Space and time in language as a pattern in general fictivity

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Systematic parallelism between spatial and temporal expressions in a language is conceived here as a pattern in general fictivity arising from an underlying cognitive manifold. Under this situation, we try to articulate some of the questions pertinent to the spatial and temporal cognition from the viewpoint of patterns in general fictivity.

In recent times, cognitive science research is overwhelmed by two distinct, though interrelated, trends of enquiries. One group[1–6] concentrates on the metaphorical structuring of time, whereas the other group[7–11] is struggling hard to identify those domains of cognition which are crucial in shaping our spatial competence. These two directions, if taken together, reveal another reality that is significant in broadening the scope of current research agenda. The first kind of research agenda considers space as primary in comparison to time, whereas researchers belonging to the latter tradition presuppose the existence of a frame of reference with respect to which space is described. If so, then how primal is space? The answer to this question will lead us to an understanding about how space and time are paradigmatically represented and processed by the human mind.

Problem statement

Some[2,4,12–16] have argued that we talk about time in language in terms of space. For example, 'looking ahead for a brighter tomorrow, troubles that we left behind', etc. These and other similar parallelisms across languages have led the researchers to examine the relationship between temporal and spatial cognition. In one such instance, Casasanto *et al.*[5] frame the question as the problem of relationship between space and time inside the human mind. Levinson and Wilkins[11] have also accepted the centrality of spatial metaphors in language-based reasoning, and considered space 'as a fundamental intuition built into the (human) nature'. These studies are significant in explaining how abstract temporal cognition is grounded in a more concrete spatial cognition. Spatio-temporal cognition from the perspective of conceptual grounding, then in turn, explains what type of spatial structures and structuring principles are

employed by the temporal cognition. What remains implicit in all these approaches is that space is linguistically more entrenched than time. Boroditsky[17] identified the frequency of occurrence as the cause of entrenchment. A nearly similar solution can also be found in the approach of Evans[16]. To Evans, the correspondence between the spatial and temporal language is an instance of principled polysemy. According to the thesis of principled polysemy, the relative significance of space over time is a consequence of pragmatic strengthening. Both the arguments of frequency of occurrence or pragmatic strengthening, following Talmy[18], can be assessed in terms of degree of veridicality under the assumption that one of the functions of human cognition is to generate such assessments. According to this view, the relative significance of space over time is simply a matter of veridicality assessment; therefore, this assessment should be considered as one of the many other patterns of general fictivity available in language. If so, then what would be the ontological status of space and time in the human mind? And, how does this proposal take into account the research findings outlined in the introduction.

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Instead of attributing the ontological priority to space over time, we argue that space and time presuppose the same underlying cognitive system, which works on the basis of the logic provided by body image and motion schema. According to this proposal, body image and motion schema provide primary interpretive procedures which determine the functioning of language-based secondary-interpretive-procedures associated with various spatial and temporal expressions.

The conceptualization of various asymmetries crucial to spatial and temporal

reasoning in language is relative to that of the human body, physical entities and motion[19–22]. In due course of development, these structures are abstracted away from their source domains and are used in linking disparate entities like space and time. This metaphorical capacity of forming patterns in general fictivity rests on the associate properties of, what Edelman[23] calls, 'a reentrant degenerate system'. Though these conceptual structures are decoupled from their original instantiations, they somehow preserve the reified structure of original input and output. According to this understanding the reified referential frames – evolving out of the conceptualization of human body, physical entities and motion – constitute that underlying cognitive manifold which is crucial to both linguistic and non-linguistic cognitive abilities. This has an obvious impact on language. Jackendoff[24], and Habel and Eschenbach[25] argue that an underlying unique thematic structure is responsible for the systematic parallelism found in spatial and temporal languages.

Under this situation, it can be argued that the various schematic representations of human body, motion and object may provide some important insights about the functioning of the underlying cognitive manifold in licensing different patterns in general fictivity. Therefore, it would probably be commendable to question how the underlying cognitive manifold that we have talked earlier is formed, and how it functions while licensing the fictive patterns of space and time in language.

Conclusion

This note conceives the systematic parallelism between spatial and temporal languages as the most commonly found pattern of general fictivity. Further studies will confirm the spatio-temporal unity on the one hand, in virtue of being

reflections of the underlying cognitive manifold and recognize the fictive aspect of spatial and temporal expressions in language on the other.

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Pervasive transcription

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Pervasive transcription or interleaved transcription is the transcription of the interspersed genes which are embedded within the normal coding sequence. The quintessential factor is that, it is believed that the entire stretch of the genome is transcribed, whether it is coding for a particular protein or not. The other underlying factor is that not all coding sequences lie juxtaposed; they may also overlap one another. In other words, they may lie interspersed. The unconventional fact is that these overlapping sequences may be a non-coding region or an interspersed coding region which is still transcribed. The question is, how often are these interspersed regions getting transcribed and does all of the transcribed sequence get translated into protein coding messages?

Transcription is a term associated with the genic region. However, recent findings help extend this concept to include intergenic region, many non-functional elements, pseudogenes, etc.[1–8]. The shear size of the mRNA transcripts produced does not correspond to the mRNA translated; neither do the data relating to the number of coding regions correspond to the multitude of transcripts obtained[9,10]. The genomic framework and transcription process have to be reviewed for better understanding of transcription of interleaved and intragenic regions. Non-coding, stably unannotated transcripts (SUTs) are also produced, which may have a vital function as a regulatory molecule[11]. Some of these might translate to peptides and hence are called transcripts of unknown function (TUFs)[12–14]. Projects such as 'ENCODE' are aimed at exploring what is transcribed to what is translated to what is expressed. The results of the ENCODE project revealed new sectors of RNA and new layers of the transcription machinery. However, the precision of the positioning of the CUTs and SUTs is still to be studied, because of the diverse mechanism of generation of transcripts and also that the number of transcripts generated does not correlate with the findings of Xu *et al.*[1]. Some interesting cases that involve promoter-associated pervasiveness are discussed below, as they are the major source of SUTs[1].

Multiple transcription start site (TSS) points, which control transcription of single annotated genes, are found by mapping the 5′-end of capped RNAs to their corresponding TSSs[8,14–16]. TSS shifts result in the production of snRNAs and snoRNAs, as seen in the shift between upstream and downstream TSS of *IMD2* gene in yeasts[17]. Additionally, pervasive