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Time and consciousness in intuitionism

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Brouwer's claims that time is a primordial intuition of consciousness has been considered in terms of the complex systems physics. The time continuum that is based upon a processual definition of real numbers concerns a skeletal category of such intuitionism which should be related to the measurement problem. A multiresolution hierarchy of the measurement process corresponds to the time operator that is a formalism of complex systems which was developed by the Brussels school of thermodynamics. The wavelet domain hidden Markov model that recapitulates statistical properties of the hierarchy has been proven tremendously useful in a variety of applications, including speech recognition and artificial intelligence. The model provides switching between outer and inner psychophysics, due to a change in representation which is the operational function of time. The inner psychophysics, which is a relation between sensation and neural activity, corresponds to the recognition of structural information that has been reflected by the increase of statistical complexity in the temporal domain. The optimal measurement corresponds to the most prominent increase that is an indicator of the system's self-organization, which presents an evident link between time and consciousness.

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直覺主義中的時間和意識

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Brouwer 關於時間是意識的原始直覺的主張已從複雜系統物理學的角度考慮。基於實數過程定義的時間連續體涉及這種直覺主義的骨架範疇，它應該與測量問題有關。測量過程的多分辨率層次對應於時間算子，它是布魯塞爾熱力學學院開發的複雜系統的形式主義。概括層次結構統計特性的小波域隱馬爾可夫模型已被證明在各種應用中非常有用，包括語音識別和人工智能。由於表示的變化是時間的操作功能，該模型提供了外部和內部心理物理學之間的切換。內在心理物理學是感覺和神經活動之間的關係，對應於結構信息的識別，這種結構信息已反映在時域統計複雜性的增加上。最佳測量對應於最顯著的增加，這是系統自組織的指標，它代表了時間和意識之間的明顯聯繫。

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The Lack of Systems Biology In-between the HLA-C and COVID-19 Severity

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The association between the COVID-19 severity and the *HLA-C*04:01* allele is the most replicated finding across Human Leukocyte Antigen (HLA) variants and diverse populations including the Armenian. The results have led to several hypotheses on the *HLA-C*04:01* allele contribution to the causative mechanisms. Thus, to unravel the systems biology underlying this genetic association, the present study aimed at identifying the *HLA-C*04:01*-related aberrations in whole blood leukocyte transcriptome, which may blueprint the severe pathophysiology of COVID-19.

Thus, we have performed DESeq2 bioinformatics and Gene Set Enrichment Analysis of RNA-sequencing data of a large publicly available cohort of 100 patients [Gene Expression Omnibus: accession ID GSE157103]. HLA-genotypes were acquired from the imputed data by Warren and Birol [PeerJ 2021]. Using univariate models of blood leukocyte transcriptomes of COVID-19 patients, we assessed differentially expressed genes (DEGs) between several clinical and demographical groups. The highest number of DEGs (over 3000) was found when groups of patients admitted and not admitted to the Intensive Care Units (ICU) have been compared. The biological processes, such as the positive regulation of both NK-mediated cytotoxicity and interferon-gamma production, as well as T cell activation. Relatively high numbers of DEGs were found associated with age and some ethnic groups. Nevertheless, only 15 DEGs were found between males and females. A comparison of *HLA-C*04:01* carriers and non-carriers revealed only 3 DEGs, i.e. *ANKS1B*, *PLA2G7*, and *DOCK6* ($P_{FDR} < 0.05$), with the inability to underpin any biological system. Moreover, in a multivariate model with five parameters (i.e. ICU status, *HLA-*