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Self-similarity and T-patterns from cell city to the only big-brain mass-societies formed in a recent eye blink: Proteomics as bio-sociology

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This talk concerns spatial and temporal self-similarity across more than nine orders of magnitude, implicating a self-similar fractal-like pattern, called T-pattern, a natural or pseudo-fractal pattern, recurring with statistically significant translation symmetry (Magnusson et al. eds. 2016). It is here presented in the order realized within a longstanding primarily ethological (i.e. biology of behavior) project beginning in the early 1970's concerning social interaction and organization in social insects and primates including humans and inspired mainly by the work of Lorenz, von Frisch and Tinbergen for which they shared a Nobel Prize in Medicine or Physiology in 1973. The smallest animals concerned in their ethological work were social insects and there was no implication of self-similarity. The present project has focused on developing time pattern definitions and corresponding detection tools resulting in the T-pattern type and corresponding detection algorithms implemented as the THEME software, which has allowed their abundant detection (Casarrubea et al., 2015), in many kinds of animal and human behavior and interactions and later in neuronal interactions within living brains (Nicol et al.), in this way indicating T-designed self-similarity of worldly association between and inside cerebrums. Apparently, the RNA world invented its evolving external memory as the purely informational T-patterned DNA strings and now there is only a DNA world. Similarly, humans invented their evolving external memory as the purely informational T-patterned strings of written language making possible very recently and in a biological eye-blink the development of modern science and innovation and the formation of incredibly crowded and complex human mass-social orders, the main mass-social orders among enormous brained creatures and now completely dependent on T-designed content strings. Protein and human mass-social orders appear to be the main ones utilizing such tough long memory strings outer to their residents. Strings that are highly standardized with parts being massively copied, distributed, promoted and even enforced such as those among humans called legal or holy. Both Human and protein mass-social orders make their specific residents utilizing different sub-segments of the outer T-designed memory strings.Extensive temporal and spatial self-similar patterning thus seems to exist in form and function from nano to human temporal and spatial scales regarding transient nonverbal behavior and its more durable spatial traces or products such as texts. A proposed self-similar hierarchical repeated pattern type, called T-pattern, has been found in many kinds of verbal and nonverbal human, animal and neuronal behavior and interactions (Casarrubea, 2015; Nicol, 2015) and seems characteristic of DNA patterns such as exons and genes. Functional analogies also seem to exist (Magnusson, 2005). Such structural self-similarity over a number of levels of biological organization suggests the possibility of a unified (mathematical) approach. Living beings are generally composed of organized masses of simpler units. Cities of both insects and modern humans descend from -- and are composed of -- unicellular organism, which themselves are mass societies of even smaller units, proteins. One striking difference is brain size and modern humans are the only primates and large brained animals to live in mass societies or cities. Human mass-societies invented writing, a precondition for a spectacular increase of knowledge and have evolved "holy" or "sacred" strings of words that profoundly and similarly misinform most the individuals of the same society about fundamental causal contingencies and thus sharply constrain (and aligning) their behavioral potentials? Are they analogous to molecules blocking some behavioral (even reproductive) potentials of social insect masses? Could (socio-) proteomics help to explain sometimes apparently brainless

behavior of human masses reminiscent of the behavior of the proteins they both descend from and are composed of? Finally, are human abilities possibly not much greater than those of proteins and insects relative to the complexity of their mass societies? Early on in the articulation of systems biology as a field, proteomics was recognized as an essential discipline for the accurate building of network models. While still far from how routine microarray analysis of transcriptome data has become, the past 10 y has seen a linear increase in the number of proteomic publications. Although the number of systems biology publications has also increased linearly, the absolute number of systems biology manuscripts is currently still one-third of proteomics. Interestingly, whereas the number of systems biology papers related to nutrition research has remained constant at 3–4% of the total, the percent of proteomics papers related to nutrition research is somewhat lower at 2–3% of the total. Advances in MS, first in the development of ionization techniques such as matrix assisted laser desorption ionization (MALDI) and electrospray ionization and secondly in the ability to conduct tandem MS (MS/MS) to fragment peptides by collision-induced dissociation, paved the way for the development of proteomics as a field. MS-based proteomics is now the only method used for the systemic characterization of proteins from identification, quantification, and characterization of either post-translational modifications or protein interactions.

The identification of proteins by MS can be achieved by the fragmentation of peptides or intact proteins using either a bottom-up or a top-down approach. Either approach is amenable to automation, although most high-throughput global proteomic analytical programs have favored the bottom-up approach primarily because, compared to proteins, peptides are relatively easy to handle and their physiochemical properties are more uniform. However, the analysis of complex biological matrices by MS is highly dependent on off-line separation technologies such as 2-dimensional gel electrophoresis (2DGE) or HPLC that simplify such samples prior to mass investigation; and HPLC is additionally the standard front end on-line division procedure for some fluid chromatography-MS (LC-MS) based instrumentation stages. Although the merits of 2DGE have been debated relative to multidimensional LC-MS, or “shotgun” proteomics, each approach has its advantages and disadvantages and both separation strategies are widely used. Whereas the success of bottom-up proteomic approaches has primarily been driven by the successful application of collision-induced dissociation fragmentation to peptide MS and it has had a central role in shotgun proteomics, instrument-based technological advances more recently have allowed alternate fragmentation technologies such as electron capture dissociation to be revisited as alternate and complementary fragmentation technologies. This, in association with the development of high-resolution mass analyzers such as the Orbitrap and high resolution time-of-flight mass spectrometers, has driven the intact molecular mass measurement of proteins and supported an increased interest in top-down proteomic analysis. Most recently, advances in the identification of post-translational modifications have been driven by the coupling of ion wave technology to MALDI-MS platforms, which allows the differentiation of identical mass peptide species by virtue of their 3-dimensional structure. With continuous improvements in particularity, affectability, fracture science, and an assortment of stages and techniques, MS is currently fit for protein investigation on a worldwide scale.