WHAT DOES IT MEAN TO BE "THE SAME"? A BIOLOGICAL VARIANT OF THE BORSUK-ULAM THEOREM

Arturo Tozzi
Center for Nonlinear Science, University of North Texas, Denton, Texas 76203, USA
1155 Union Circle, #311427
Denton, TX 76203-5017 USA
tozziarturo@libero.it

James F Peters
Department of Electrical and Computer Engineering, University of Manitoba
75A Chancellor's Circle Winnipeg, MB R3T 5V6 CANADA and
Department of Mathematics, Adıyaman University, 02040 Adıyaman, Turkey
James.Peters3@umanitoba.ca

Raquel del Moral
Grupo de Bioinformación / Bioinformation Group
Instituto Aragonés de Ciencias de la Salud (IACS)
Instituto de Investigación Sanitaria Aragón (IIS)

Pedro C. Marijuán
Grupo de Bioinformación / Bioinformation Group
Instituto Aragonés de Ciencias de la Salud (IACS)
Instituto de Investigación Sanitaria Aragón (IIS)
Edificio CIBA. Avda. San Juan Bosco, 13, 50009 Zaragoza, Spain
pcmarijuan.iacs@aragon.es

ABSTRACT

A unifying principle underlies the organization of physical and biological systems. It relates to a well-known topological theorem which succinctly states that an activity on a planar circumference projects to two activities with "matching description" into a sphere. Here we ask: What does "matching description" mean? Has it something to do with "identity"? Going through different formulations of the principle of identity, we describe diverse possible meanings of the term "matching description". We demonstrate that the concepts of "sameness", "equality", "belonging together" stand for intertwined levels with mutual interactions. By showing that "matching" description is a very general and malleable concept, we provide a novel testable approach to "identity" that yields helpful insights into physical and biological matters. Indeed, we illustrate how a novel mathematical approach derived from the Borsuk-Ulam theorem, termed bio-BUT, might explain the astonishing biological "multiplicity from identity" of evolving living beings as well as the logic of their intricate biochemical arrangements.

KEYWORDS: systems dynamics; topology; Borsuk-Ulam theorem; computation.

1. INTRODUCTION: SAMENESS AND MATCHING DESCRIPTIONS

The concept of "sameness" is the tenet of approximate reasoning, treatment of imprecision, assessment of physical systems and biological classification. Indeed, techniques such as pairwise comparison (Kolkodzaj et al., 2017), rough sets and Fraenkel-Zermelo group theory are based on the concept of "equality' among different features. In particular, recently introduced versions of the Borsuk-Ulam theorem (BUT) state that a feature on a n-manifold projects to two points with "matching description" onto a $n+1$ manifold (Peters, 2016; Tozzi and Peters, 2016a). Starting from this rather simple, abstract claim, a fruitful general framework has been built which is able to elucidate disparate real physical and biological phenomena, from quantum entanglement (Peters and Tozzi, 2016) to brain activity (Tozzi et al. 2017a), from biological gauge theories (Tozzi et al., 2017b) to pre- big bang scenarios (Tozzi and Peters, 2016b).

Summarizing the novel topological approach, we may observe that, by taking into account projections on functional or real dimensions of physical and biological systems onto corresponding feature spaces, a system of mappings is achieved with "matching description" that fits very well with experimental results, allowing to assess countless issues in far-flung scientific branches spaces (Angel and Leong, 1994; Benson et al., 2016; Giusti et al., 2016; Kida et al., 2016; Kleineberg et al, 2016; Simas et al., 2015). Nevertheless, what does "matching description" mean in a topological context?

Matching descriptions are termed "descriptively near sets", i.e., two (or more) features that lie on the same manifold, but that have no points in common. In a semantic framework, a matching description encompasses all information about two nodes in two structures which semantically correspond to one another. In what follows, we will describe other possible meanings of matching description in different scientific contexts, providing testable examples, and we will subsequently introduce a novel version of Borsuk-Ulam theorem (BUT), dubbed bio-BUT, that takes into account the relatedness and overwhelming evolutionary complexification of living beings. Within the bio-BUT framework, we will use the concept of "matching description" in comparing mathematical, physical, and biological features of signals such as amplitude, duration and intensity.

2. THE PROBLEM OF CONNECTION AND UNITY

Some fundamental questions

Here we may ask, paraphrasing the seminal paper by Nagel (1974), what is it like to be a matching description? In order to tackle this issue, here we need to ask before: has matching description anything to do with "identity"? In the "classical" BUT, the matching features are just points, therefore a point is equal to another and we might easily state that the two points are "identical" (Borsuk, 1933). On the other hand, in the novel BUT variants, the matching features stand not just for simple topological points, but also for more intricate features, such as shapes of space (spatial patterns), shapes of time (temporal patterns), vectors, tensors, functions, signals, thermodynamic parameters, movements, trajectories, lexical structures (either syntactic or semantic), or most generally, symmetries and symmetry breaks (Peters et al., 2017; Matousek 2003).

Thereafter, we may ask: Apart from the two adimensional points of the classical BUT, are other types of matching features identical? When you compare a pair of "equal" features, how do you state that they are equal? Do they have the same feature, or two different features with something in common? In order to solve the issue, we analyze the "principle of identity" (Heidegger, 1957), which is one of the three tenets of classical logic.

First answer: sameness

The principle of identity states that A=A. The formula expresses, in its usual description, an equality of A and A. One A is equal to another A. Therefore, we can state that A is the same as A, because "identical" (from Greek and Latin) means: "**the same**". We will see how "matching description" standing for "sameness" can be found not just in the rather abstract disciplines of philosophy, logic and mathematics, but also in the "objective" accounts of physics and biology, and in the "subjective" realm of single individual's mental activity.

Second answer: equality

In another version, the formula A=A speaks of "equality". A is A. It does not say that A is the same, but that **every A is itself the same**. Or, in other words, each thing itself is the same for itself and with itself.

Third answer: belonging together

It can also be stated that matching description "belongs to" an identity. In this case, sameness stands for a "**belonging together**". In "belonging together", the world "together" means to be assigned and placed into the order of a together, to be established in the unity of a manifold, **to be combined into the unity of a system**. Such assignment and placing occur thanks to connections and mappings of the one with the other. Belonging together means that two features are put orderly into a common feature that is outlined against the background.

This means that two interpretations are feasible: a) matching description is determined by an identity as a feature of that

identity; b) identity is represented as a feature of matching description.

To make an example, night and day belong together: if you say just "day", you do not yet acquire knowledge, if you not think the day as lasting until the night's onset. The night is night just because it stands for the day fading. Therefore, night and day are not just two interchangeable features; rather they have to be taken together. Two contrasting features such as night and day stand out in sharp relief just because they are two and meet one with each other.

Fourth answer: coincidentia oppositorum

Another possible interpretation for A=A might be extrapolated from Nicholas de Cusa (1440) and Giordano Bruno (1582): the so-called *coincidentia oppositorum*. As usual, the sign = can be understood either in terms of sameness, or equality, or belonging together. However, the two As stand for opposite, sometimes incompatible, apparently mutually excluding features or activities. In this case, we start from A different from B, where B= non A, or B= -A. At the end of the comparison, despite A is different from B, we achieve A=B, and therefore, just in terms of features A:

$$A = \text{non } A, \text{ or } +A = -A$$

The As stand either for mathematical, or physical, or biological features. The principle of *coincidentia oppositorum* is in touch with the counter-intuitive lack of the principle of identity in quantum dynamics and superimposition of wave/particles. This formulation is particularly useful in quantum dynamics, where experimental findings have "wrecked" the classical formulations of the principle of identity. To make an example, think about the Schrodinger cat. He can be alive or dead in the same instant, so that $A = -A$.

3. WHAT DOES MATCHING DESCRIPTION MEAN IN BUT TERMS?

Here we draw some conclusion about the BUT counterparts of the above given definitions of the principle of equality. A BUT system, i.e., a system equipped with two manifolds in lower and higher dimensions and with reciprocal mappings, can be defined as follows (see **Figure**):

1) A single feature in lower dimensions specifies equality.
2) Two corresponding matching features in higher dimensions describe the same, the purely identical signal.
3) A BUT-oriented system describes signal values that belong together, that are copies of each other. In belonging together, the opposites do not disappear, rather they reach unity, although still existing separately but joined by a force, by something that binds them together. In the BUT case, such force stands for the mappings between manifold of different dimensions. The whole BUT system may also describe the *coincidentia oppositorum.*

Lower dimensions

The equal is the single feature that stands alone in lower dimensions. In lower dimensions, we are assessing a single, undifferentiated, homogeneous feature; therefore we cannot catch the differences between two activities, the latter being distinguishable just in higher dimensions. Indeed, the equal is correlated with the indistinguishable unity, because it encompasses the whole description of the feature, leaving apart the possible differences endowed in the higher-dimensional systems' features. To make an example, by the standpoint of an observer located in the feature A and with an observational horizon limited to A, the BUT account in lower dimensions stands for the unity, for the complete available description of the feature.

Higher dimensions

In turn, higher dimensions describe the standpoint of the separation. In higher dimensions, the differences between features become evident, as they can be separately assessed. Two features are the same just in case of the difference, the not-undifferentiated, the absence of singularity is thought. From the separation, the duality emerges. The same is never identified with the equal: the same expunges the risk to smooth the different in the always equal. The same may also stand for the reciprocal belonging together of different features, based on the assembly operated by the differences imposed by an observer. While he same joins the different in a primitive union, the equal scatters into the unity of what is one just for uniformity. In solving the different, the joining core of the same comes into light. In higher-dimensional levels, the same reaches the multiplicity of the almost incompatible. The BUT higher-dimensional account stands for

the indeterminate and the unknown. Indeed, an observer located in one A cannot have knowledge of the antipodal A, placed at the opposite side of the high-dimensional manifold, and disjointed from the A where the observer stands. Therefore, our secluded observer in higher dimensions is able to catch neither the whole system, nor the possible existence of an identity, of a sameness, of a belonging together, of a matching description. The observer cannot encompass the whole system in a single sight. Incidentally, this might explain, for example, why we detect in our Universe the matter, but not the antimatter, and why we perceive a baryon asymmetry (a *baryon* is a composite subatomic particle that consists of three quarks). BUT might also explain why we detect, by our standpoint inside the Universe, the arrow of time, e.g., time asymmetry.
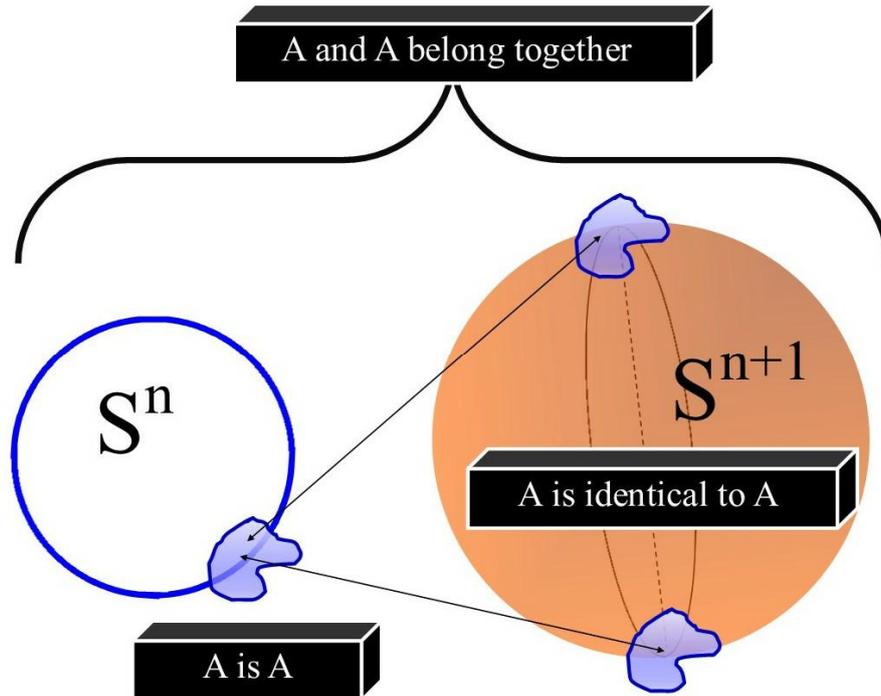

Figure 1. Topology and the principle of identity. The figure illustrates the Borsuk-Ulam theorem's counterparts of sameness, identity, belonging together (i.e., the first three answers to our main question). The shapes stand for the feature termed A.

4. A NOVEL BUT VARIANT IN MACROSCOPIC PHYSICS AND IN BIOLOGY

As stated above, our previous framework, developed through different papers in various scientific disciplines, suggests that BUT and its variant might explain relevant biological phenomena. To make an example, based on novel topological considerations, Tozzi et al. (2017b) have proposed a gauge symmetry for living cells. The reference system is the living cell, equipped with general symmetries standing for the intertwined biochemical, metabolic and signaling pathways that allow its global homeostasis. Environmental stimuli stand for "forces" able to locally break the symmetry of metabolic/signaling pathways, while the species-specific DNA is the gauge field that restores the global homeostasis after external perturbations. The authors applied BUT in order to operationalize a methodology in terms of topology/gauge fields and subsequently inquire about the evolution from inorganic to organic structures, proposing that, from prokaryotes to eukaryotes, an increase in complexity (standing in topological terms for an increase of dimensions on an abstract manifold) gives rise to a progressive increase of matching features (Chaisson 2010).

During evolution, life gives rise to a formidable increase in complexity. The latter is an increase of dimensions in a manifold where the nth dimension stands for the level of complexity. To make a few examples, living beings have descriptively proximal appearance, their inorganic constituents have single description; seeds (as fibres) have single

descriptions, fruits (projections from sets of fibres) have similar descriptions (for mathematical details, see **next section**). Such increase elucidates the countless biochemical functions of the more advanced living beings, such as mammals and primates. However, if an increase of matching description is correlated with an increase in dimensions (in the living cells' case, an increase in complexity), we would achieve a countless number of identical antipodal features, termed A, that are equal. Therefore, advanced cells might be equipped with a countless number of serial, monotonous, repeating features, which number increases with complexity, and the astonishing diversity of living beings would be lost (contrary to what happens in the real world).

Indeed, in terms of the principle of identity, our high complex macroscopic world is made of equal, but of different objects, achieved through the joining together of different microscopic particles endowed in lower levels of complexity. In particular, separation is a factor, achieved through oppositions against the undifferentiated, REQUIRED for life taking place. Two opposites prevail over the power of the singularity, because the order of life overtakes the primeval unity. The exit from the singularity gives rise to splits and to disjointed opposites, e.g., the huge variety evolving living beings. With increase in complexity (and therefore in dimensions) in living cells, the fixed points disappear, while differences and oppositions are produced in their full vitality.

We propose another version of BUT, the bio-BUT: a single feature in n-dimensions, say A, projects to two matching points in n+1 -dimensions (for mathematical details, see **Section 6**). The difference from the classical BUT is that, instead of achieving the two typical matching descriptions termed A and its opposite A, we achieve the two matching descriptions termed A and ΔA. In every subsequent mapping in higher dimensions, the diversity among the matching features increases, allowing a high rate of evolutionary variety. The identity (in the sense of equality or sameness) among matching features A gradually disappears, giving rise to more and more various living entities: in other words, the mapping from lower to higher dimensions gives rise to two features that are slightly different and belong together, instead of being the equal or the same. Therefore, life can be explained just by taking into account the total BUT system, and not just one of its manifolds.

5. BIOLOGY AND TOPOLOGY: AN INTIMATE INTERRELATIONSHIP

Every physical and biological structure has a history. Based on their features, every structure has a description. The physical and biological world is a collection of structures with shapes defined by fibre bundles of the form $X \xrightarrow{f} E \xrightarrow{\pi} B,$ where X is a set of particles, f maps X to a set of selected fibers (generators) E in an m-dimensional space, and π is a 1-1, continous, bijective mapping that projects E onto a space B with a well-formed

shape such that $\pi(e) \in \begin{cases} n-\text{dimensional space, n} \geq \text{m, or,} \\ n-\text{dimensional space, n} < \text{m,} \end{cases}$ for $e \in E, \ \pi(e) \in B.$

The collection of particles in X sweep out world canals as they move through space. Hence, the world canals defined by X resemble a multi-layer ham sandwich (layers of world sheets). For example, metabolic pathways are worldsheets, while homeostasis is intertwined worldsheets.

The fibres in E are selected segments (slices) of the sandwich in X. The projection π is a piecewise continuous mapping on E onto B. During evolution, life is a composition of fibre bundle projection mappings with concomitant dimensional changes (changes in complexity). Instead of a causality view of the physical structure, the origin of the species can be defined by projection mappings. Evolutionary systems are defined by sequences of projections of the form

$E \xrightarrow{\pi_1} B_1 \xrightarrow{\pi_2} B_2 \cdots B_i \xrightarrow{\pi_{i+1}} B_{i+1} \cdots \xrightarrow{\pi_k} B_{k+1}$ (evolved shape).

In other words, the fabric of the physical (and biological) world has an underlying fibre bundle structure, apart from thermodynamic and information relationships.

Projections among the structures of different dimensions are piecewise continuous. The projection $E \xrightarrow{\pi} B$ is piecewise continuous inasmuch as, for $A \ \delta \ B, A, B \subset E$ implies $\pi(A) \ \delta^{\wedge\wedge} \ \pi(B),$ i.e., whenever A is close to B in E, then $\pi(A) \in B$ is close to $\pi(B) \in B.$ The closeness of projects results from endowing the sets E and B with a proximity relation with all projections defined in a proximity space $\left(E, B, \delta^{\wedge\wedge}\right),$ where $\delta^{\wedge\wedge}$ is a strong (overlap) Lodato proximity (Peters, 2016). In sum, world structures with changing shapes are defined by a collection of piecewise continuous projections.

6. A BIOLOGICAL VERSION OF THE BORSUK-ULAM THEOREM

Here we propose another development of BUT, termed bio-BUT, that can be useful in the experimental assessment of both macroscopic physical and biological (linear and nonlinear) systems. Summarizing our approach, the Borsuk-Ulam theorem (BUT) from algebraic topology introduces a continuous mapping from an *n*-sphere into itself. A biological counterpart of BUT dubbed bio-BUT introduces a piecewise continuous mapping from signals in space time R^{3+1} into a k-dimensional space R^k, k ≥ 1, containing feature vectors that describe antipodal spacetime signals. In other words, antipodal signals in spacetime signal can have matching descriptions in a 1-dimensional space or matching descriptions in a k-dimensional space $R^{3+1} \rightarrow R^k$, k ≥ 1. Let us briefly clarify the terms we are using in order to establish the bio-BUT.

n-sphere

An *n*-sphere S^n is the set of points in Euclidean space R^{n+1} with unit distance to the origin (0,0,...,0), a point whose coordinates are $n+1$ zeros. An *n*-sphere is an *n*-dimensional manifold (Ghrist, 2014). That is, there is a continuous 1-1 map on the set of points on S^n onto R^n. For example, $S = S^1$ denotes the Euclidean plane R^2, an S^2 denotes the Euclidean 3-space R^3. At the physical level, S^2 is the set of all points with unit distance from (0,0,0). The analogue of S^2 is the set of all points in the system (e.g., the brain), which physically is in the 3-space R^3.

Antipodes

Let *x* be a point on S^n. The antipode of *x* is the point –*x* (Munkres,2000), i.e., the antipode of x is a point opposite *x* on an *n*-sphere. For example, the antipode of a point x on the circumference of a circle is a point –x on that part of the circumference opposite *x*. Again, for instance, a physical analogue of Munkres antipode is the antipode of cone at location x in one eye, is a cone at the same location in the opposite eye. Another physical analogue of a Munkres antipode is an alternative description of a signal x, represented by a feature vector of the form $\Phi\left(\varphi_1(x), \cdots, \varphi_k(x)\right)$ with k components, where each $\varphi_i(x)$ is a feature value that represents an observation about the variable x.

Continuous Mapping

A continuous mapping $f : X \rightarrow Y$ is a correspondence between a point x in X and a point y = f(x) in Y, such that x and x' are close, then f(x) is close to f(x') (Naimpally and Peters, 2013). The physical analogue of a continuous mapping $\Phi: R^3 \rightarrow R^k$ defines a correspondence between a set of signals in R^3 and set of descriptions in R^k. See Table 1 for an example.

Piecewise Continuous Mapping

A piecewise continuous mapping $f : A \rightarrow B$ is a correspondence between a subset A in X and a subset B in Y so that if a and a' are close in A, then, then f(a) and f(a') are close in B. In other words, we only assume that the closeness rule applies to a subset of the set X and a subset in the image space B that is a subset of the larger set Y but does not necessarily apply to the larger sets X and Y. The physical analogue of a piecewise continuous mapping is a mapping $\Phi: R^{3+1} \rightarrow R^k$ that is a correspondence between a set of signals A in R^{3+1} (spacetime) and a set of descriptions B in R^k so that if signals a and a' are close in A, then description $\Phi\left(\varphi_1(a), \cdots, \varphi_k(a)\right)$ and description $\Phi\left(\varphi_1(a'), \cdots, \varphi_k(a')\right), k \geq 1$ are close in B.

Table 1. Analogues of Mathematical Structures Underlying bio-BUT

Structure(s)	Mathematics	Physics
2-sphere S^2	Euclidean space R^3	Biosphere space
Antipodes (left vs. right eye)	$x, -x \in \mathsf{R}^{3+1}$	Cone at x in left eye, cone at –x in right eye.
Antipodes (signal x vs. description of the signal)	$x, -x \in \mathsf{R}^3$	$\Phi\left(\varphi_1(x),\cdots,\varphi_i(x),\cdots,\varphi_k(x)\right)$ is a feature vector Φ with n observations that describes signal x, and $\Phi\left(\varphi_1(-x),\cdots,\varphi_i(-x),\cdots,\varphi_k(-x)\right)$ is a feature vector that describes signal –x, $k \geq 1$.

From the Borsuk-Ulam Theorem

If x is a point in S^n, then its antipode is the point –x. A continuous map $h: S^n \to S^n$ is antipode-preserving, provided h(x) = h(-x) for all $x \in S^n$.

A conjecture

There is a biological analogue of the Borsuk-Ulam Theorem. The following theorem proves this conjecture.

Towards the Bio-Borsuk-Ulam Theorem (bio-BUT)

Given a signal a in R^{3+1}, then its antipode is a signal –a in spacetime. A piecewise continuous map $\Phi: \mathsf{R}^{3+1} \to \mathsf{R}^k$, k ≥ 1 is antipode-preserving in spacetime, provided the antipodes have matching description, *i.e.*, $\Phi\left(\varphi_1(a),\cdots,\varphi_k(a)\right) = \Phi\left(\varphi_1(-a),\cdots,\varphi_k(-a)\right), k \geq 1$ for all signals α, -α $\in \mathsf{R}^{3+1}$.

Proof: Let x be a signal in a set of signals $X \subseteq \mathsf{R}^{3+1}$ and let –x be an antipodal signal in X. Every signal x has a description $\Phi\left(\varphi_1(x),\cdots,\varphi_k(x)\right) \in \mathsf{R}^k, k \geq 1$, where $\varphi_i(x)$ is feature value for x and R^k is a feature space such that every point in R^k defined by the mapping Φ. Each antipodal signal $-x$ occupies the same position as x after translation. Hence, $\Phi\left(\varphi_1(x),\cdots,\varphi_k(x)\right) = \Phi\left(\varphi_1(-x),\cdots,\varphi_k(-x)\right)$ after translation.

In other words, bio-BUT guarantees that the antipodal signals x, -x have matching descriptions in some k-dimensional spacetime, $k \geq 1$. In addition, bio-BUT relaxes the requirement that the domain and the range of the mapping Φ have the same dimension. For example, $\Phi\left(\varphi_1(x)\right)$ is 1-dimensional (i.e., only one perceived feature of signal x is described), whereas signal x itself is 3+1 dimensional in spacetime.

The concept of biological closeness

It looks like bio-BUT occurs in spacetime. Each description would reside on a string on a worldsheet. Descriptions emanate in parallel from systems' features that are also branes. Antipodal signals would "live" on parallel worldsheets of different functional dimensions. It is piecewise continuity in spacetime that gives rise to a perception of the closeness of antipodal signals and their descriptions. Closeness (proximity) of antipodal signals means that one signal A and its antipodal signal A are within some distance of each other (within kissing distance). Then bio-BUT tells us that the descriptions of the As will also be within kissing distance, thanks to the piecewise continuity of mappings in spacetime.

The **Figure 2** provides an example on the evolution of two dynamical systems, according to bio-BUT. How does such decrease in feature homogeneity occur, in topological terms? It might occur through slightly changes in the strength of the projections. They could stand for slight changes in biological general symmetries that give rise to a not complete restoration of the locally broken Lagrangian.
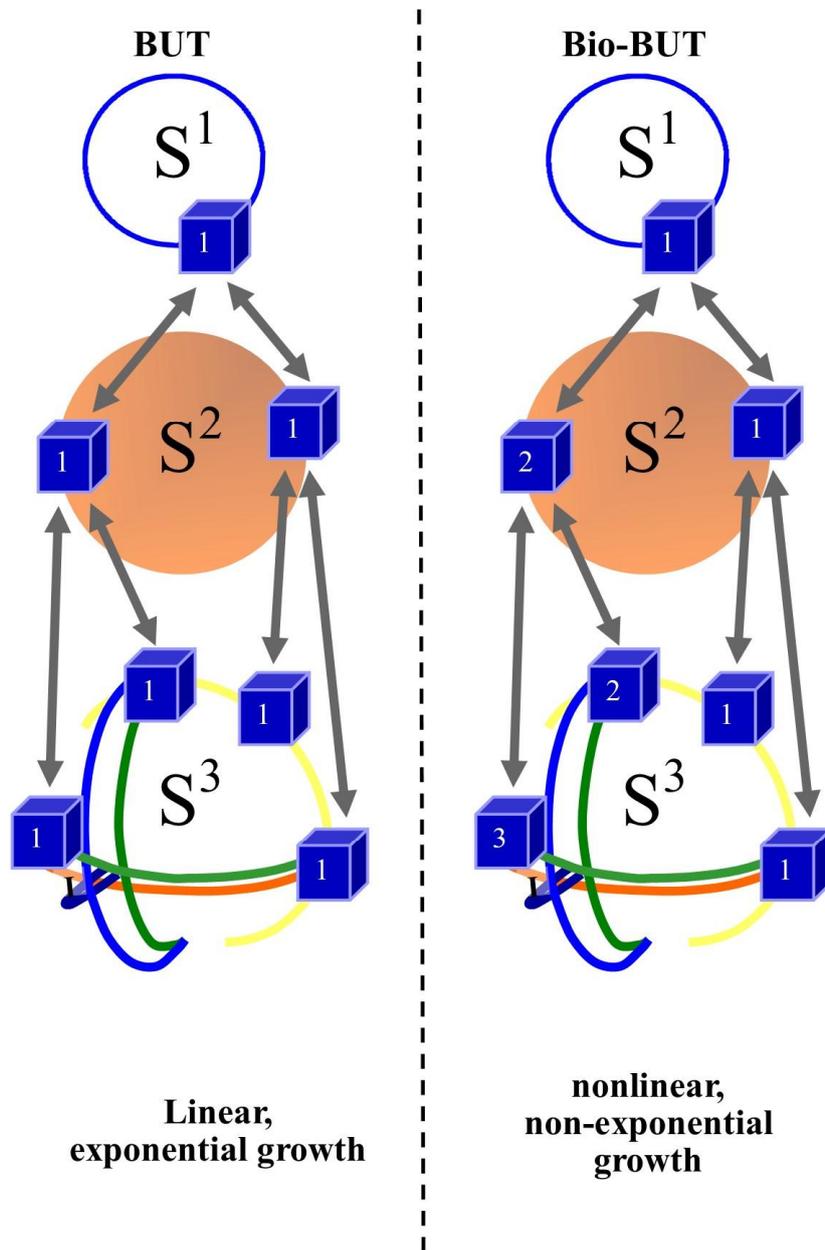
Figure 2. Evolution of two dynamical systems. In BUT terms (left side), every increase in manifold dimensions (in case of life, complexity), gives rise to redoubling of "the same" matching points, and vice versa. In bio-BUT terms, every increase in manifold dimensions gives rise to redoubling of matching points that "belong together", i.e., they display slight different changes for every duplication. The two dynamics gives rise, through the manifold evolution towards increases or decreases of dimensions, to different systems' outputs.

Assessment of brain function in terms of the identity principle

A further example from neuroscience shows how the identity principle and BUT may pave the way to novel approaches. We describe the meaning of "belonging together". However, as we have seen before, "belonging together" can also mean: **the together is determined by the belonging**. Therefore, the possibilities here are two:

a) representing belonging in terms of the unit of together;

b) experiencing this together in terms of belonging.

This point b leads us into the psychological standpoint of the observer. Indeed, "thinking" and matching description can also be thought as the same, so that they belong together in the same, and by virtue of the same. If we attempt to represent together the thinking and matching description as a coordination, we can establish and explain the latter either in terms of thinking or in matching description. If thinking and matching description belong to each other, matching description belongs with thinking to an identity, whose active essence stems from that "letting belong together" which we call "mental representation". Identity becomes, in this version, a functional property of the event of mental representation.

Identity (including the ego, i.e., the subjective identity of the human individual) can be presupposed as a feature of the matching description, or as a spring that departs from it. In this account, the principle of identity becomes a spring into the psychological origin of identity. We can therefore assess matching description and thinking in terms of that which joins the two, by virtue of the event of mental representation. This allows us to assess brain function in terms of projections among manifolds with different dimensions.

7. CONCLUSION: ENCOMIUM OF DIVERSITY

We have shown how to generalize and operationalize the concept of BUT's matching description, correlating it with the principle of identity from logic and philosophy, and provided some applications in physics, biology, and neuroscience. We have described BUT's "descriptively near sets", a concept that appears to be rather vague (because it may refer not just to a physical content such as energy or vectors, but also to a semantic content, such as two "felines") in terms of identity features. Further, the BUT concept of identity and matching description can be applied also to fields where the principle of identity is traditionally excluded, such as, for instance, the quantum entanglement. For more details, see Peters and Tozzi (2016).

We have also proposed a novel variant of BUT, termed bio-BUT, that elucidates the astonishing variety of living structures. Indeed, generation after generation slight changes in DNA occur. The same might occur during the life of the single individual, for example during the ageing process. This means that, if we are able to find the topological source of the above-mentioned slight changes in features A in single individuals, we might partially counteract ageing, or to alleviate diseases due to an accelerated disarrangement of matching points.

One of the main concerns in the BUT topological approach to systems features is that it talks in rather general terms, leaving apart the peculiar features of individuals and of single physical and biological processes. This paper highlights that the concept of matching description displays the widest range of possible uses, in particular when the concept of matching description is well developed. In particular, matching description does not assess just "the same" feature, but also features that are "different".

Our framework also provides a lesson or two about our knowledge capabilities: the unity is never given directly, and knowledge is feasible just when coming back to unity. Therefore, we need to talk of unity BEFORE the separation. This implementation makes BUT and its variants not just the standpoint for a novel interpretation of a number of elusive biological and physical phenomena, but also a suitable tool in order to evaluate the slight (objective and subjective) differences that make our intellectual world an astonishing realm of rich heterogeneity.

REFERENCES

1) Angel E, Leong P. 1994. Multidimensional dynamic programming on massively parallel computers. Computers & Mathematics with Applications. 27, 9–10: 67-75

2) Benson AR, Gleich DF, Leskovec J. 2016. Higher-order organization of complex networks. Science, 353, 6295: 163-166. DOI: 10.1126/science.aad9029

3) Borsuk M. 1933. Drei satzeuber die n-dimensionale euklidische sphare. Fundamenta Mathematicae XX, 177–190.

4) Bruno G. 1582. De umbris idearum. In: Jordani Bruni Nolani opera latine conscripta (Giordano Bruno the Nolan's Works Written in Latin), Dritter Band (1962) / curantibus F. Tocco et H. Vitell

5) Chaisson EJ. 2010. Energy Rate Density as a Complexity Metric and Evolutionary Driver. Complexity, v 16, p 27, 2011; DOI: 10.1002/cplx.20323.

6) Crabb MC, Jaworowski J. 2013. Aspects of the Borsuk-Ulam Theorem, J. of Fixed Point. Theory and Applications 13: 459–488, DOI 10.1007/s11784-013-0130-7, MR3122336.

7) de Cusa N. 1440. De docta ignorantia. English translation in Bond, H. Lawrence (ed.), Nicholas of Cusa: Selected Spiritual Writings, Classics of Western Spirituality. New York: Paulist Press, 1997.

8) Ghrist R. 2014. Elementary Applied Topology, Amazon, ISBN: 978-1-5028-8085-1.

9) Giusti C, Ghrist R, Bassett DS. 2016. Two's company, three (or more) is a simplex. Algebraic-topological tools for understanding higher-order structure in neural data. Journal of Computational Neuroscience, 41; 1:1–14

10) Heidegger M. 1957. Identity and difference. Harper & Row, Publishers (New York, Evanston, and London).

11) Kida T, Tanaka E, Kakigi R. Multi-Dimensional Dynamics of Human Electromagnetic Brain Activity. Front Hum Neurosci. 2016 Jan 19;9:713. doi: 10.3389/fnhum.2015.00713. eCollection 2015.

12) Kleineberg K-K, Boguñá M, Serrano MA, Papadopoulos F. 2016. Hidden geometric correlations in real multiplex networks. Nature Physics, in press. doi:10.1038/nphys3812

13) Koczkodaj WW, Magnot J-P, Mazurek J, Peters JF, Rakhshani H, Soltys M, Strzałka D, Szybowski J, Tozzi A. 2017. On normalization of inconsistency indicators in pairwise comparisons. International Journal of Approximate Reasoning. 86, 73–79. http://doi.org/10.1016/j.ijar.2017.04.005.

14) Matoušek J. 2003. Using the Borsuk–Ulam Theorem. Lectures on Topological Methods in Combinatorics and Geometry (Springer-Verlag Berlin Heidelberg).

15) Munkres JR. 2000. Topology, 2nd Ed. Prentice-Hall, Upper Saddle River, NJ, MR0464128

16) Nagel T. 1974. What Is It Like to Be a Bat? The Philosophical Review, 83, 4, 435-450.

17) Naimpally SA, Peters JF. 2013. Topological spaces via near and far. With a foreword by Iskander A. Taimanov. *World Scientific Publishing Co. Pte. Ltd., Hackensack, NJ,* 2013. xvi+277 pp. ISBN: 978-981-4407-65-6, MR3075111

18) Peters JF. 2016a. Computational Proximity. Excursions in the Topology of Digital Images. Edited by Intelligent Systems Reference Library. Berlin: Springer-Verlag. doi:10.1007/978-3-319-30262-1.

19) Peters JF, Tozzi A. 2016c. Quantum Entanglement on a Hypersphere. Int J Theoret Phys, 1–8. doi:10.1007/s10773-016-2998-7.

20) Peters JF, Ramanna S, Tozzi A, Inan E. 2017. Frontiers Hum Neurosci. BOLD-independent computational entropy assesses functional donut-like structures in brain fMRI image. doi: 10.3389/fnhum.2017.00038.

21) Simas T, Chavez M, Rodriguez PR, Diaz-Guilera A. 2015 An algebraic topological method for multimodal brain networks comparisons. Front Psychol. 6;6:904. doi: 10.3389/fpsyg.2015.00904. eCollection 2015.

22) Tozzi A, Peters JF. 2016a. A Topological Approach Unveils System Invariances and Broken Symmetries in the Brain. Journal of Neuroscience Research 94 (5): 351–65. doi:10.1002/jnr.23720.

23) Tozzi A, Peters JF. 2016b. Symmetries, Information and Monster Groups before and after the Big Bang. Information, 7(4), 73; doi:10.3390/info7040073.

24) Tozzi A, Peters JF, Fingelkurts AA, Fingelkurts AA, Marijuán PC. 2017a. Topodynamics of metastable brains. Physics of Life Reviews. http://dx.doi.org/10.1016/j.plrev.2017.03.001.

25) Tozzi A, Peters JF, Navarro J, Kun W, Lin B, Marijuán PC. 2017b. Cellular Gauge Symmetry and the Li Organization Principle. Progress in Biophysics and Molecular Biology. doi.org/10.1016/j.pbiomolbio.2017.06.004.