Evidence of Novel Structured Behaviors from Intact Tissue Measures

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Allostatic adjustments to inflammatory signaling is a common feature of chronic disease, affecting peripheral tissues and CNS behaviors. Applying novel strategies, we have explored features of the resting-state Hb-signal from intact, whole-breast measures in women with (N = 18) and without (N = 45) breast cancer under the hypothesis that adjustments to the molecular interactome of tissues will yield definable changes in resting-state dynamics that drive hemodynamic and neurogenic behaviors thereby bridging *macroscale* non-invasive phenomena with *microscale* 'omic-style measures.

Using a custom-fabricated fNIRS tomography system, simultaneous-bilateral volumetric time-series imaging of the whole breast in the resting state was performed. Applying a novel time-series-to-network mapping procedure, short-term (< 1 sec), voxel-dependent, network-transition behaviors were explored with the aim of defining associated kinetic and thermodynamic features.

Network adjacency matrix measures were identified for a 10-State nodal model of the Hb-signal. Among the 18 classes identified, most appear weakly correlated to each other and were strongly disease sensitive, suggesting access to a high degree of differential information. Also explored were various forms of co-dependent behaviors among the matrices. Contrary to the null-hypothesis of independence between network transition probabilities, dwell-time and mean coefficient amplitude, evidence of smoothly varying behaviors was observed, including various forms of saturable (hyperbolic) behaviors for both kinetic and thermodynamic feature classes. Building on classical enzyme-action theory, evidence of enzyme-like behaviors was observed from intact tissue and are consistent with known actions of NO on vascular smooth muscle.

The consider approach appears extendable to all forms of on-demand, physiologic time-series measures.