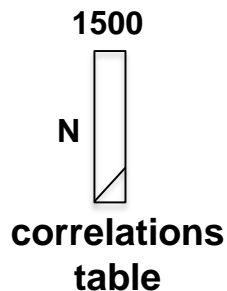
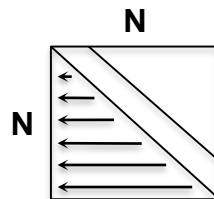
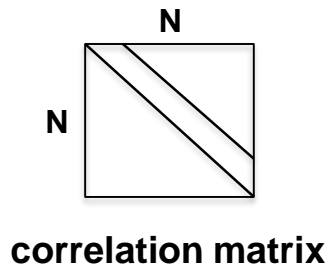
- Dense pipeline that stores the narrow band as a table
- Sparse pipeline that stores the matrix in compressed sparse row (CSR) form

Correlation matrix

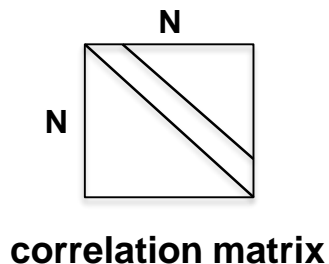


# Data representation

– Dense



– Sparse



CSR format

column indices

start of row

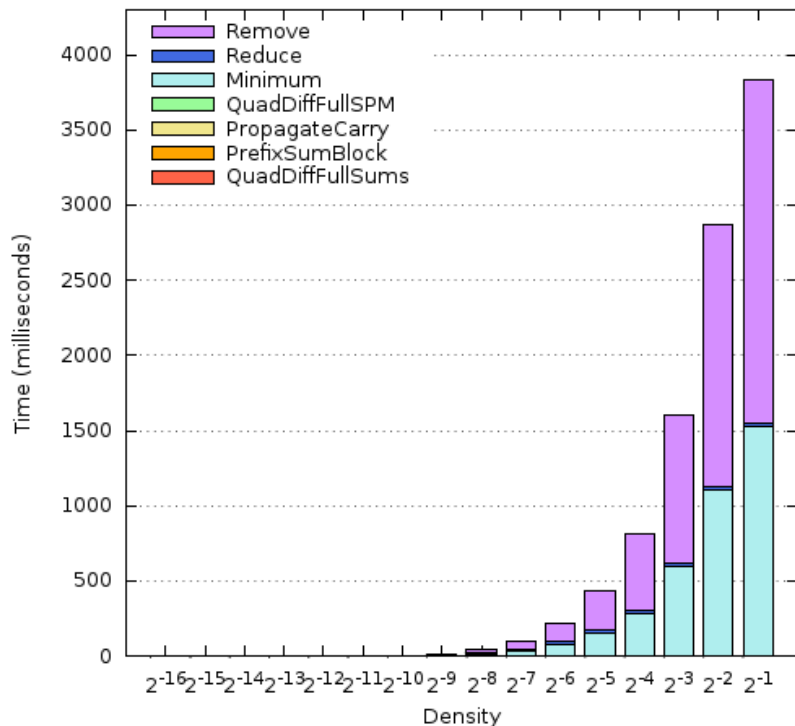
# correlations



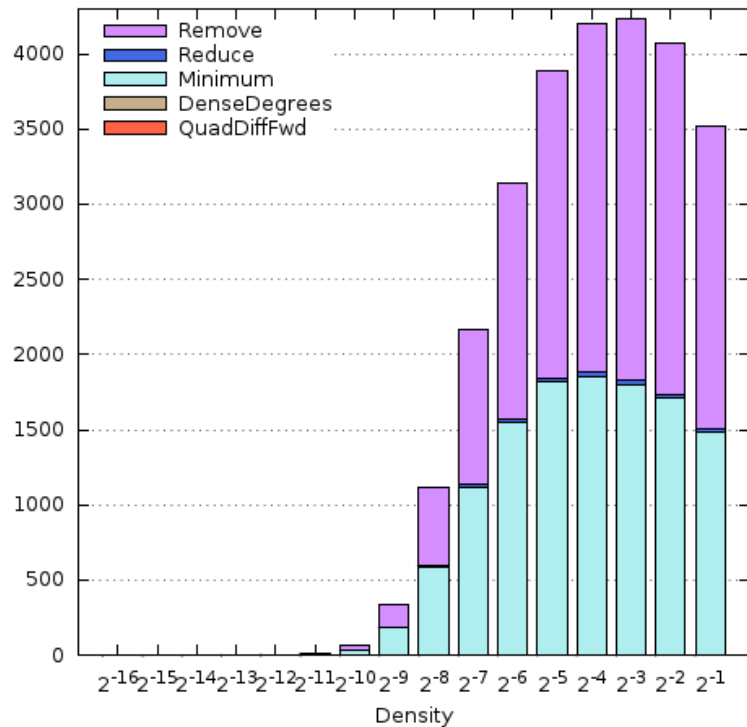


# Comparing performance

Sparse pipeline



Dense pipeline

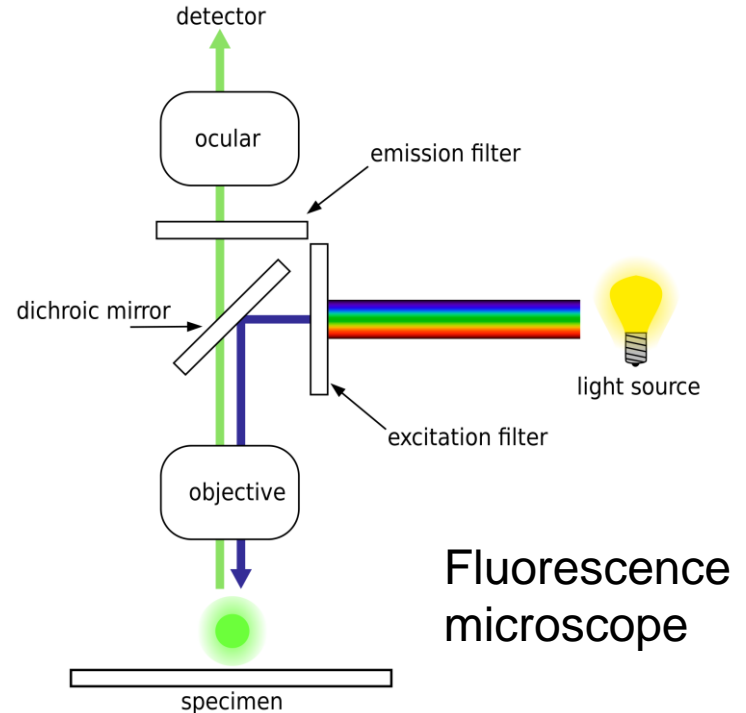


A fluorescence microscopy image showing several cells. The nuclei are stained blue, the cytoskeleton is green, and other organelles are red. The cells are interconnected by a network of filaments.

# Super-resolution microscopy

# Super-resolution microscopy

- Collect a large number of images from fluorescence microscope
- Localize fluorophores using fitting code
- Create single super-resolution image from all localized fluorophores
- Segment all individual molecules in the image
- Create single reconstruction by combining identical copies in the data





# Existing GPU code

- **GPU code for maximum likelihood estimation developed in 2009-2010**
  - ”Fast, single-molecule localization that achieves theoretically minimum uncertainty”  
Smith et al. *Nature Methods* (2010)
- **Estimates the locations and several other parameters of points in noisy image data for various fitting schemes and pixel area sizes**
- **State of the code:**
  - Each thread worked on exactly one fitting
  - Pixel area analyzed by single thread is 7x7, 19x19, and expected to grow in future
  - Requires many registers and a lot of shared memory per thread block
  - Results in low utilization on modern GPUs
  - Multiple fitting schemes implemented with lots of code duplication



# New parallelization

- One fitting is now computed by a whole thread block cooperatively
- Used CUB library for thread block-wide reductions
- Code quality
  - Used function templates to de-duplicate code between different fitting methods
  - Wrote scripts for testing and tuning of device functions and kernels
- Results
  - Currently, speedup of 5.8x to 6.6x over old GPU code on Nvidia GTX Titan X
  - Code can handle arbitrary pixel area per fitting
  - Makes it possible to do termination detection
  - Easier to maintain and extend the code with new fitting schemes



# Lessons Learned



# Software Engineering Practice

*“Throw all good practices out of the window for the sake of high performance”*

- **Examples:**
  - Thousands of code lines in a single function
  - Only acronyms as variable names
  - No comments or external documentation about the code
  - Unnecessary optimization
- **Recommendations:**
  - Start GPU code from simple code
  - Write and use tests
  - Write C++ and not C, whenever possible
  - Trust the compiler to handle simple stuff



# Evaluating results

Results from the CPU and GPU codes are not bit-for-bit the same

- GPUs today implement the IEEE standard just like CPUs
- CPU compilers sometimes more aggressive than GPU compilers
- Fused multiply-add rounds differently
- Floating-point arithmetic is not associative

Things to keep in mind

- It depends on the application whether bit-for-bit difference is a problem
- Testing with random input can give a false sense of correctness



# Talking about performance

- **Many computer scientists I know think**
  - The only way to properly way to discuss GPU performance is to fully optimize and tune for both CPU and GPU
  - Then (and only then) you are allowed to say anything about GPU performance
  - Answering the question: “Which architecture performs the best for this application?”
- **Many scientists from others fields that I work with just want to know:**
  - “How much faster is that Matlab/Python code I gave you on the GPU?”





# Summary

- Choose your starting point carefully
- High-performance and high quality software can co-exist
- Application dependent if small differences in results is a problem
- When talking about performance, be very clear on what is compared to what

[www.esciencecenter.nl](http://www.esciencecenter.nl)

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# Project Partners



Nederlands Forensisch Instituut  
*Ministerie van Veiligheid en Justitie*



ASTRON



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