Software bottlenecks for 3D AI

X-IA #16 Santé : Molécules, Protéines et 3D

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- 1. What is an image?
- 2. Software bottlenecks for AI research

3. What you can expect going forward

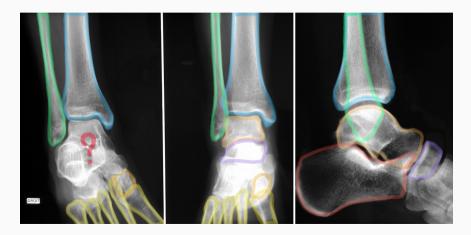
What is an image?



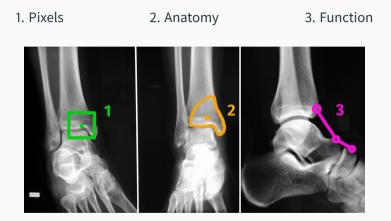
1. Pixels



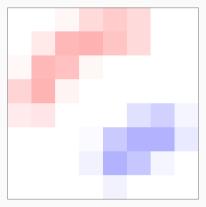
1. Pixels 2. Anatomy







Simplifying a bit, each level of analysis corresponds to a way of **grouping pixels** with their neighbors.

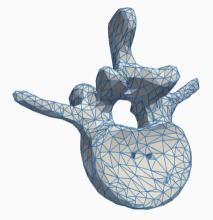


 $N_x \times N_y \times N_z$ array of pixels.

Bitmap images and volumes:

- .bmp, .png, .jpg
- Standard in **radiology**.
- + Ordered memory structure.
- + Explicit neighborhoods.
- + Fast **local** filters.
- \rightarrow **Texture** analysis.
- \rightarrow Organ segmentation.
- \rightarrow Pattern **detection**.

2nd level: point clouds and 3D surfaces



 $N_{\text{points}} \times 3 \text{ array of } (x,y,z) \text{ coordinates.}$

Clouds of points (\pm triangles):

- .svg
- Standard for video games.
- + Compact representation.
- + High precision geometry.
- + Easy to deform.
- ightarrow 3D visualization.
- \rightarrow Anatomical **atlas**.
- \rightarrow **Shape** analysis.

3rd level: biomechanical and/or physiological model [Zyg]



Volumetric mesh, graph of interactions.

Mechanical/biological model:

- Finite elements, networks.
- Standard for CAD.
- + Prior knowledge.
- + Robust to noise.
- + Realistic behaviour.
- \rightarrow **Physiological** interpretation.
- $\rightarrow~$ Infer what cannot be seen (stress).
- \rightarrow **Simulate** a surgery.

Looking for the **neighbors** of a point in 3D space?

- On a grid : read adjacent memory cells.
- With N **points** (x, y, z) : computation of N distances.

Want to **rotate** a bone by 10°?

- On a grid : artifacts, loss of details, transfers between memory cells.
- With N **points** (x, y, z) : simple arithmetics on the coordinates.

Computational **speed** \iff Training on **large datasets**.

To summarize

AI = statistical regression method + relevant computational model.

In biomedical imaging, we represent data as:

- 1. A 2D or 3D pixel grid.
- 2. An array of (x, y, z) coordinates.
- 3. A **web** of complex interactions.
- 4. All three at once!

In most cases, we define a large structured formula:

 $\mathsf{image} \xrightarrow{F} F(\mathsf{image}) \simeq \mathsf{diagnostic}$

F is a parametric computing **architecture** \simeq **model** to fit \simeq **network** to train.

Software bottlenecks for AI research

The AI revolution is driven by gaming computers

Digital images and machine **learning** have been studied for **decades**. **Breakthrough** in 2010-15 : using **PlayStations** to do **science** became **easy**.

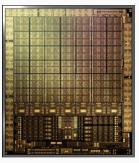
Research effort at all levels towards:

- Increasingly powerful computers.
- Increasingly convenient **software toolkits**.
- Increasingly relevant models.

Spectacular results in a few applications

⇒ massive **investments**, industry + governments.





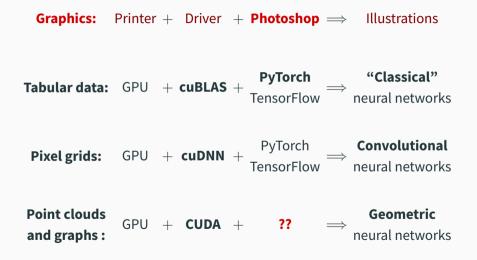
For grid images: a mature ecosystem



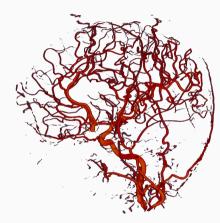
Main motivation for AI in 2012-2022: **self-driving cars**. Key challenges: **segment** the environment, **detect** other actors.

Two full software suites to manipulate **images as grids of pixels**: TensorFlow (Google) and PyTorch (Facebook-Meta).

To go beyond prototypes, AI engineers need a full software suite



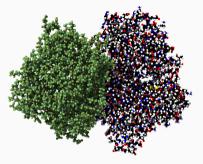
For point clouds and graphs: work in progress



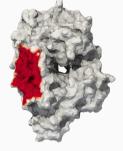
Brain arterial network. How do we **process this object**? An ecosystem under construction:

- KeOps : since 2017
 - Fast learning with **point clouds**.
- **PyG** : since 2018
 - Fast learning with graphs.
- Warp, FEniCSx and PhiFlow : since 2018
 - Fast learning with **physics**.
- PyVista and Vedo : since 2019
 - 3D visualisation.
- scikit-shapes: released soon
 - Easy morphometrics.

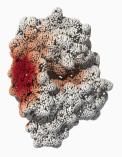
Applications to protein sciences [SFCB20]



(a) Raw protein data.

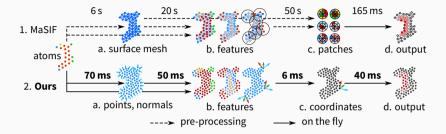


(b) Interface.



(c) Prediction.

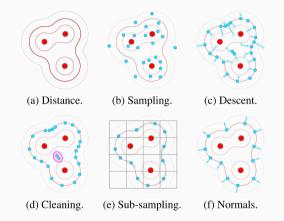
Fast end-to-end learning on protein surfaces





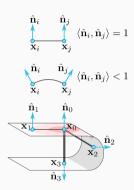
 $\times 100$ - $\times 1,000$ faster, lighter and fully differentiable.

Idea 1: on-the-fly sampling of protein surfaces

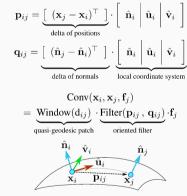


Fast, fully differentiable, heterogeneous batches (without padding).

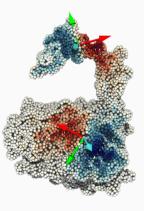
Idea 2: quasi-geodesic convolutions



(a) Quasi-geodesic distance d_{ij}.



(b) Quasi-geodesic convolution.



Fast, fully differentiable, heterogeneous batches (without padding).

KeOps (www.kernel-operations.io) lets us implement:

- Custom operations that best reflect a biological prior.
- Zero need to talk about CUDA blocks, threads, etc.
- Great tool for prototyping with geometric ideas.

Main limitation: beyond 32 channels per convolution, register spilling.

This is just **one example** of architecture that is equivariant to isometries.

(Some?) general E3NN layers could also be accelerated.

- Gaming computers (GPUs) are the workhorses of AI.
 A full software suite is required to rein in these machines.
- Since 2015, **biomedical imaging** rides a wave of investment from the **FAANG** for **natural** image processing.
- Breakthroughs: **segmentation**, **texture** analysis and lesion **detection**. What about **surgical** planning, **morphometrics**, **vascular** analysis...?
- An **investment in the numerical foundations** of the field is under way. **Tradeoffs** between ease of use, versatility, speed, portability, etc.

References

Freyr Sverrisson, Jean Feydy, Bruno E. Correia, and Michael M. Bronstein.

Fast end-to-end learning on protein surfaces.

bioRxiv, 2020.



Solid 3d human foot and ankle model.

https://www.zygote.com/cad-models/solid-3d-human-anatomy/cad-human-foot-ankle-model.