

Cobiode

Bari, 16 Ottobre 2024



Contesto

- **Big data** era: strong need for a tool capable of performing **fast** and **efficient comparisons** to **find patterns** in large amounts of data, provide solutions to **unsolved problems**, and **speed up** pattern search times.
 - **Pattern recognition** is a fundamental process across numerous industries: from healthcare to finance, from technology to agriculture.
 - It involves identifying **regularities and trends** within large datasets to extract valuable insights and make **informed decisions**.
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La nostra soluzione

- A system that enables **ultra-fast data comparison** (bitwise) based on **dedicated hardware**, that delivers **superior performance**, allowing our customers to achieve accurate comparisons
 - **significantly less time.**
 - **Low power**
 - Our **patented** technology is based on **Associative Memories (AM)**.
 - Funded by **INFN/CERN** with about **5 M€** for tracking particle at CERN.
 - Prototype available in the laboratory: **CoBioDe**
 - genomics
 - medicine
 - pharmacology
 - The system is **scalable** with many AM chip in parallel.
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COBIODE's origins

At hadron colliders:

- **Common problem:** identification of particle tracks in vertex detector

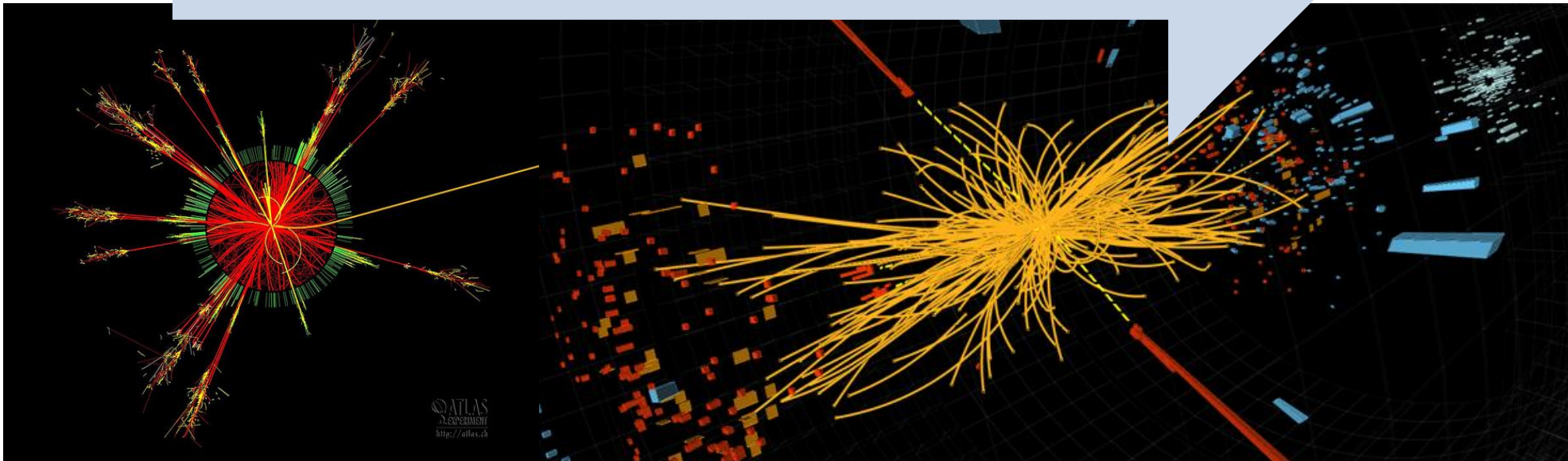
Huge amount of produced data

- **Limited** amount of events can be transferred

Data reduction must be performed

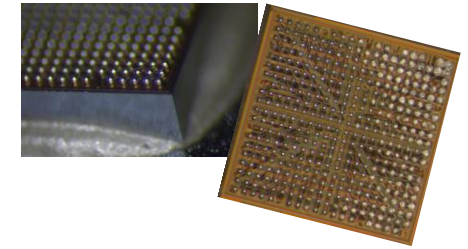
Trigger system

- Particle track recognition in **real time**



The core device: AM CHIP

Associative Memory



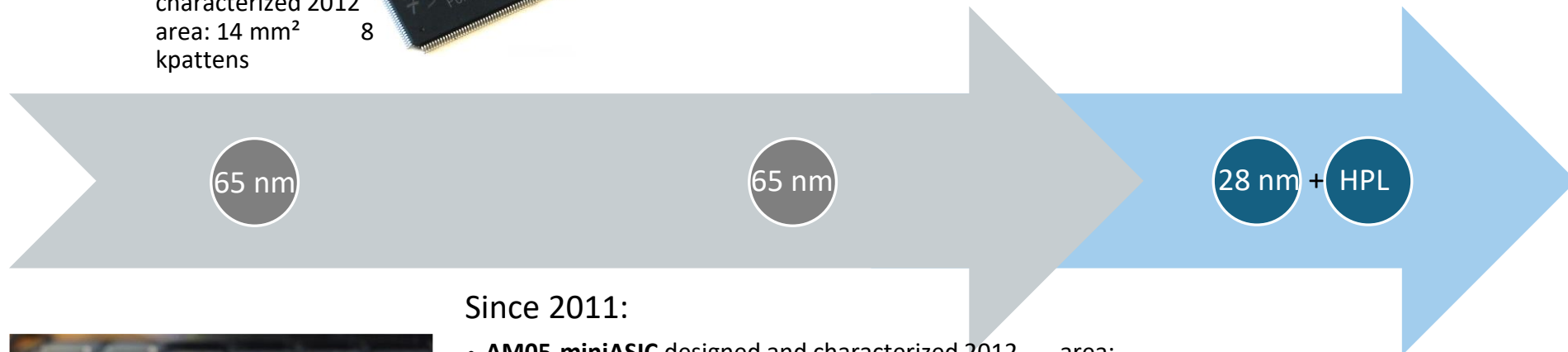
Since 2010:

- **AM chip v. 4** designed and characterized 2012
area: 14 mm² 8
kpattens



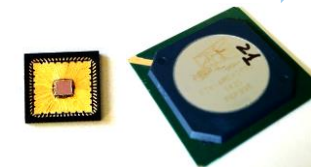
2015-2017:

- **AM07 has been** designed and characterized within the project for several disciplines:
 - **Trigger DAQ (ATLAS* + CMS*)**
 - **Image analysis**
 - **DNA sequencing**



Since 2011:

- **AM05-miniASIC** designed and characterized 2012 area: 4 mm² – 256 patterns for cell test
- **AM05-mpw** designed and characterized 2013 area: 12 mm² – 5 kpattens
- **AM06** designed and characterized 2016 – area: 160 mm² – 128 patterns – **421 millions transistors**



*https://cds.cern.ch/record/2263760/files/CR2017_117.pdf

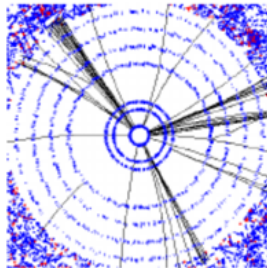
*<https://cds.cern.ch/record/2285584>

THE AM CHIP ARCHITECTURE

For each bus and for each pattern there is a small **CAM cell array (layer x)**

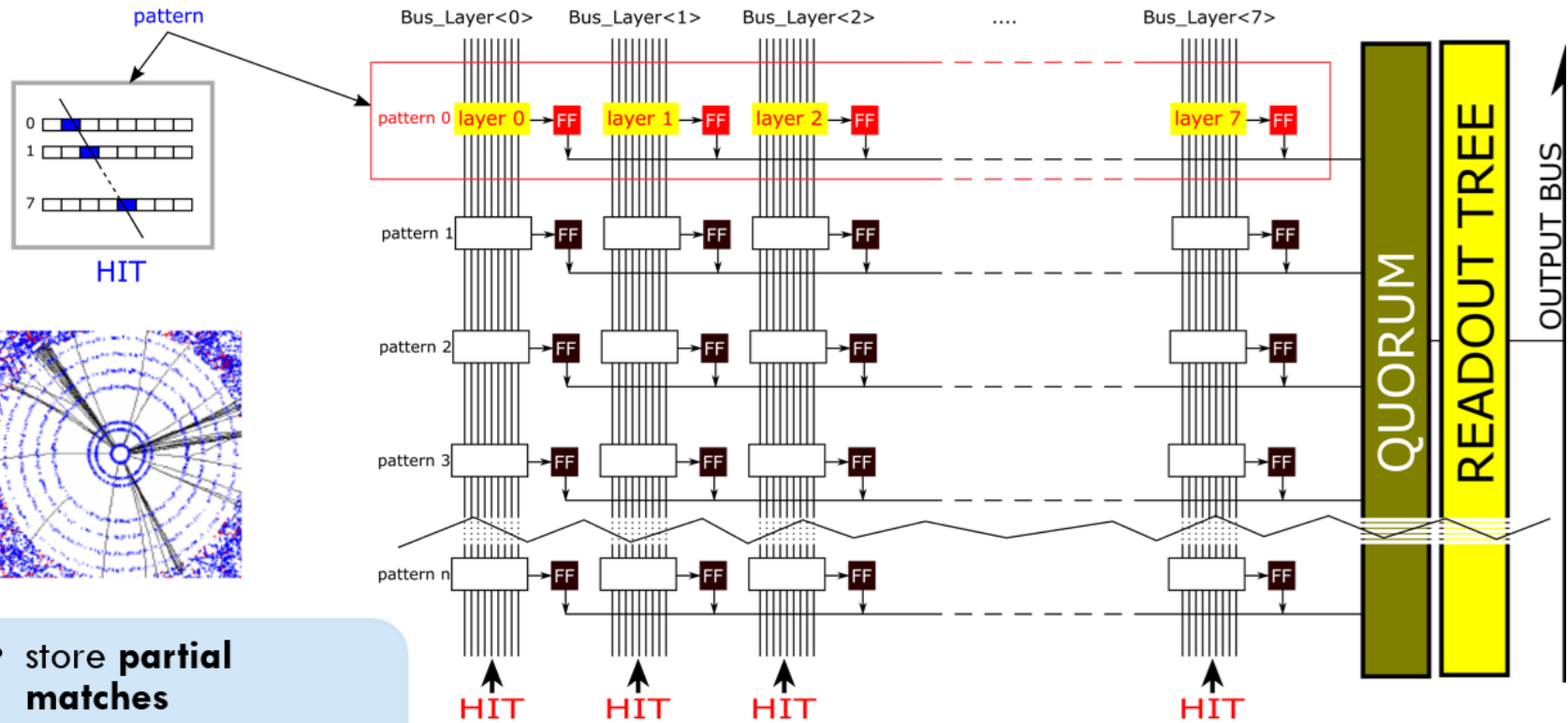
- It compares its own content with all data received. If it matches a **memory is set (FF)**
- The partial matches are analyzed by **Quorum logic** and compared to the desired threshold
- A **readout encoder (Fischer Tree)** reads the matched patterns in order

The AM and commercially available CAMs differs substantially



The AM provides the unique capability:

- store **partial matches**
- find correlations at **different times**



Columns can compute the information independently

AM Performances

Comparison rate (bit-wise):

- AM06 (65 nm) $\sim 15 \cdot 10^{18}$ comparisons per second per chip - (XORAM cell)
- AM07/08 prototype (28 nm) $\sim 6.25 \cdot 10^{18}$ comparisons per second per chip

AM07/08 are based on New Generation Low-power Design Cells

DOXORAM

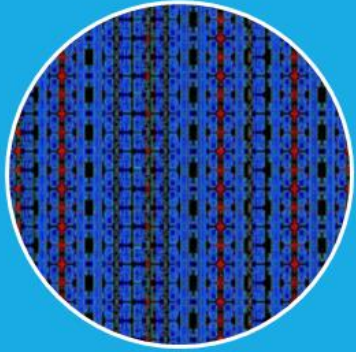
KOXORAM

Italian Patent: A. Annovi, L. Frontini, V. Liberali, A. Stabile,
"MEMORIA CAM",
UA2016A005430

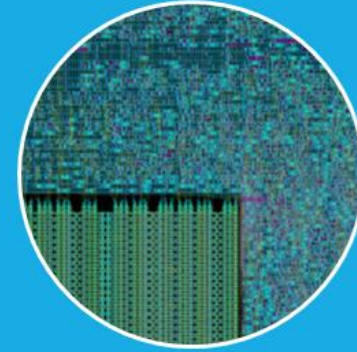
AMchip complexity

<i>Chip name</i>	<i>Transistor count</i>	<i>Year</i>	<i>Brand</i>	<i>Technology</i>	<i>Area</i>
Core 2 Duo Conroe	291,000,000	2006	Intel	65 nm	143 mm ²
Itanium 2 Madison 6M	410,000,000	2003	Intel	130 nm	374 mm ²
Core 2 Duo Wolfdale	411,000,000	2007	Intel	45 nm	107 mm ²
AM06	421,000,000	2014	AMteam	65 nm	168 mm²
Itanium 2 with 9 MB cache	592,000,000	2004	Intel	130 nm	432 mm ²
Core i7 (Quad)	731,000,000	2008	Intel	45 nm	263 mm ²
Quad-core z196 ^[20]	1,400,000,000	2010	IBM	45 nm	512 mm ²
Quad-core + GPU Core i7 Ivy Bridge	1,400,000,000	2012	Intel	22 nm	160 mm ²
Quad-core + GPU Core i7 Haswell	1,400,000,000	2014	Intel	22 nm	177 mm ²
AMBIO future chip	1,684,000,000		COBIODE	28 nm	150 mm²
Dual-core Itanium 2	1,700,000,000	2006	Intel	90 nm	596 mm ²

DESIGN METHODOLOGY

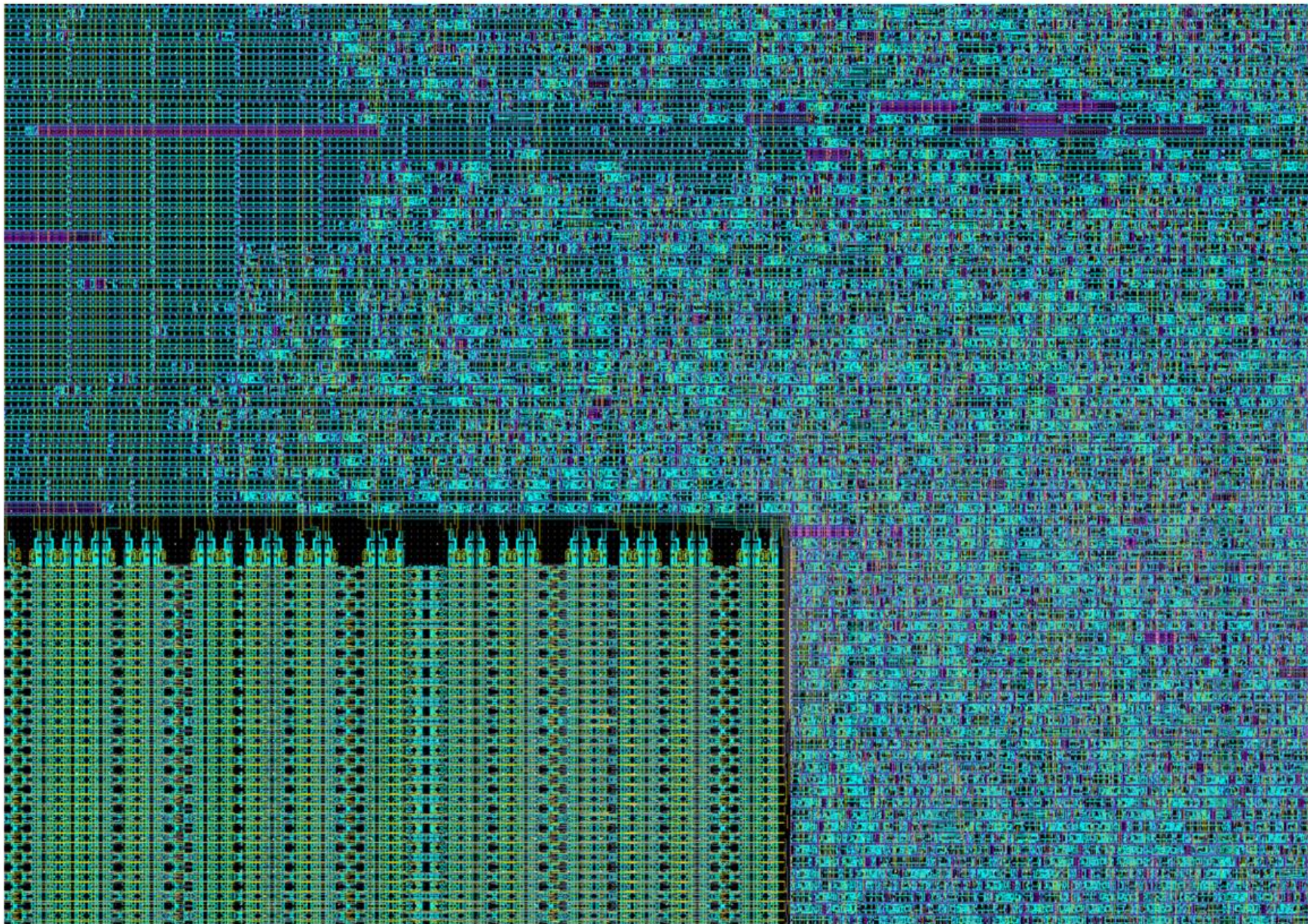


More repetitive parts have been design “by hand” with a full custom approach



More complex logics have been design with automatic tools based on standard cells (synthesis, place & route)







Standard
cells

A photograph of a microchip die with a circular label in the upper right corner. The die surface is covered in a dense grid of small, square cells, which are the standard cells of a programmable logic device. The label 'Standard cells' is written in white text on a blue circular background.



Full
custom

A photograph of a microchip die with a circular label in the lower left corner. The die surface is covered in a dense grid of small, square cells, which are the full custom cells of a programmable logic device. The label 'Full custom' is written in white text on a blue circular background.

COMPLEXITY

Comparison rate:

AMBIO about 0.2 zeta
comparisons per second
per chip

AM06 about 15 exa
comparisons per second
per chip

Call "Research 4 Innovation - 2022"

- COBIODE propone l'uso di HW costituito da 10 chip contenenti le celle di Memoria Associativa (AM) oggetto del brevetto e da un System On Chip (SOC) contenente FPGA e processori ARM. L'integrazione tra SOC ed AM chip permette di sfruttare sia le potenzialità e le prestazioni di un HW dedicato, sia la flessibilità di un FPGA, sia la capacità di calcolo di una CPU ARM.
- Obiettivo: velocizzare le procedure di confronto fra sequenze biologiche di almeno 1000x qualora si confrontino i tempi di elaborazione di CPU convenzionali rispetto all'HW proposto

Nome del progetto:	COMparatore di sequenze BIOlogiche basato su HW Dedicato (COBIODE)
Persona Responsabile delle attività:	Gabriella Trucco
Strutture INFN partecipanti:	Sezione di Milano
Altri Enti o soggetti coinvolti:	Università degli Studi di Milano
Indicare l'esperimento o altro progetto nell'ambito del quale la tecnologia è stata generata:	ATLAS – AMchip
Indicare progetti in corso o finanziati negli ultimi cinque anni su tematiche analoghe sia all'interno dell'INFN, sia a livello di progetti europei/nazionali/regionali:	GenData 2020 project: https://gendata.weebly.com/ DATA-DRIVEN GENOMIC COMPUTING (GeCo): http://www.bioinformatics.deib.polimi.it/geco/?home
Descrizione sintetica del progetto di sviluppo tecnologico proposto (max 500 caratteri, spazi inclusi). Gli algoritmi di analisi genomica richiedono tempi di calcolo talvolta ingestibili. Si propone l'uso di un HW dedicato basato su ASIC e FPGA per accelerare l'analisi di sequenze genomiche. Vantaggio: velocizzare i tempi di calcolo e ridurre i costi; l'ASIC da noi progettato permette di aumentare la parallelizzazione di calcolo con bassi consumi. Impatto sulla società: l'HW consentirà analisi ad oggi irrealizzabili in tempi utili nell'ambito della ricerca biologica e medicina personalizzata.	

Pattern recognition and BLAST

- WP 2.2: 2 Month Activity was devoted to the study of BLAST (Basic Local Alignment Search Tool) software in order to understand BLAST seeding mechanism with C++ library primitive functions

Escherichia coli strain 2011C-3911, complete genome

Sequence ID: [CP015240.1](#) Length: 4863599 Number of Matches: 4

Range 1: 4671753 to 4701689 [GenBank](#) [Graphics](#)

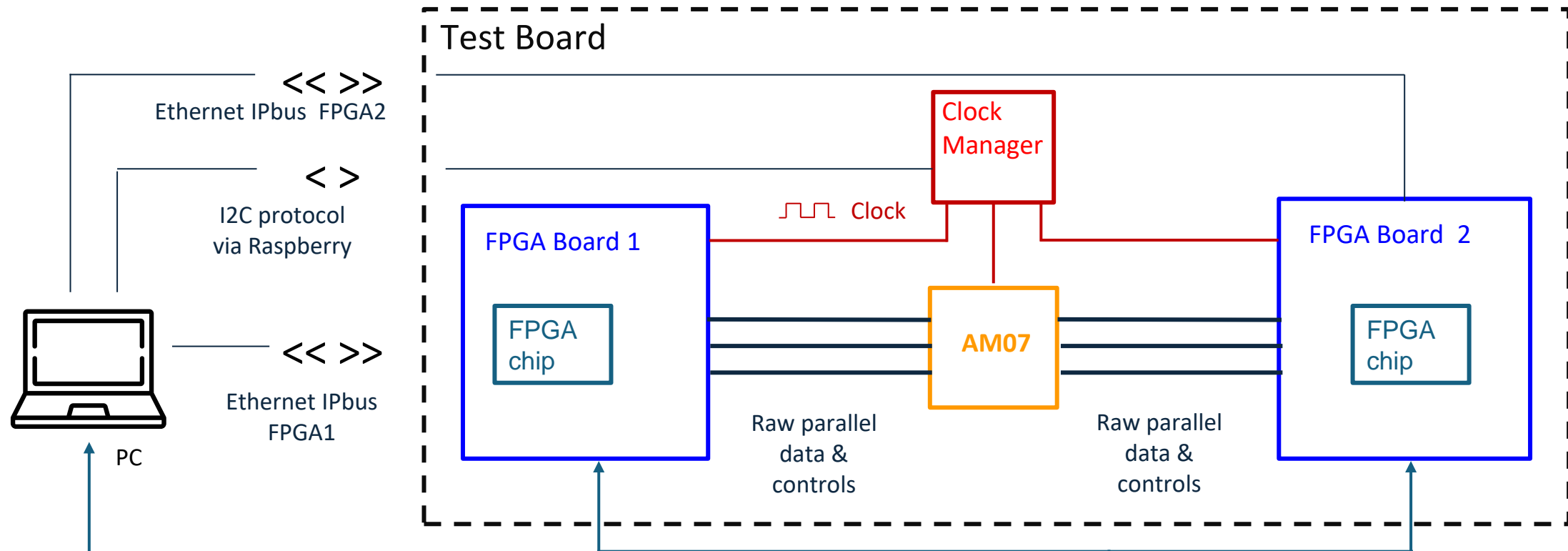
[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
55042 bits(29806)	0.0	29896/29940(99%)	3/29940(0%)	Plus/Plus
Query 1	CCTCCCAAACCTGGCGATATCCAGTCTGGTAAACAGCCTCAAAGGCGTATCGGGTAGGTTA	60		
Sbjct 4671753	CCTCCCAAACCTGGCGATATCCAGTCTGGTAAACAGCCTCAAAGGCGTATCGGGTAGGTTA	4671812		
Query 61	CTGCGACGAGATCGACCAGATATTGCAGTCAGGTATTACTACAAAGGCGTTTTGTGGAGT	120		
Sbjct 4671813	CTGCGACGAGATCGACCAGATATTGCAGTCAGGTATTACTACAAAGGCGTTTTGTGGAGT	4671872		
Query 121	CCTGGCTATTTTGCCAGTAGCTGCGGAGGTGCGCCAATATCCGTCATCCGCCAATACATT	180		
Sbjct 4671873	CCTGGCTATTTTGCCAGTAGCTGCGGAGGTGCGCCAATATCCGTCATCCGCCAATACATT	4671932		

- Original goal was to adapt BLAST module to connect to COBIODE HW and achieve interoperability
- BLAST seeding algorithm is based on sequential CPU optimization: not easy to adapt to massively parallel interfaces of AMs

Research has been addressed to AM internal pattern matching algorithm

Test Board Architecture

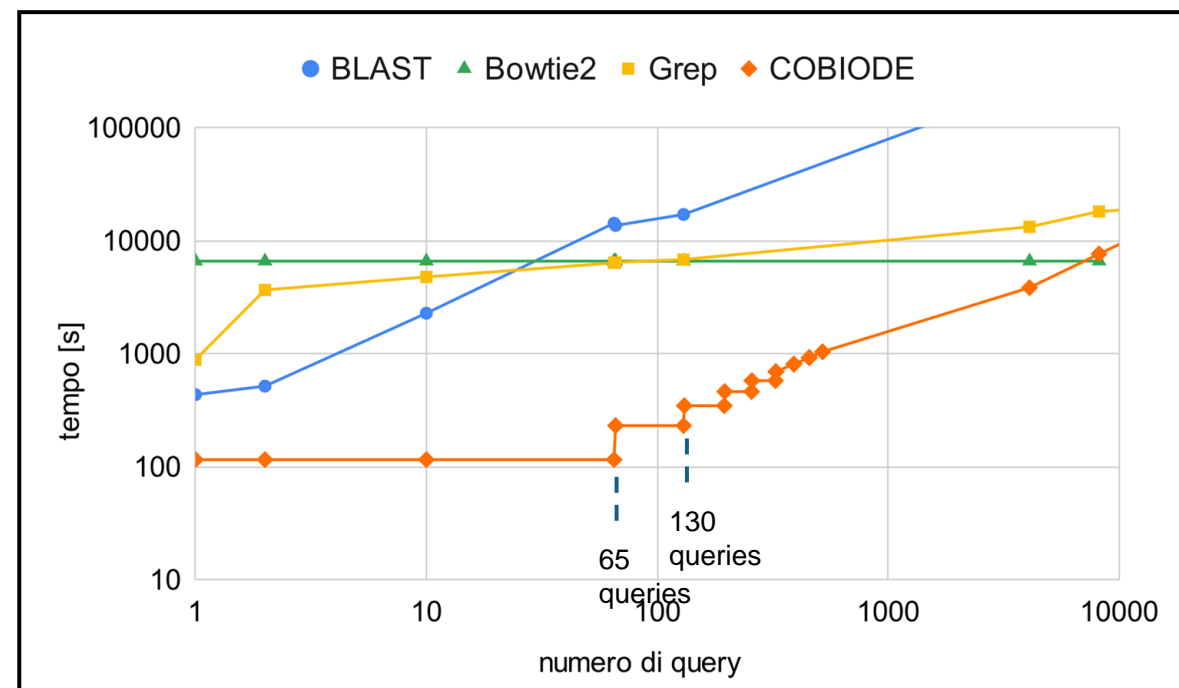


- C++ code: IPbus endpoints to FPGA1 + FPGA2
- I2C - Clock Manager

- VHDL FirmWare (FW):
 - FPGA 1 + FPGA 2

Risultati

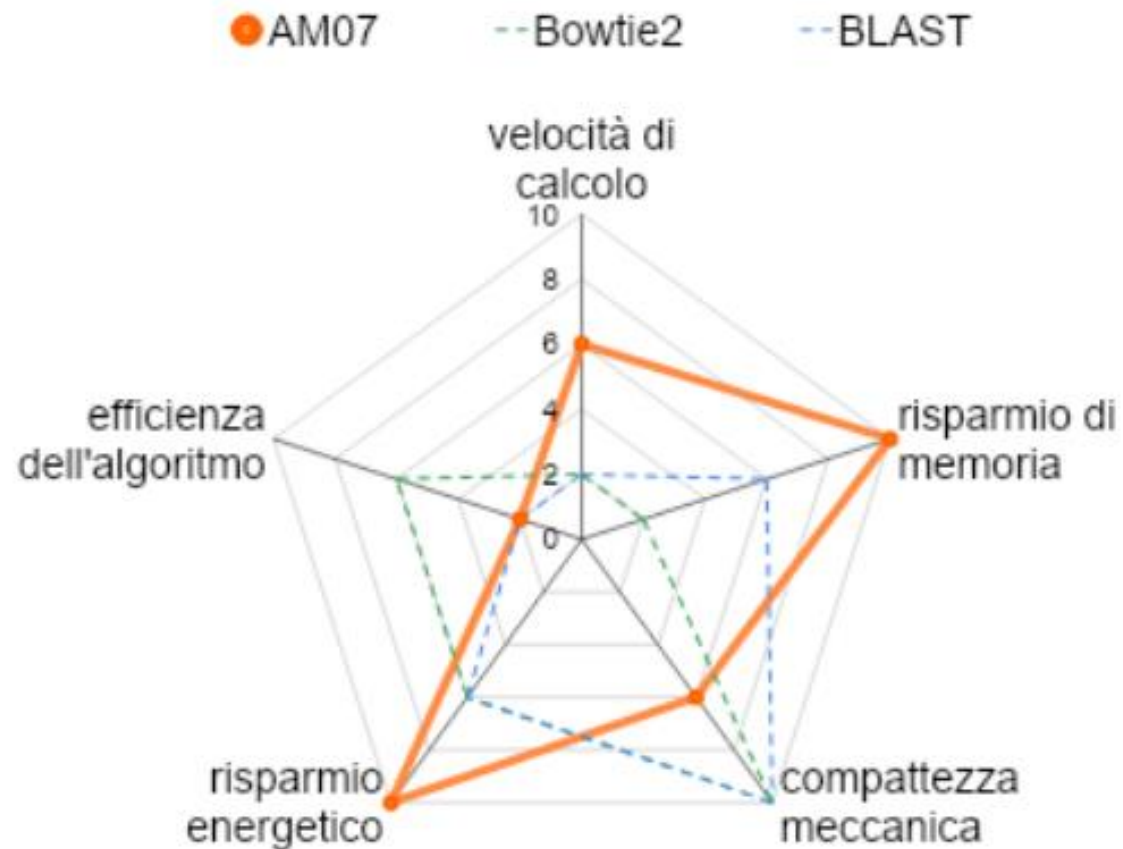
- Genoma umano completo (3GB)
- Il tempo di processamento di COBIODE rimane costante fino a 65 query.
- Ad ogni multiplo di 65 query il tempo raddoppia a causa della riscrittura del secondo set di query sull' AM.



Risultati

Punteggio basato su una scala posizionale:

- alla soluzione migliore viene assegnato un punteggio di 10,
- a quella peggiore un punteggio di 2,
- la soluzione intermedia riceve un punteggio di 6.



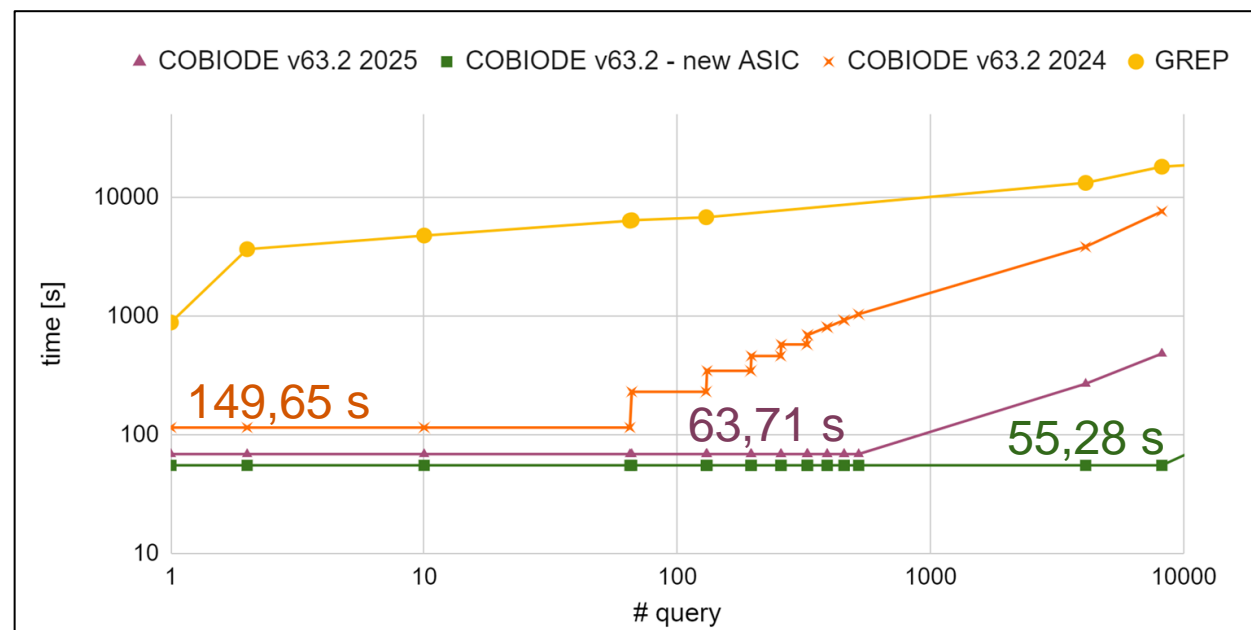
Sviluppi futuri

- COBIODE 2025

- Aumentare la frequenza di AM07
- Aumentare la trasmissione dei dati
- Realizzazione di una nuova PCB performante
- Abilitazione di tutti i 4 cores
- Utilizzo intensivo della CPU

- COBIODE nuovo ASIC

- Nuovo ASIC con 128 cores in una singola AM
- Connessione di più AM in serie
- Aumento della frequenza delle AM fino a 1 GHz





E se facessimo una startup?

- Finito il progetto, TT di INFN ritiene promettente il nostro progetto e ci propone di procedere con startup.
 - Livello raggiunto:TRL4
 - Corso di un anno per imprenditorialità GSOMxCDP (INFN + PoliMI):
 - 3 moduli
 - Mentorship
 - Secondo modulo: andare in giro a raccogliere necessità mercato (prodotto che deve soddisfare le esigenze di mercato)
 - Potenziali clienti
 - Investitori
 - Persone non tecniche, con competenze complementari
 - Costruire una squadra che funzioni
-



Competitor

- Why are we **different from software**? We are much faster at processing data due to the parallelism of our hardware solution.
 - Why are we **different from GPUs**? AM offer a higher degree of parallelism specifically for search and comparison operations compared to GPUs. They can perform these operations simultaneously on all words in memory in a single clock cycle, making them extremely efficient for tasks that require rapid comparisons.
 - Why are we **different from AI**? We differentiate ourselves by providing an exact, deterministic solution.
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Modello di business

- **Freemium with subscription**
 - Set up a **cloud** and give customer access online to our service
 - Prices: to be chosen → we are working on the BP definition

 - **Hardware sale**
 - Directly sell our IP (layout + schematic) to big tech (Intel, AMD, ...)
 - Directly sell our chip or our system to a potential customer
 - Updates and maintenance
-



Piano di crescita

- **First phase (about 2 years):**
 - consolidate and improve the tools for DNA comparison (for human health, breeding, crops, etc.);
 - offer the most suitable solutions for different fields, considering different customer needs in term of performance, availability of tools, privacy of data
 - cooperation with customers as a key point to improve our solutions.
 - **Second phase (after 2 years):**
 - investment rounds to expand the application to other fields, such as information theory, cryptography, image analysis, generic pattern recognition.
 - application, In principle, to all fields requiring fast comparison can benefit from a hardware solution
 - special attention to different requirements (data size, comparison time, power constraints)
 - increase in workforce
-



Perché la nostra soluzione avrà successo

- A **hardware-based solution** has obvious **advantages w.r.t. a software-based one**, both in time and in power consumption.
 - Hardware programmability can offer flexibility, to **adapt our solution to different customers' needs**.
 - **Attention to customers' needs**, to innovate and provide better and better solutions with a problem-driven approach.
-

I fondatori



Alberto Stabile
CTO



Gabriella Trucco
CEO



Luca Palini
Lead Tecnico



A che punto siamo

- Concentrarsi su una fetta di mercato specifica: ambito genomico
 - Partecipazione a Taranto Biotech days
 - Opportunità di ampliare networking
 - Esperti sia dell'accademia che dell'industria
 - Serve validazione industriale: ricerca di un caso studio industriale
 - Fondazione Occhi azzurri e AISJAC per ricerca su malattie genetiche rare
 - Zootecnia e agrifood
 - NextGenomics
-



Prossimo appuntamento

25 Novembre: presentazione finale a Roma a conclusione del corso
GSOMxCDP



Mission e vision

- **Mission:** potenziare la ricerca e l'industria con una tecnologia che permetta di fare riconoscimento di pattern in modo innovativo; fornire uno strumento in grado di sfruttare l'enorme potenziale dei big data per guidare la ricerca e l'innovazione in modo efficiente e rapido.
 - **Vision:** diventare lo standard globale per un confronto rapido, accurato e a basso consumo di potenza, trasformando il modo in cui aziende e ricercatori sfruttano il potere dei dati per risolvere sfide complesse e migliorare il benessere di tutti.
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