From size functions to GENEOs:
an in(form)al journey
from the form of data to the form of observers

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Seeing, Learning, Evolving:
An asymptotic journey
through 65 Years of Alessandro Verri
November 27-28, 2025, Genoa

Outline

Size functions

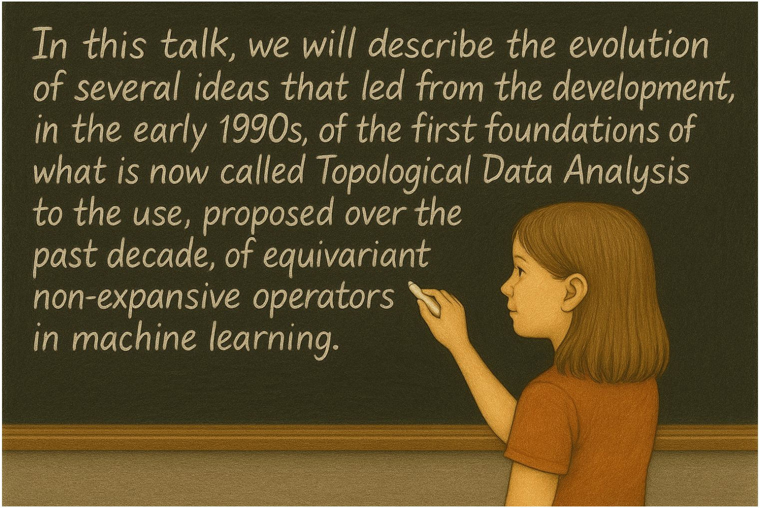
Natural pseudo-distance

Multidimensional data

From Persistent Homology to GENEOs

GENEOs and XAI

Introduction



In this talk, we will describe the evolution of several ideas that led from the development, in the early 1990s, of the first foundations of what is now called Topological Data Analysis to the use, proposed over the past decade, of equivariant non-expansive operators in machine learning.

Size functions

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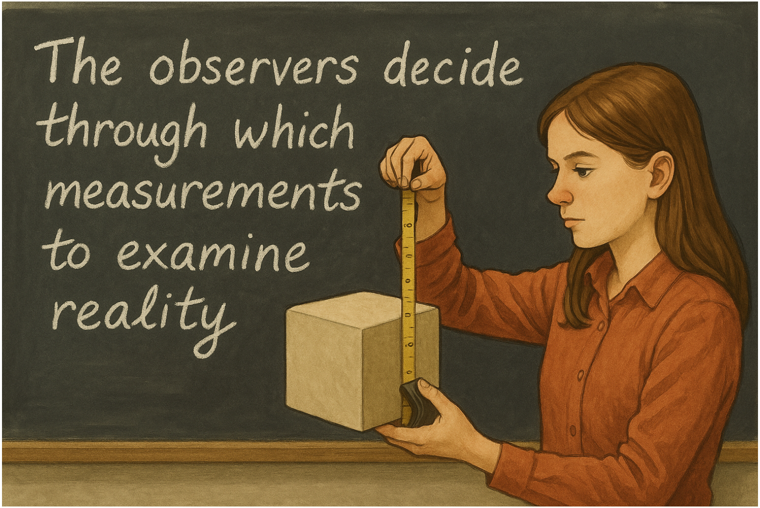
Idea n.1


The observers decide
through which
measurements
to examine
reality

Size functions

This idea led to the concept of the **size function**:

- Filter a topological space S by taking the sublevel sets of a continuous function $\varphi : S \to \mathbb{R}$.
- Consider the function $\ell(x,y)$ that, for each pair (x,y) with $x < y$, counts the number of connected components of the sublevel set below y that contain at least one point below x.

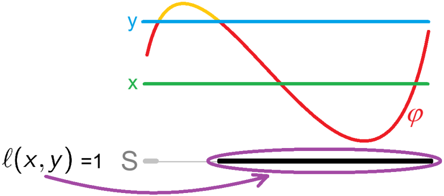
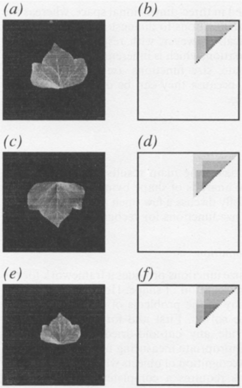
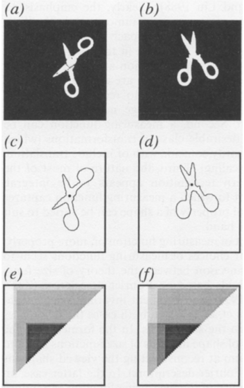


Figure: In this example, the topological space S is a line segment.

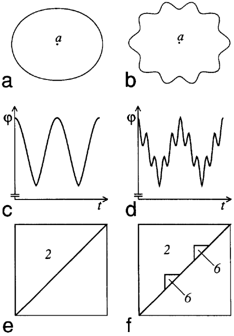
Size functions

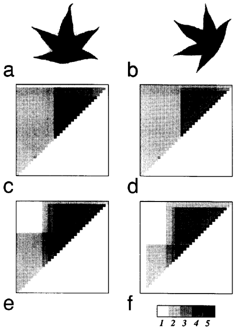




A. Verri, C. Uras, P. Frosini, M. Ferri. *On the use of size functions for shape analysis*. **Biological Cybernetics**, 70, 99–107 (1993).

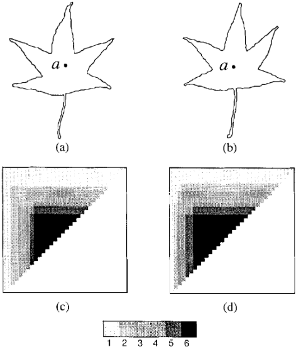
Size functions

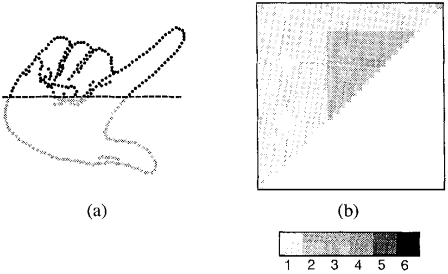




A. Verri, C. Uras. *Metric-topological approach to shape representation and recognition*. **Image and Vision Computing**, 14(3), 189-207 (1996).

Size functions

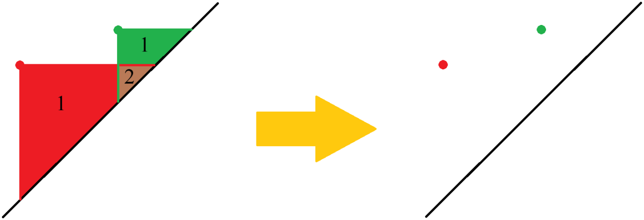




C. Uras, A. Verri. *Computing Size Functions from Edge Maps*. **International Journal of Computer Vision**, 23, 169-183 (1997).

Size functions

Size functions are equivalent to persistence diagrams in degree 0. In other words, they record the birth and death times of connected components as the level of a filtering function varies, interpreting the level as time.



size function

persistence diagram

Persistence diagrams can be generalized to higher degrees, counting holes of higher dimensions. These diagrams are used in Topological Data Analysis.

Size functions

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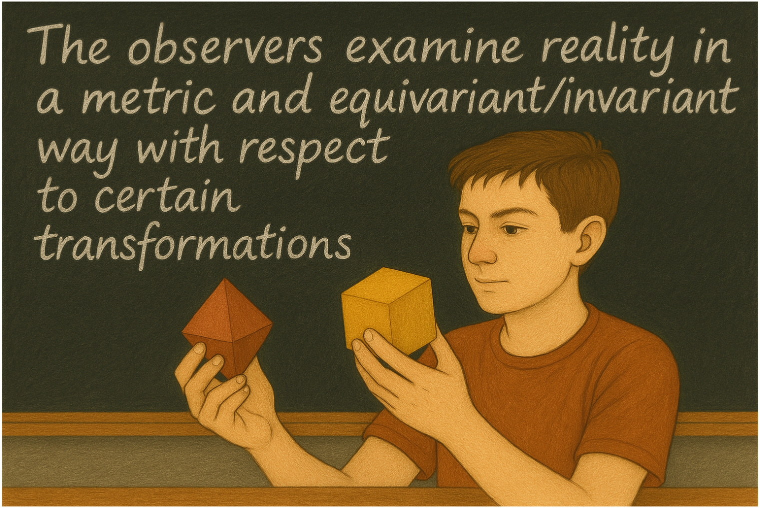
Idea n.2



The observers examine reality in a metric and equivariant/invariant way with respect to certain transformations

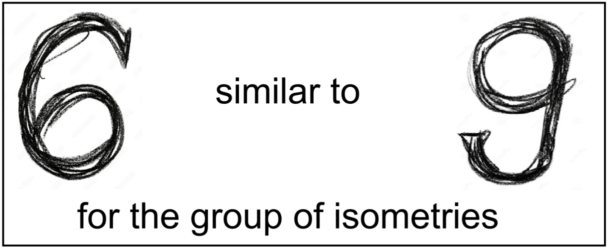
The definition of d_G

Let X and G be a **compact metric space** and a **subgroup of the group** $\mathrm{Homeo}(X)$ of all homeomorphisms from X to X, respectively. If φ_1, φ_2 are two continuous and bounded functions from X to $\mathbb{R}$ we can consider the value $\boxed{\inf_{g \in G} \|\varphi_1 - \varphi_2 \circ g\|_\infty}$. This value is called the **natural pseudo-distance** $d_G(\varphi_1, \varphi_2)$ between φ_1 and φ_2 with respect to the group G.

In plain words, the natural pseudo-distance associated with group $\boldsymbol{G}$ measures how similar two signals are under the action of $\boldsymbol{G}$.

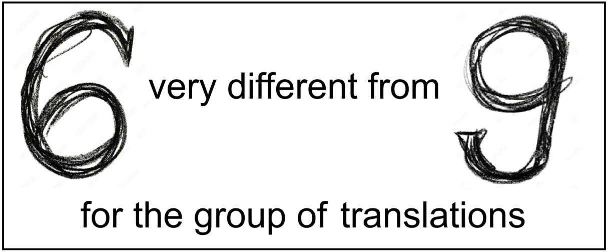
P. Donatini, P. Frosini. *Natural pseudodistances between closed surfaces*. **Journal of the European Mathematical Society**, 9(2), 331-353 (2007).

The definition of d_G



similar to

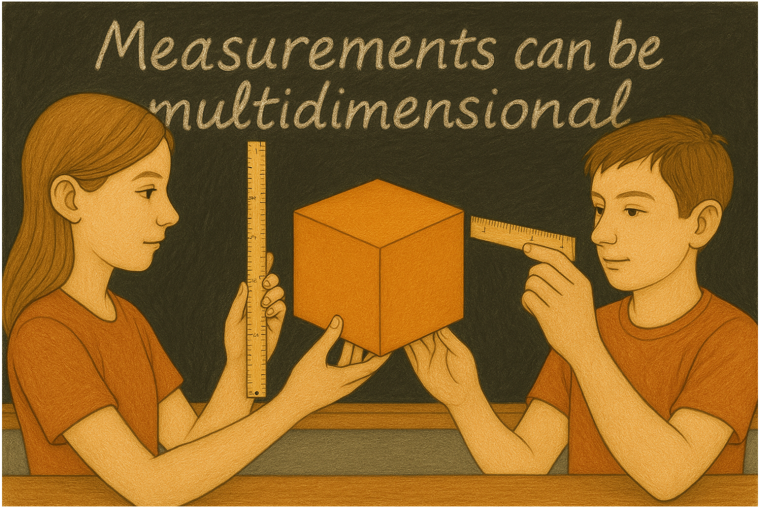
for the group of isometries



very different from

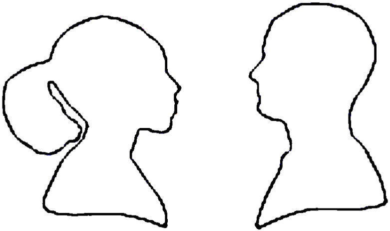
for the group of translations

Idea n.3



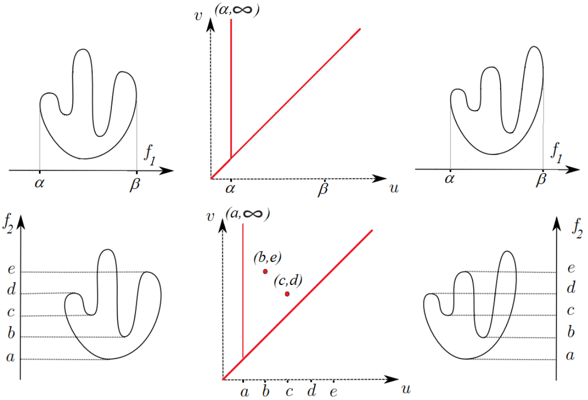
What can we do for vector-valued functions?

In topological data analysis we often have to consider vector-valued functions instead of scalar functions. As an example, we could have to compare two closed curves in $\mathbb{R}^2$, i.e., two functions $f_1, f_2 : S^1 \to \mathbb{R}^2$. How can we extend the concept of persistence diagram to this setting?



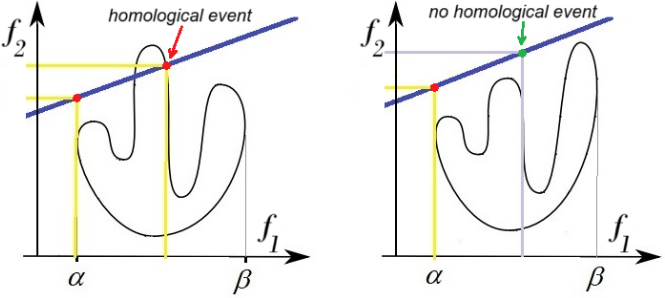
The foliation method

A not very useful idea is to study the two components f_1 and f_2 separately. In this case, the two curves below cannot be distinguished.



The foliation method

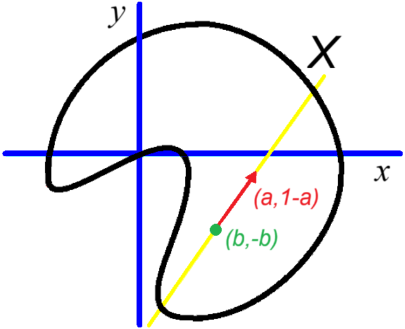
A better idea is to study each filtration associated with a line of positive slope.



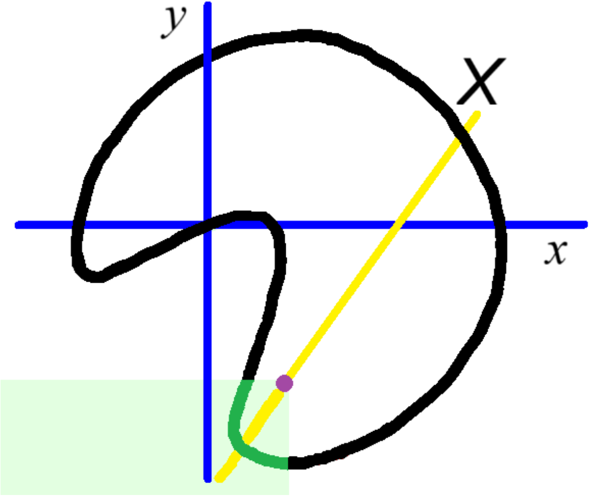
The chosen line allows to distinguish between these curves.

Bifiltrations and positive slope lines

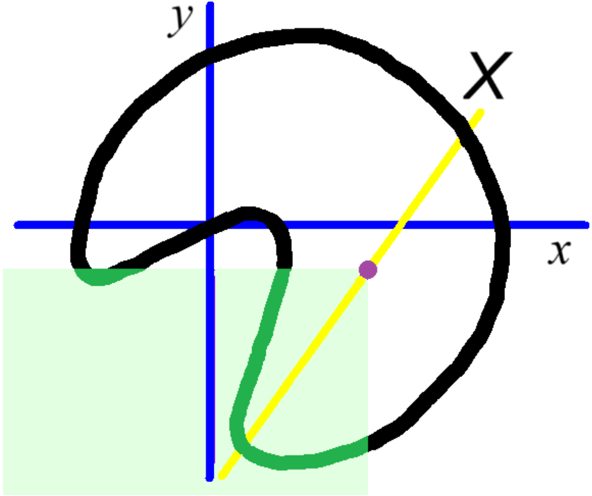
If we have a bifiltration given by a function $\boldsymbol{f} = (f_1, f_2) : X \to \mathbb{R}^2$, we can consider a unit vector (w.r.t. $\|\cdot\|_1$) $w = (a, 1-a)$ with a positive slope, and a point $P = (b, -b)$. Every choice of P and w defines a filtration $\{X_t\}$ of X, where X_t is the set of points of X whose image by $\boldsymbol{f}$ is both under and on the left of the point $P + tw$. As a consequence, each choice of P and w defines a persistence diagram.



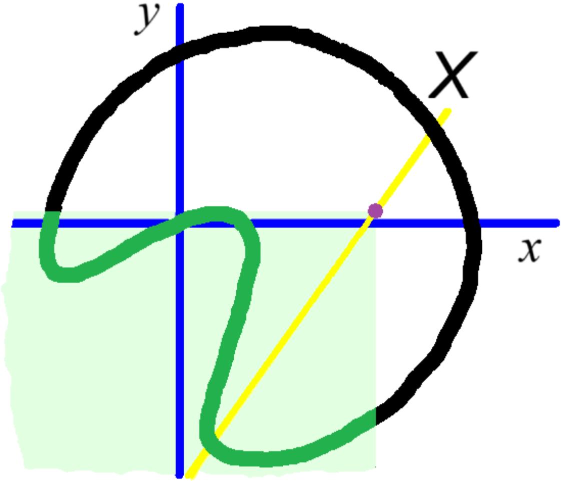
Bifiltrations and positive slope lines



Bifiltrations and positive slope lines



Bifiltrations and positive slope lines



The normalized function $f^*_{(a,b)}$

If we set $(x, y) = P + tw = \big(at + b, (1-a)t - b\big)$ and define the function $f_{(a,b)}(p) := \max\left\{\frac{f_1(p)-b}{a}, \frac{f_2(p)+b}{1-a}\right\}$, then we can write $X_{(x,y)} = \{p \in X : f_1(p) \leq x, f_2(p) \leq y\}$ as the set $X_t = \{p \in X : f_{(a,b)}(p) \leq t\}$.
As a consequence, the bifiltration $\{X_{(x,y)}\}$ of X leads us to consider the persistence diagram $\mathrm{Dgm}_k(f_{(a,b)})$ of the function $f_{(a,b)}$.
In order to get a stability theorem we have to normalize $f_{(a,b)}$ by setting

$$f^*_{(a,b)}(p) := \min\{a, 1-a\} \cdot f_{(a,b)}(p).$$

The persistence diagram $\mathrm{Dgm}_k(f^*_{(a,b)})$ can be obtained by multiplying the persistence diagram $\mathrm{Dgm}_k(f_{(a,b)})$ by the value $\min\{a, 1-a\}$.

Stability of $\mathscr{D}_{\mathrm{match}}$

We can define a 2D matching distance $\mathscr{D}_{\mathrm{match}}(\boldsymbol{f}, \boldsymbol{f}')$ by setting
$\mathscr{D}_{\mathrm{match}}(\boldsymbol{f}, \boldsymbol{f}') := \sup_{(a,b)\in]0,1[\times\mathbb{R}} d_{\mathrm{match}}\left(\mathrm{Dgm}_k(f^*_{(a,b)}), \mathrm{Dgm}_k(f'^*_{(a,b)})\right)$.

Theorem (Stability Theorem for the matching distance)

$\mathscr{D}_{\mathrm{match}}(\boldsymbol{f}, \boldsymbol{f}') \le \|\boldsymbol{f} - \boldsymbol{f}'\|_\infty$.

The distance $\mathscr{D}_{\mathrm{match}}$ has been introduced in the paper

S. Biasotti, A. Cerri, P. Frosini, D. Giorgi, C. Landi. *Multidimensional size functions for shape comparison*. **Journal of Mathematical Imaging and Vision**, 32(2), 161-179 (2008).

Some key remarks

- We have seen that biparameter persistence can be compared by a method that is based on these operators $F_{a,b}$:

$$F_{a,b}(f_1, f_2) := \mathrm{Dgm}_k \left(\min\{a, 1-a\} \max\left\{ \frac{f_1(p)-b}{a}, \frac{f_2(p)+b}{1-a} \right\} \right).$$

- The operators $F_{a,b}$ are invariant under reparametrization: if $h : X \to X$ is a homeomorphism, then

$$F_{a,b}(f_1, f_2) = F_{a,b}(f_1 \circ h, f_2 \circ h).$$

- The operators $F_{a,b}$ are non-expansive:

$$d_{\mathrm{match}} \left(F_{a,b}(f_1, f_2), F_{a,b}({f'}_1, {f'}_2) \right) \leq \|(f_1, f_2) - ({f'}_1, {f'}_2)\|_\infty.$$

Operators of this kind fall under the definition of group equivariant non-expansive operators (GENEOs).

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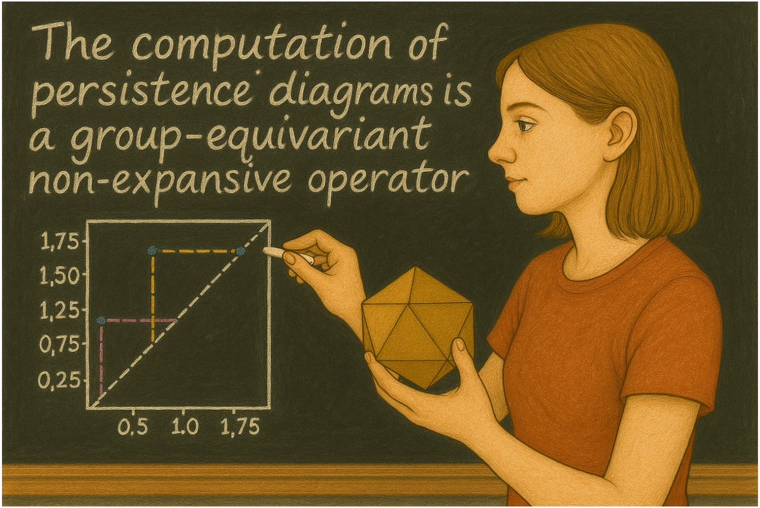
Idea n.4


The computation of persistence diagrams is a group-equivariant non-expansive operator
1,75
1,50
1,25
0,75
0,25
0,5
1.0
1,75

What is a GENEO?

- A Group Equivariant Non-Expansive Operator (GENEO) is a mathematical tool used to approximate observers that act on data.
- The theory of GENEOs is based on the idea that the geometric characteristics of observers significantly influence the interpretation of data.
- In the next slides, we'll take a quick look at the core properties of GENEOs, their role in machine learning, and how they can be applied to explainable artificial intelligence.

Let us begin by recalling the concept of a group action

A *group* $\mathbf{G} = (G, \circ, \mathrm{id}_G)$ consists of a set G, an associative operation $\circ\colon G \times G \to G$ having a unit element $\mathrm{id}_G \in G$ such that, for all $g \in G$, there exists $g^{-1} \in G$ satisfying $g \circ g^{-1} = g^{-1} \circ g = \mathrm{id}_G$.

A *group homomorphism* $T\colon (G, \circ_G, \mathrm{id}_G) \to (K, \circ_K, \mathrm{id}_K)$ is a function $T\colon G \to K$ such that, for all $g_1, g_2 \in G$,
$T(g_2 \circ_G g_1) = T(g_2) \circ_K T(g_1)$.

Given a group $(G, \circ, \mathrm{id}_G)$ and a set X, a *group left action* is a function $*\colon G \times X \to X$ such that, for all $x \in X$ and $g_1, g_2 \in G$,

$$\mathrm{id}_G * x = x \qquad \text{and} \qquad (g_2 \circ g_1) * x = g_2 * (g_1 * x).$$

An example of a group action

Let R be the group of rigid motions (isometries) of the Euclidean plane $\mathbb{R}^2$. The group operation is composition $\circ$:

- Composition is associative: $f_3 \circ (f_2 \circ f_1) = (f_3 \circ f_2) \circ f_1$.
- The *identity* rigid motion id is the unit: $\mathrm{id} \circ f = f \circ \mathrm{id} = f$.
- Every $f \in R$ has an inverse $f^{-1} \in R$ with $f \circ f^{-1} = f^{-1} \circ f = \mathrm{id}$.

The group R acts on $\mathbb{R}^2$ on the left by evaluation:

$$f * P := f(P), \qquad f \in R,\ P \in \mathbb{R}^2.$$

This is a well-defined left action since

$$\mathrm{id} * P = P \quad \text{and} \quad (f_2 \circ f_1) * P = (f_2 \circ f_1)(P) = f_2\big(f_1(P)\big) = f_2 * (f_1 * P).$$

Perception spaces

Recall that a pseudo-metric is a distance function d satisfying nonnegativity, symmetry, and the triangle inequality, but not necessarily the property $d(x_1,x_2)=0 \implies x_1=x_2$.

Definition

Let us consider:

1. A nonempty set Φ endowed with a pseudo-metric D_Φ.
2. A group $(G,\circ)$ acting on Φ on the left, denoted by $*$. We assume the action is by isometries, i.e., for every $\varphi_1,\varphi_2\in\Phi$ and every $g\in G$, $D_\Phi(g*\varphi_1,g*\varphi_2)=D_\Phi(\varphi_1,\varphi_2)$.

We call (Φ, G) an (extended) perception space.

Moreover, the action induces a pseudo-metric D_G on G defined by

$$D_G(g_1,g_2):=\sup_{\varphi\in\Phi} D_\Phi(g_1*\varphi,\, g_2*\varphi), \qquad g_1,g_2\in G.$$

Perception spaces

The set $\varPhi$ represents the data we may obtain from our measuring tools (functions, graphs, point clouds, ...). The group G represents the possible transformations of the data that the observer may be interested in.

For example, $\varPhi$ can be a set of grey-level images represented as functions from $\mathbb{R}^2$ to $[0,1]$, while G can be the group of isometries of the real plane.

A more interesting example arises when the data consist of neural networks, viewed as functions. In this case, the group G acts on each neural network F by composition:

$$F \overset{g}{\mapsto} F \circ g.$$

GEOs and GENEOs

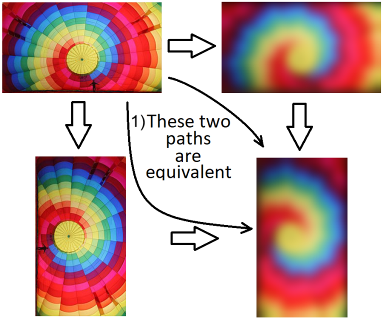
Definition

- Let (Φ, G), (Ψ, K) be two perception spaces. If a map $F : \Phi \to \Psi$ and a group homomorphism $T : G \to K$ are given, such that $F(g * \varphi) = T(g) * F(\varphi)$ for every $\varphi \in \Phi$, $g \in G$, we say that (F, T) is an (extended) *group equivariant operator* (GEO).
- If (F, T) is non-expansive (i.e., $D_\Psi(F(\varphi_1), F(\varphi_2)) \leq D_\Phi(\varphi_1, \varphi_2)$ for every $\varphi_1, \varphi_2 \in \Phi$ and $D_K(T(g_1), T(g_2)) \leq D_G(g_1, g_2)$ for every $g_1, g_2 \in G$), we say that (F, T) is an (extended) *group equivariant non-expansive operator* (GENEO).

An example of GENEO

When we blur an image by applying a **convolution** with a rotationally symmetric kernel whose mass is less than 1 in L^1, we apply a GENEO:

- $T : \mathrm{Isom}(\mathbb{R}^2) \to \mathrm{Isom}(\mathbb{R}^2)$ is the identity homomorphism;
- $(F, T) : \left(C_c\left(\mathbb{R}^2, [0,1]^3\right), \mathrm{Isom}(\mathbb{R}^2)\right) \to \left(C_c\left(\mathbb{R}^2, [0,1]^3\right), \mathrm{Isom}(\mathbb{R}^2)\right)$ is a GENEO.



1)These two paths are equivalent

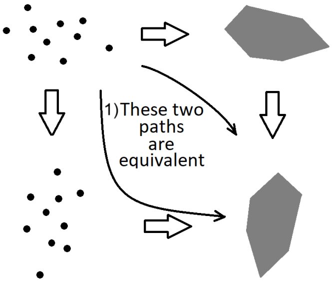
Here, the max-norm distance between functions is used.

2) Blurring does not increase the distance between the images.

Another example of GENEO

When we compute the **convex hull** of a cloud of points, we apply a GENEO:

- $\mathscr{F}$ = the collection of all finite nonempty subsets of the real plane;
- $\mathscr{C}$ = the collection of all convex nonempty subsets of the real plane;
- $T : \mathrm{Isom}(\mathbb{R}^2) \to \mathrm{Isom}(\mathbb{R}^2)$ is the identity homomorphism;
- $(F, T) : (\mathscr{F}, \mathrm{Isom}(\mathbb{R}^2)) \to (\mathscr{C}, \mathrm{Isom}(\mathbb{R}^2))$ is a GENEO.



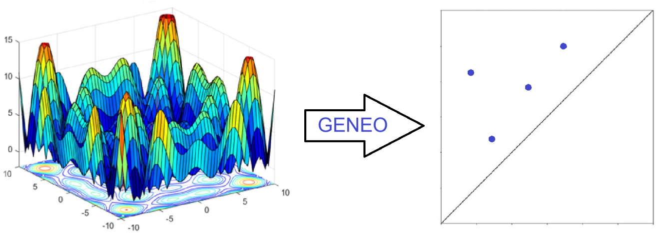
Here, the Hausdorff distance between compact sets is used.

2) The operation of taking the convex hull does not increase the Hausdorff distance between sets.

Another example

The operator taking each filtering function $f : X \to \mathbb{R}$ to its persistence diagram is another example of GENEO:

- DGM is the metric space of all persistence diagrams of real-valued continuous functions defined on a topological space X;
- $\{\mathrm{id}\}$ is the trivial group acting on DGM, consisting only of the identity map;
- T is the trivial homomorphism from $\mathrm{Homeo}(X)$ to $\{\mathrm{id}\}$;
- $(F, T) : (C_c(X, \mathbb{R}), \mathrm{Homeo}(X)) \to (DGM, \{\mathrm{id}\})$ is a GENEO.

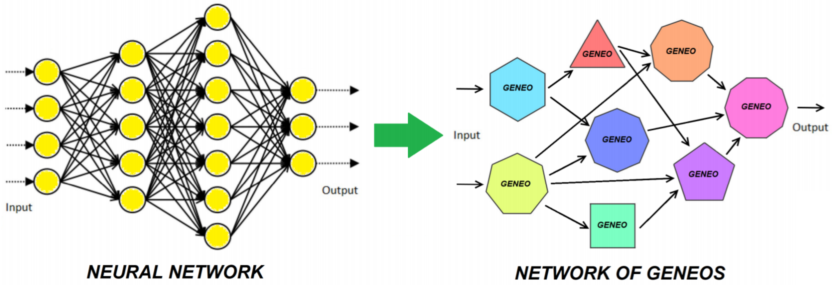


Why are GENEOs interesting?

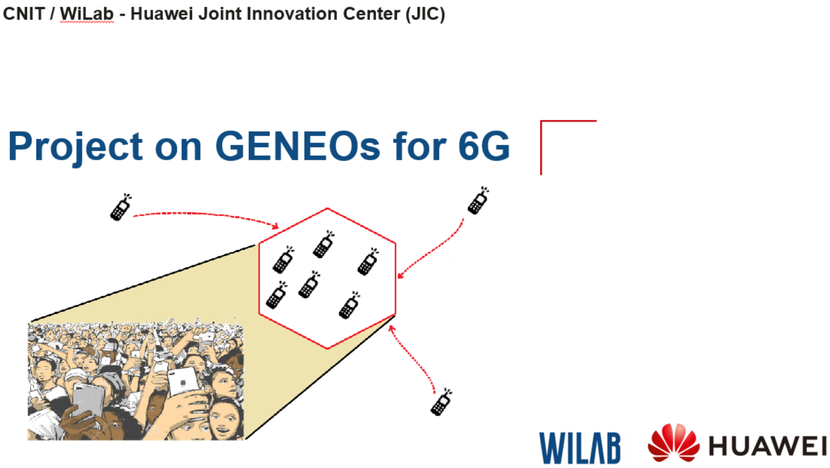
- GENEOs rest on a **rigorous topological/geometric framework** (in what follows we outline several results).
- GENEOs encode **prior knowledge about the chosen observer**.
- The non-expansiveness property of GENEOs imposes a strong constraint that enables meaningful **data simplification**.
- GENEOs enable a **compositional approach to deep learning**.
- Analyzing the **geometry of the observer space** (as represented by GENEOs) is often more informative than analyzing the geometry of the data space.

The main point in the approach based on GENEOs

In perspective, we are looking for a good compositional theory for building efficient and transparent networks of GENEOs.
Some preliminary experiments suggest that replacing neurons with GENEOs could make some applications in deep learning more transparent and interpretable and speed up the learning process.



Some research projects concerning GENEOs (I)

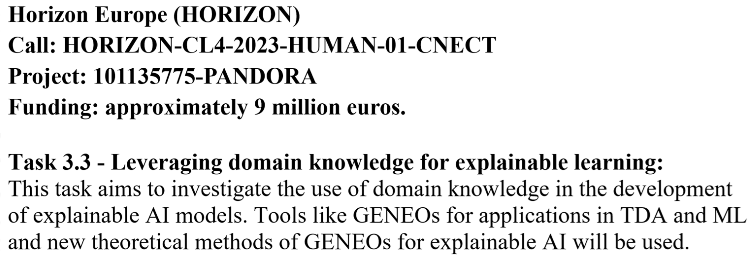


CNIT / WiLab - Huawei Joint Innovation Center (JIC)

Project on GENEOs for 6G

Some research projects concerning GENEOs (II)

PANDORA



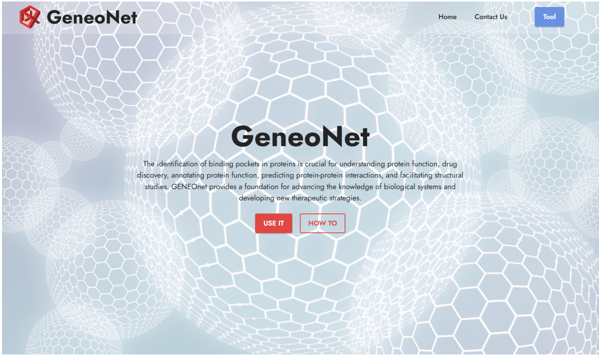
Horizon Europe (HORIZON)
Call: HORIZON-CL4-2023-HUMAN-01-CNECT
Project: 101135775-PANDORA
Funding: approximately 9 million euros.

Task 3.3 - Leveraging domain knowledge for explainable learning: This task aims to investigate the use of domain knowledge in the development of explainable AI models. Tools like GENEOs for applications in TDA and ML and new theoretical methods of GENEOs for explainable AI will be used.

The project has received funding form the
European Union's Horizon Europe
Framework Programme (Horizon) under
grant agreement No 101135775

https://pandora-heu.eu/consortium/

Some research projects concerning GENEOs (III)



The identification of binding pockets in proteins is crucial for understanding protein function, drug discovery, annotating protein function, predicting protein-protein interactions, and facilitating structural studies. GENEOnet provides a foundation for advancing the knowledge of biological systems and developing new therapeutic strategies.

The GENEOnet webservice represents the outcome of a partnership with Italian Pharmaceutical Company Dompé Farmaceutici S.p.A.: `https://geneonet.exscalate.eu/`

Good news for applications

A metric can be naturally defined on the space of GENEOs between two fixed perception pairs (Φ, G) and (Ψ, K), given a fixed homomorphism T between the transformation groups G and K.

The following result holds.

Theorem

- *If the input and output spaces of admissible data are compact, then the space of GENEOs is also* **compact**. *(NOT TRUE FOR GEOS!)*
- *If the output space of admissible data is convex, then the space of GENEOs is also* **convex**.

Good news for applications

As a consequence,

- If the input and output spaces of admissible data can be approximated with arbitrarily small error, then the **space of observers** has the same property.
- If the output space of admissible data is convex, then the **space of observers** is also convex.

The functional case of GENEOs

A particularly important case of GENEO is the one in which the perception spaces involved consist of sets of data expressed as functions with values in $\mathbb{R}$ or $\mathbb{R}^n$.

In the remainder of this talk we shall restrict our attention to the case of data expressed as real-valued functions.

In every perception space (Φ, G) under consideration, Φ will be a set of $\mathbb{R}$-valued functions defined on a domain X (denoted by $\mathrm{Dom}(\Phi)$) and endowed with the metric $D_\Phi(\varphi, \varphi') = \|\varphi - \varphi'\|_\infty$).

The group G will be a group of permutations of X such that, if $\varphi \in \Phi$ and $g \in G$, then $\varphi \circ g^{-1} \in \Phi$ as well, and the left action of G on Φ will be given by $g * \varphi = \varphi \circ g^{-1}$.

Representation Theorem for linear GENEOs

Let X be a finite set and G a group of permutations of X.
A **permutant measure** is a measure on the set $\mathscr{P}$ of all permutations of X that is invariant under the conjugation action of G on $\mathscr{P}$.
The following theorem illustrates the significance of the notion of a permutant measure.

Theorem (Representation Theorem for linear GENEOs)

Let us assume that the group G transitively acts on the finite set X and that F is a map from $\mathbb{R}^X$ to $\mathbb{R}^X$. The map F is a linear GENEO from $\mathbb{R}^X$ to $\mathbb{R}^X$ with respect to the identical homomorphism $\mathrm{id}_G : g \mapsto g$ **if and only if** *a permutant measure μ with respect to G exists, such that $F(\varphi) = \sum_{h \in \mathrm{Bij}(X)} \varphi h^{-1} \mu(h)$ for every $\varphi \in \mathbb{R}^X$, and $\sum_{h \in \mathrm{Bij}(X)} |\mu(h)| \leq 1$.*

Some references about GENEOs (I)

- P. Frosini, G. Jabłoński, *Combining persistent homology and invariance groups for shape comparison*, **Discrete & Computational Geometry**, 55(2), 373-409 (2016).
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- G. Bocchi, S. Botteghi, M. Brasini, P. Frosini and N. Quercioli, *On the finite representation of linear group equivariant operators via permutant measures*, **Annals of Mathematics and Artificial Intelligence**, 91(4), 465-487 (2023).
- A. Micheletti, *A new paradigm for artificial intelligence based on group equivariant non-expansive operators*, **European Mathematical Society Magazine**, 128, 4–12 (2023).

Some references about GENEOs (II)

- G. Bocchi, M. Ferri, P. Frosini, *A novel approach to graph distinction through GENEOs and permutants*, **Scientific Reports**, 15, 6259 (2025).
- G. Bocchi, P. Frosini, A. Micheletti et al. *GENEOnet: a breakthrough in protein binding pocket detection using group equivariant non-expansive operators.* **Scientific Reports**, 15, 34597 (2025).
- D. Lavado, A. Micheletti, G. Bocchi, P. Frosini, C. Soares, *SCENE-Net: Geometric induction for interpretable and low-resource 3D pole detection with Group-Equivariant Non-Expansive Operators*, **Computer Vision and Image Understanding**, 262, 104531 (2025).

Size functions

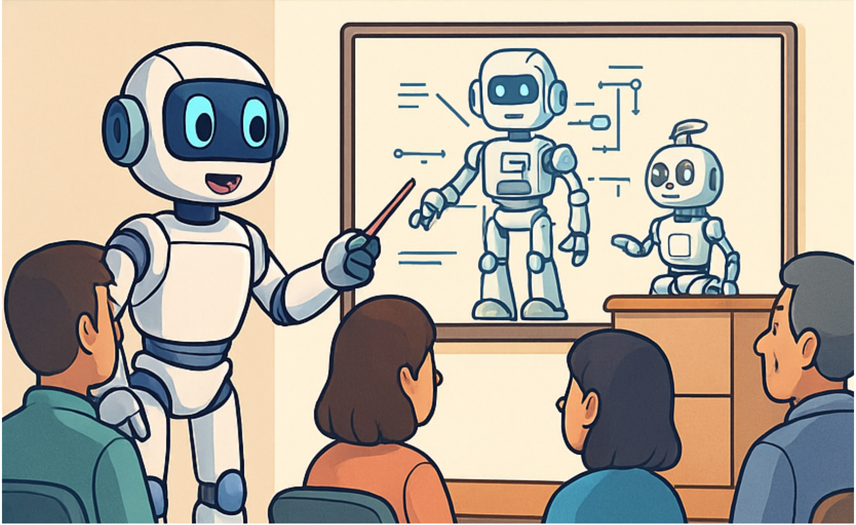
Natural pseudo-distance

Multidimensional data

From Persistent Homology to GENEOs

GENEOs and XAI

GENEOs and XAI



GENEOs and XAI

GENEOs as a mathematical framework to quantify distances between operators with distinct domain–codomain pairs

How close are these two operators?

Basic idea

How can we mathematically and generally formalize the concept of an explanation provided by an agent, viewed as an operator?

Informal idea: We could say that the action of an agent A is explained by another agent B from the perspective of an agent C if:

1. C perceives A and B as similar to each other;
2. C perceives B as less complex than A.

E.g., let's consider two neural networks represented as two GEOs.

Note that a GEO can take another GEO as an input.

Basic idea

How can we transform our informal idea into a precise mathematical model?

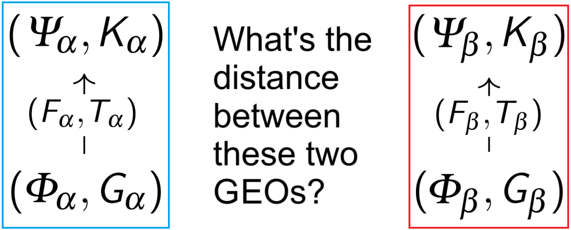
Let us begin by formalizing property 1.

Informal idea: We could say that the action of an agent A is explained by another agent B from the perspective of an agent C if:

1. C perceives A and B as similar to each other;
2. C perceives B as less complex than A.

An extended pseudo-metric for *ALL* GEOs

We have to introduce a pseudo-metric between GEOs that remains well-defined even when the GEOs operate on **different** domains and produce outputs in **distinct** codomains. This is a non-trivial challenge.



$$\begin{tikzcd}(\Psi_\alpha, K_\alpha) \\ (\Phi_\alpha, G_\alpha) \arrow[u, mapsto, "{(F_\alpha, T_\alpha)}"]\end{tikzcd}$$

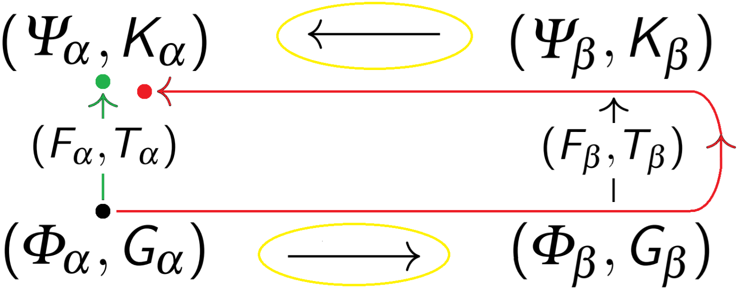
What's the distance between these two GEOs?

$$\begin{tikzcd}(\Psi_\beta, K_\beta) \\ (\Phi_\beta, G_\beta) \arrow[u, mapsto, "{(F_\beta, T_\beta)}"]\end{tikzcd}$$

In other words, what does it mean for two GEOs to behave approximately the same way?

An extended pseudo-metric for *ALL* GEOs

Informally speaking, two GEOs are considered similar if there exist two horizontal GENEOs that make this diagram "nearly commutative", with the same holding true in the opposite direction:



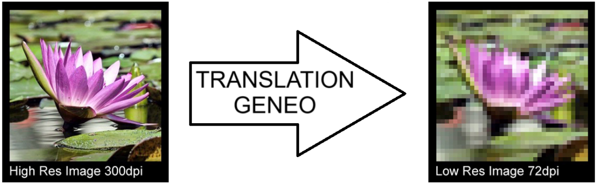
$$\begin{tikzcd}
(\Psi_\alpha, K_\alpha) & (\Psi_\beta, K_\beta) \arrow[l] \\
(\Phi_\alpha, G_\alpha) \arrow[u, mapsto, "{(F_\alpha, T_\alpha)}"] \arrow[r] & (\Phi_\beta, G_\beta) \arrow[u, mapsto, "{(F_\beta, T_\beta)}"']
\end{tikzcd}$$

We can measure the non-commutativity of each diagram by a **cost function**.

An extended pseudo-metric for *ALL* GEOs

To formalize our new pseudo-metric d_E between GEOs, let us consider the category $\mathbf{S}_{all}$ whose objects are all perception spaces, and whose morphisms $(F,T):(\Phi,G)\rightarrow(\Phi',G')$ are GENEOs. The morphisms in $\mathbf{S}_{all}$ are called *translation GENEOs*. These morphisms describe the possible "logical correspondences" between data represented by different perception spaces.

For example, a translation GENEO might transform high-resolution images into low-resolution images.



An extended pseudo-metric for *ALL* GEOs

Let us choose a set $\mathscr{G}$ of GEOs. Therefore,

$$\mathscr{G} = \{(F_\alpha, T_\alpha) : (\Phi_\alpha, G_\alpha) \to (\Psi_\alpha, K_\alpha)\}_{\alpha \in A}.$$

To proceed with the definition of our pseudo-metric on $\mathscr{G}$, we need to specify which logical correspondences between data we consider admissible. To this end, let us consider a small subcategory $\mathbf{S}$ of the category $\mathbf{S}_{all}$. Recall that a category is **small** if it has a set (rather than a proper class) of objects and a set (rather than a proper class) of morphisms.

$\mathscr{G}$ will be the set of GEOs on which we will define our pseudo-metric, while the morphisms in $\mathbf{S}$ will be the translation GENEOs considered admissible.

Definition of the explainability distance

Let

$$(F_\alpha, T_\alpha) : (\Phi_\alpha, G_\alpha) \to (\Psi_\alpha, K_\alpha)$$
$$(F_\beta, T_\beta) : (\Phi_\beta, G_\beta) \to (\Psi_\beta, K_\beta)$$

be two GEOs in the given set of GEOs $\mathscr{G}$.
Let us consider a pair

$$\pi = \Big((L_{\alpha,\beta}, P_{\alpha,\beta}), (M_{\beta,\alpha}, Q_{\beta,\alpha})\Big)$$

of morphisms in **S**, with

- $(L_{\alpha,\beta}, P_{\alpha,\beta})$ a morphism from (Φ_α, G_α) to (Φ_β, G_β),
- $(M_{\beta,\alpha}, Q_{\beta,\alpha})$ a morphism from (Ψ_β, K_β) to (Ψ_α, K_α),

Note that the two GENEOs have opposite directions. We say that π is a crossed pair of translation GENEOs from (F_α, T_α) to (F_β, T_β).

Definition of the explainability distance

$$\begin{tikzcd}
(\Psi_\alpha, K_\alpha) & & (\Psi_\beta, K_\beta) \arrow[ll, "{(M_{\beta,\alpha}, Q_{\beta,\alpha})}"'] \\
 & \pi & \\
(\Phi_\alpha, G_\alpha) \arrow[uu, "{(F_\alpha, T_\alpha)}"] \arrow[rr, "{(L_{\alpha,\beta}, P_{\alpha,\beta})}"] & & (\Phi_\beta, G_\beta) \arrow[uu, "{(F_\beta, T_\beta)}"']
\end{tikzcd}$$

Figure: A crossed pair of translation GENEOs.

Definition of the explainability distance

To proceed, we need to equip each metric space Φ_α with a Borel probability measure μ_α. In simple terms, the measure μ_α represents the probability of the data points in Φ_α appearing in our experiments.

We will assume that all GENEOs in **S** are not just distance-decreasing (i.e., non-expansive) but also measure-decreasing, i.e., if $(L_{\alpha,\beta}, P_{\alpha,\beta}) : (\Phi_\alpha, G_\alpha) \to (\Phi_\beta, G_\beta)$ belongs to **S** and the set $A \subseteq \Phi_\alpha$ is measurable for μ_α, then $L_{\alpha,\beta}(A)$ is measurable for μ_β, and $\mu_\beta(L_{\alpha,\beta}(A)) \leq \mu_\alpha(A)$.

Definition of the explainability distance

We also assume that the function that takes each $\varphi \in \Phi_\alpha$ to $f_{\alpha,\beta}(\varphi) := D_\Psi\Big((M_{\beta,\alpha} \circ F_\beta \circ L_{\alpha,\beta})(\varphi), F_\alpha(\varphi)\Big)$ is integrable with respect to the probability measure μ_α defined on the dataset Φ_α. The functional cost of π is defined by setting

$$\mathrm{cost}(\pi) := \int_{\Phi_\alpha} D_\Psi\Big((M_{\beta,\alpha} \circ F_\beta \circ L_{\alpha,\beta})(\varphi), F_\alpha(\varphi)\Big)\ d\mu_\alpha.$$

The value $\mathrm{cost}(\pi)$ quantifies how far the two paths in the next figure are from being equivalent, on average, when φ is randomly selected in Φ_α according to the probability measure μ_α.

A similar cost can also be defined for the group component.

Definition of the explainability distance

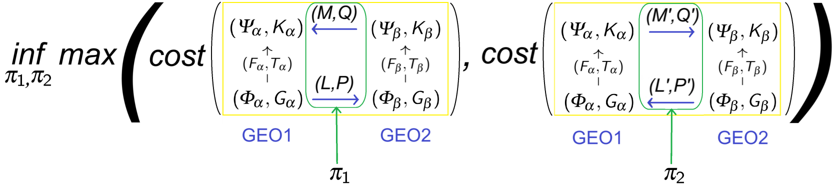
$$\begin{tikzcd}
(\Psi_\alpha, K_\alpha) & & (\Psi_\beta, K_\beta) \arrow[ll] \\
(F_\alpha, T_\alpha) \arrow[u, green] & & (F_\beta, T_\beta) \arrow[u] \\
(\Phi_\alpha, G_\alpha) \arrow[u, green] \arrow[rr] \arrow[rr, red, bend right] & & (\Phi_\beta, G_\beta) \arrow[u] \arrow[uu, red, bend right] \arrow[uull, red, bend right]
\end{tikzcd}$$

Figure: The explainability distance we are going to define measures how far the green path and the red path are from being equivalent, on average.

Definition of the explainability distance

We can formalize the new pseudo-metric d_E on $\mathscr{G}$ by defining $d_E(GEO1, GEO2)$ as the infimum of the maximum between the cost of π_1 and the cost of π_2, over all crossed pairs π_1 of admissible translation GENEOs from GEO1 to GEO2 and all crossed pairs π_2 of admissible translation GENEOs from GEO2 to GEO1.

Formally, $d_E(GEO1, GEO2)$ is equal to



$$\inf_{\pi_1,\pi_2} \max\left(cost\left(\begin{tikzcd} (\Psi_\alpha, K_\alpha) & (\Psi_\beta, K_\beta) \arrow[l, "(M{,}Q)"'] \\ (F_\alpha, T_\alpha) \arrow[u] & (F_\beta, T_\beta) \arrow[u] \\ (\Phi_\alpha, G_\alpha) \arrow[u, dash] \arrow[r, "(L{,}P)"] & (\Phi_\beta, G_\beta) \arrow[u, dash] \end{tikzcd}\right), cost\left(\begin{tikzcd} (\Psi_\alpha, K_\alpha) \arrow[r, "(M'{,}Q')"] & (\Psi_\beta, K_\beta) \\ (F_\alpha, T_\alpha) \arrow[u] & (F_\beta, T_\beta) \arrow[u] \\ (\Phi_\alpha, G_\alpha) \arrow[u, dash] & (\Phi_\beta, G_\beta) \arrow[u, dash] \arrow[l, "(L'{,}P')"'] \end{tikzcd}\right)\right)$$

Definition of the explainability distance

Proposition

d_E is an extended pseudo-distance.

The non-expansiveness of GENEOs is a key component in the definition of d_E.

In simple terms, the value $d_E((F_\alpha, T_\alpha),(F_\beta, T_\beta))$ measures the *cost* of changing (F_α, T_α) into (F_β, T_β).

When $d_E((F_\alpha, T_\alpha),(F_\beta, T_\beta))$ is small, it indicates that the GEOs (F_α, T_α) and (F_β, T_β) act approximately in the same way on the data they process, on average.

Back to the basic idea of explanation

Let us recall our informal idea.

Informal idea: We could say that the action of an agent A is explained by another agent B from the perspective of an agent C if:

1. C perceives A and B as similar to each other; $\boxed{\checkmark}$
2. C perceives B as less complex than A.

The formalization of 1 is completed using the pseudo-metric d_E.
How about the formalization of 2?

Complexity of GEOs

Let us assume a set $\Gamma = \{(F_i, T_i) : (\Phi_i, G_i) \to (\Psi_i, K_i)\}$ of GEOs is given. We will say that Γ is our internal library. For each GEO $(F_i, T_i) \in \Gamma$ we arbitrarily choose a value c_i representing the complexity $\mathrm{comp}((F_i, T_i))$ of (F_i, T_i).

The set Γ represents the elementary GEOs that we can use to build other more complex GEOs.

Let us now consider the closure of Γ, i.e., the minimal set $\bar{\Gamma}$ such that

- $\bar{\Gamma} \supseteq \Gamma$;
- $\bar{\Gamma}$ is closed under composition (i.e., if $(F, T), (F', T') \in \bar{\Gamma}$ are composable, then $(F', T') \circ (F, T) \in \bar{\Gamma}$);
- $\bar{\Gamma}$ is closed under direct product (i.e., if the GEOs $(F, T), (F', T') \in \bar{\Gamma}$, then $(F, T) \otimes (F', T') \in \bar{\Gamma}$).

Complexity of GEOs

Each composition and direct product is associated with a complexity.

The complexity of each GEO $(F, T) \in \bar{\Gamma}$ is obtained by minimizing the sum of the complexities of the GEOs (F_i, T_i) that we use and the complexities of the compositions and direct products that we apply to build (F, T).

Other forms of composition of GEOs can be added to the model.

Back to the basic idea of explanation

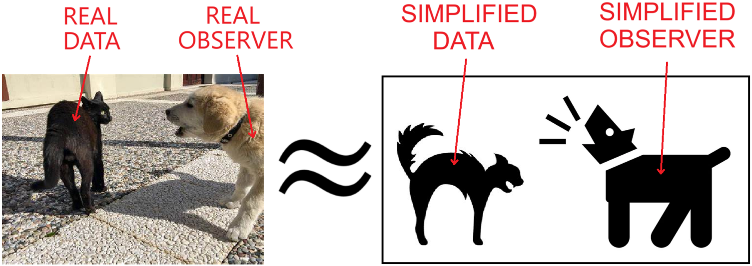
Informal idea: We could say that the action of an agent A is explained by another agent B from the perspective of an agent C if:

1. C perceives A and B as similar to each other; $\boxed{\checkmark}$
2. C perceives B as less complex than A. $\boxed{\checkmark}$

Our theoretical construction is now complete.

A mathematical concept of explanation

Now we can formalize our mathematical concept of **explanation**. Specifically, we can define it as follows: The action of an agent represented by a GEO (F_α, T_α) is explained **at a level ε** by the action of another agent of **complexity less than k** represented by a GEO $(F_\beta, T_\beta) \in \bar{\Gamma}$ when $d_E((F_\alpha, T_\alpha), (F_\beta, T_\beta)) \leq \varepsilon$.

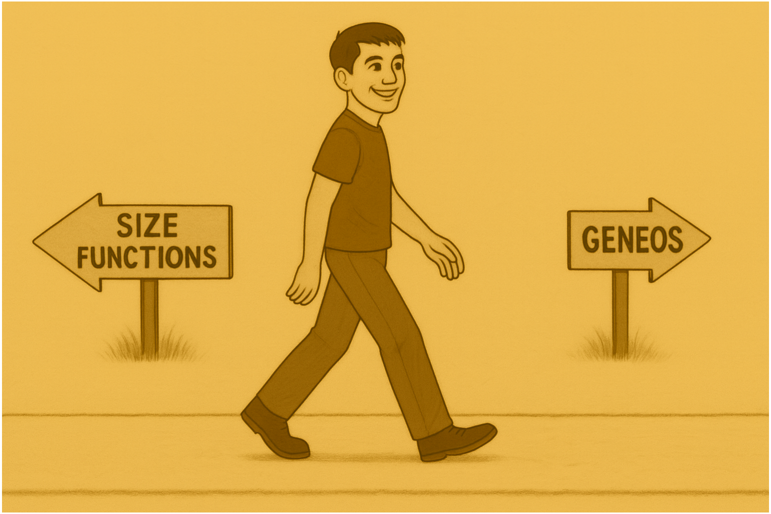


A reference

Further details on the explainability distance can be found in this paper:

J. J. Colombini, F. Bonchi, F. Giannini, F. Giannotti, R. Pellungrini and P. Frosini, *Mathematical Foundation of Interpretable Equivariant Surrogate Models*, In: Guidotti, R., Schmid, U., Longo, L. (eds) Explainable Artificial Intelligence. xAI 2025. **Communications in Computer and Information Science**, Springer, Cham, 2577, 294-318 (2026).

The journey continues...




Thanks for your attention!