MLconf Online^{**}



Accelerated ML, instantly

Chris Kachris CEO, Co-founder

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Need for Computing power



"computing power needed to carry out machine learning neural networks is doubling every 3.5 months."

Cliff Young, Google

New ML models need more powerful platform

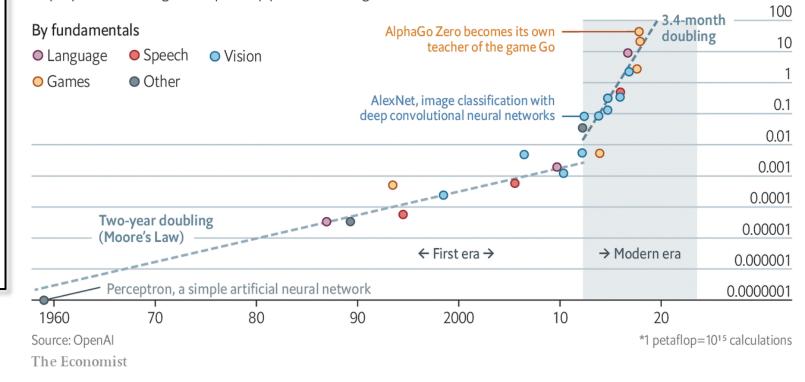
In 2018, OpenAI found that the amount of computational power used to train the largest AI models had doubled every 3.4 months since 2012.

https://www.technologyreview.com/s/614700/the-computing-powerneeded-to-train-ai-is-now-rising-seven-times-faster-than-ever-before/

Open Al

Deep and steep

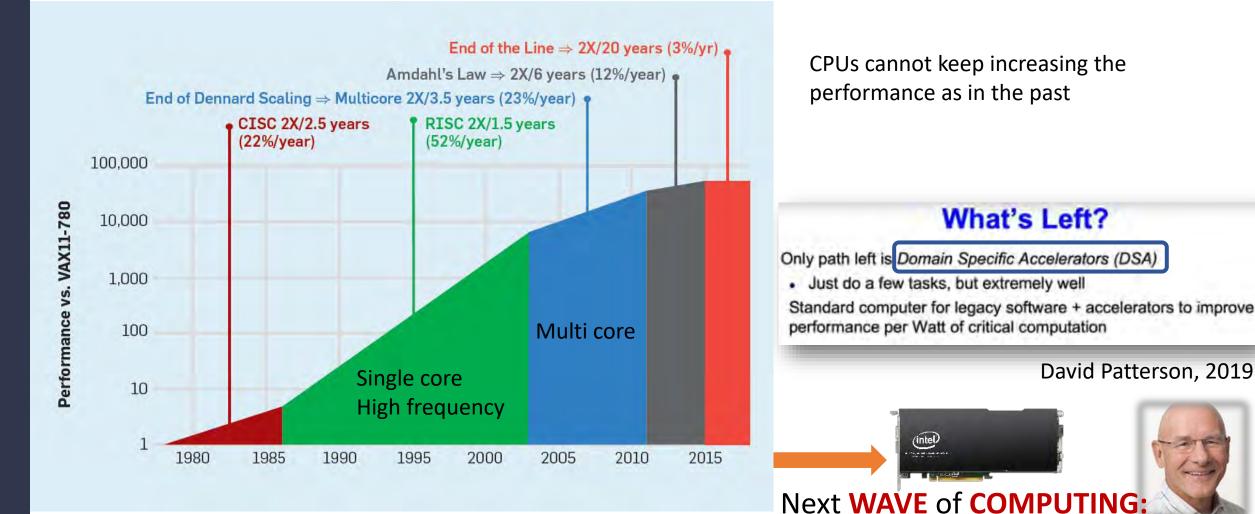
Computing power used in training AI systems Days spent calculating at one petaflop per second*, log scale



https://www.economist.com/technology-quarterly/2020/06/11/the-cost-of-training-machines-is-becoming-a-problem

What's left for faster computing?



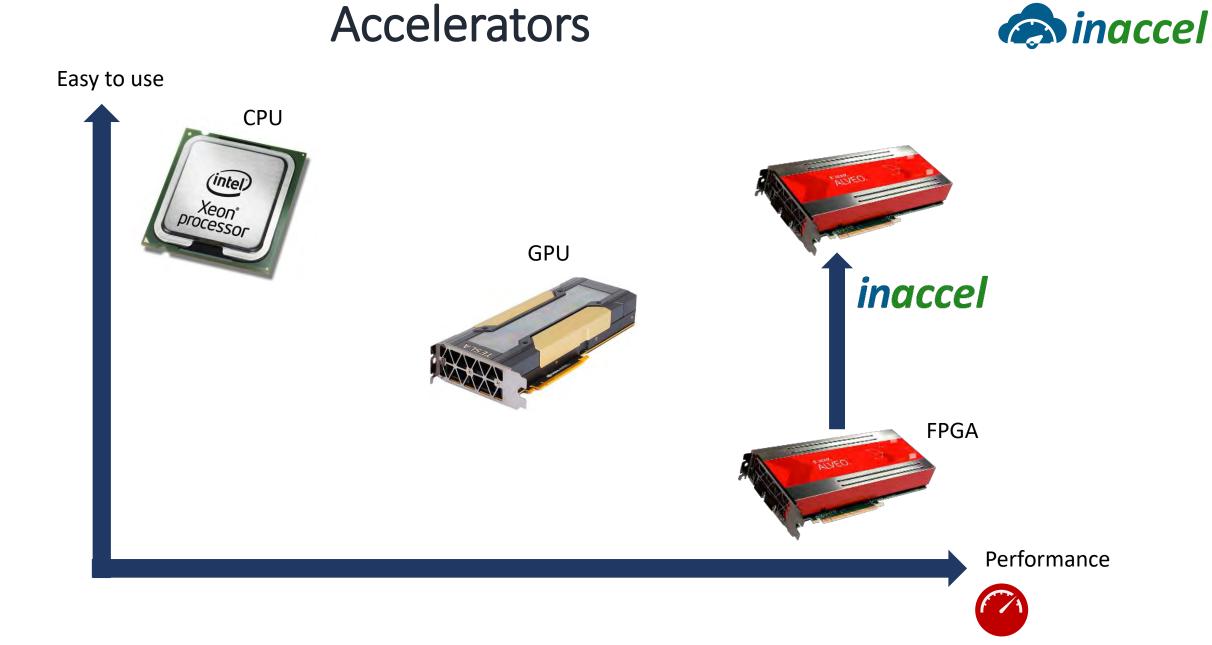


Accelerators

Source: John Hennessy and David Patterson, Computer Architecture: A Quantitative Approach, 6/e. 2018 A domain-specific architecture for deep neural networks Norman P. Jouppi, Cliff Young, Nishant Patil, David Patterson

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Accelerated Machine Learning





https://inaccel.com/accelerated-data-science/

https://inaccel.com/

What we do: Accelerated Machine Learning



Help companies **speedup** their ML applications by using **accelerators** (FPGAs) seamlessly (**ML as a Service**):



10x – 20x Faster





Integrated Accelerated Machine Learning/DNN Platform

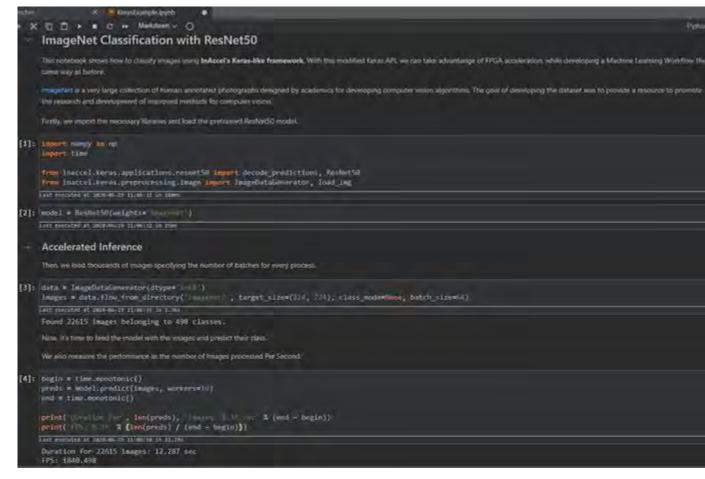


https://www.youtube.com/watch?v=hDLAYNsF39s

Same tools (Python), Faster results



InAccel Studio is a unique portal for Accelerated Machine learning



Familiar tools



Faster results

- 10x-20x faster
- Zero code changes

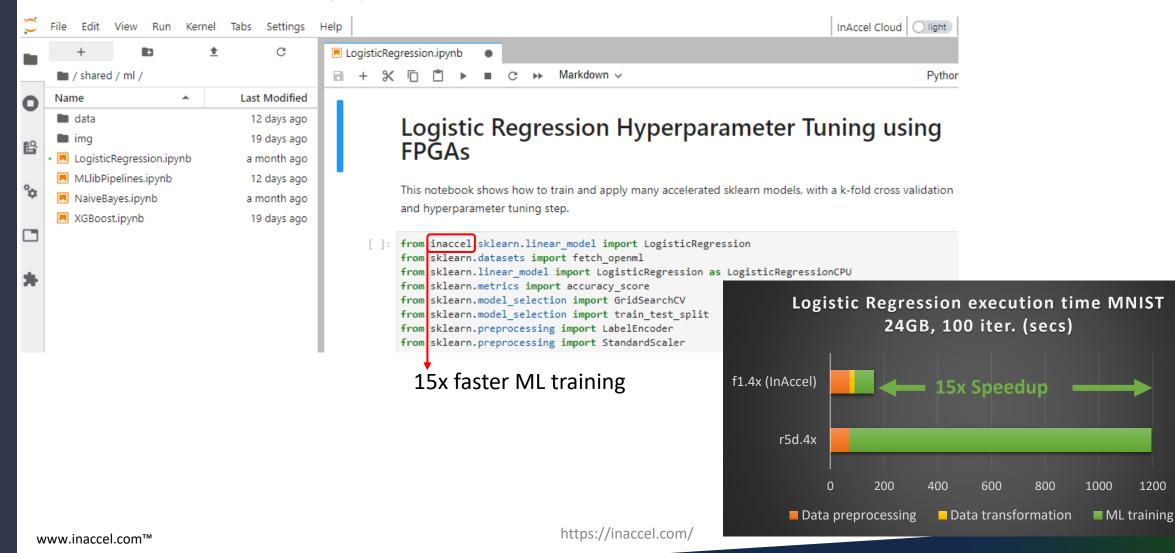
https://inaccel.com/accelerated-machine-learning/

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Instant Acceleration



Just add inaccel and enjoy 15x faster execution



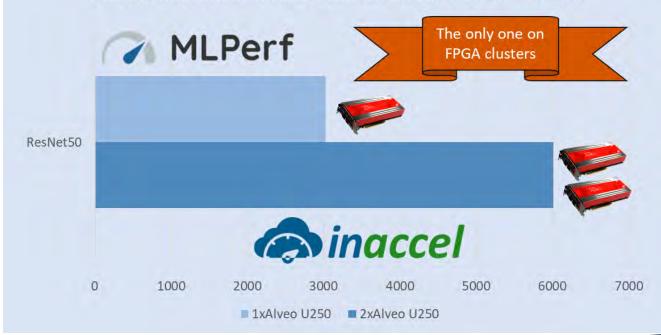
1400





							Results						
									Task	Image classificatior	1		
										ResNet			
									Accuracy (%FP32 ref				99.00
									Scenario	Single Stream	Multiple Stream	Server	Offline
			_							latency in			
	Submitte		Processor	#	Accelerator	#	Software	Model Used	Units	ms	streams	query/s	samples/s
)RY: Availa	able											
0.7-158	Deci	n2-highcpu-16	Intel(R) Xeon(R) Cascade Lake CPU	1			openvino_2020.4.287	resnet		2.13			1,093
0.7-159	Deci	n2-highcpu-2	Intel(R) Xeon(R) Cascade Lake CPU	1			openvino_2020.4.287	resnet		6.77			148
0.7-160	dividiti	AWS g4dn.4xlarge	Intel(R) Xeon(R) Platinum 8259CL CPU @ 2.50GHz	1			OpenVINO 2020	resnet50		2.67			
0.7-161	dividiti	AWS g4dn.4xlarge	Intel(R) Xeon(R) Platinum 8259CL CPU @ 2.50GHz	1			OpenVINO 2020	ssd-resnet34					
0.7-162	InAccel	alveo2.ethz.ch	Intel(R) Xeon(R) Gold 6234	2	Xilinx Alveo U250	1	InAccel Keras 2.3.1.2	resnet		7.00	58		3,026
0.7-163	InAccel	alveo2.ethz.ch	Intel(R) Xeon(R) Gold 6234	2	Xilinx Alveo U250	2	InAccel Keras 2.3.1.2	resnet					6,008

MLPerf inference of ResNet50 on an Alveo U250 cluster





Instant Acceleration by more than 10x



Now we're ready to build a pipeline and fit it. This puts the data through all of the feature processing, model tuning & training we described in a single call.

In [*]: from pyspark.ml import Pipeline

pipeline = Pipeline(stages=[labelIndexer, featuresScaler, cv, indexToLabel])

```
%time model = pipeline.fit(train)
```

	Contraction of the second second	The second se		T REMINING	6 COMPLETED	
27 March	16:45					
38	39		10	41		42
				3	4	5
		27 March 16:45 38 39				

The next cell converts the test set from LibSVM to Parquet memory format, in order to serve as our streaming source.

15x faster

Video analytics: Face detection





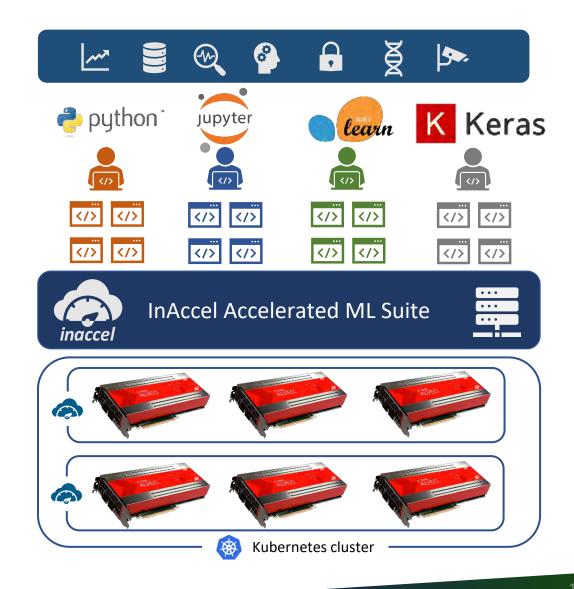


1700fps per server

How we do it



- We leverage the power of programmable accelerators (FPGA)
- A unique platform for easy deployment, scaling and resource management of FPGA
- **Pricing model**: Pay-as-you-go (Subscription)



Use cases

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(intel

Written by Steven Leibson | August 2, 2019



https://blogs.intel.com/psg/inaccels-accelerated-ml-suite-boosts-spark-ml-performanceby-as-much-as-7x-on-fpga-based-alibaba-cloud-f1-instances/

Quantitative Finance



Written by Steven Leibson | June 11, 2020



https://blogs.intel.com/psg/flumaion-acceleratesquantitative-financial-calculations/



intel.

ğ Genomics

Solution Brief FPGA Genomic Analytics

Acceleration of Sequence Alignment and Variant Calling for Genomic Analytics Using Intel® FPGAs

(a) inaccel



Natalia Poliakova

Ioannis Stamelos

Aspasia Stavrianou

Genomic Analytics aligns a selected genome to a reference genome to detect genetic variants in that selected genome as compared to the reference genome his technique is fundamental to the diagnosis and cure of rare, inherited disease as well as for medical breakthroughs and personalized care. The medical industry is progressing towards personalized medicine, which will require the storage of many, many human genomes. There are 3 billion nucleotide base pairs in a human enome, which trai genome.

As the Coronavirus has raced around the world, thousands of genome sequence of the virus have been shared on GISAID¹, an online global platform for genomic data. One Cornavirus genome sequence contains good platform of genome data. One Cornavirus genome sequence contains good to 32K to 32K bases in the RNA strand located inside the coronavirus. These shared sequence variants offer clues about how the virus, named SARS-CoV-2; is spreading and evolving. But because these shared sequences represent a tiny fraction of cases and show few tell-tale differences, they are easy to overinterpret.²

Virologist Eeva Broberg of the Centre for Disease Prevention and Control³ states that "there are more plausible scenarios for how the disease reached northern Italy than an undetected spread from Bavaria."1 This statement underscores the importance of fast sequence alignment of the Coronavirus mutations.

"The very first SARS-CoV-2 sequence, in early January, answered the most bas question about the disease: What pathogen is causing it? The genomes that followed were olmost identical, suggesting the virus, which originated in an animal, Authors had crossed into the human population just ance. If it had jumped the species barrier multiple times, the first human cases would show more variety. Some diversity is now emerging. Over the length of its 30,000-base-pair genome, SARS-CoV-2 accumulates an average of about one to two mutations per month. Using these little changes, researchers draw up phylogenetic trees, much like family trees make connections between cases, and gauge whether there might be undetected spread of the virus.²¹ Fast analysis and tracking of the mutations is critical for better protection of the population as the virus evolves and migrates between the countries and geographies. Elias Koromilas

Scientists will be scouring the genomic diversity of these viral genome sequences for signs that the virus is getting more dangerous. Caution is warranted. An analysis of 103 genomes published by Lu Jian of Peking University and colleagues on 3 March 2020 in the National Science Review argued that they fell into one of two distinct types, named 5 and L, and are distinguished by two mutations. Because 70% of sequenced SARS-CoV-2 genomes belong to a newer type L genome, the authors concluded that the type L genome has evolved to become more aggressiv and spreads faster.

Chris Kachris Genomic scientists and researchers within different groups around the world have been trying to uncover genetic determinants of susceptibility, severity, and outcomes of COVID-19 crow the genomes of COVID-19 patients. COVID-19 is the **Calvin Hung** pandemic disease caused by the SARS-CoV-2 coronavirus

Using genomic analytics on the sequences of novel viruses to track mutations is a computationally intensive algorithm and requires powerful processing platforms for the efficient processing of huge amounts of data. Fast genome sequencing



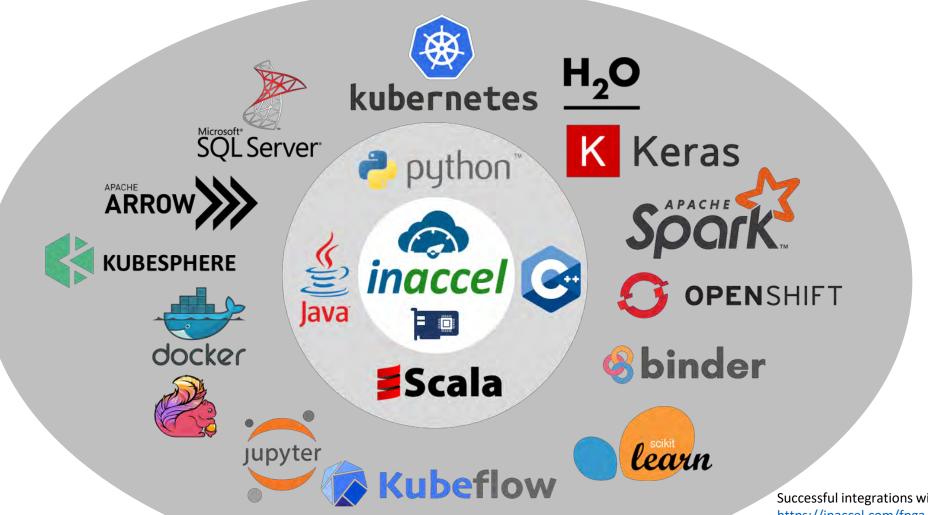
On line free Data Science platforms



	GPU	FPGA
<i>inaccel</i>		10x
Azure Notebooks		
Amazon SageMaker		
colab		
OataCamp		
kaggle		

Seamless Integration with any framework





Successful integrations with Multiple Frameworks https://inaccel.com/fpga-integration-easier-than-ever/

Market size – FPGAs in Data Centers



InAccel is targeting the Market size for FPGA Data Center and HPC Accelerators for application Acceleration

- Machine learning
- Genomics
- Quantitative Financial
- Analytics
- Databases
- Security
- Vision



2023

TAM: \$500 Million

(Compute acceleration not including smartNIC and storage)

SAM: \$200 Million

(Compute acceleration not including smartNIC and storage)





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Co-founders Team



• Dr. Chris Kachris

- Xilinx Research labs (2007)
- Book: Hardware Accelerators in Data Centers
- First paper on FPGAs for MapReduce
- 80+ publications on FPGAs, 1800+ citations

• Elias Koromilas

- Winner of the Xilinx Open Hardware Contest, Spark on PYNQ 2017
- Ioannis Stamelos
 - Winner of the Xilinx Open Hardware Contest, Spark on PYNQ 2017

Christoforos Kachris · Babak Falsaf Dimitrios Soudris Editors Hardware Accelerators in Data Centers Springer

ID United States

Kulkarni et al.

(12) Patent Application Publication

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(43) Pub. Date

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InAccel Team



Advisory board





Christos Makiyama Founder and President at Silicon Planet Corporation Genelle Heim Managing Director at Grayson Hayden Group

(Ex-Vice President of Marketing at Xilinx)



Chris Kachris CEO, co-founder



Elias Koromilas CTO, co-founder



Ioannis Stamelos COO, co-founder



Vasilis Amourgianos FPGA Engineer



Vangelis Gkiastas ML Engineer



Aspasia Stavrianou DevOps engineer

InAccel, Inc. Corporate overview



- Founded in January 2018 (Seed fund: \$600 USD in June'18)
- Registered in Delaware, USA



• Membership:





QUESTIONS?







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THANK YOU!

@inaccel /in/kachris

