Epigenetic factor competition can reshape the EMT landscape in breast cancer cells



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We are nearing the tenth anniversary of the first papers applying methods of computational systems biology to the study of the epithelial-mesenchymal transition (EMT) and its relevance to cancer metastasis. This undertaking has been a major success, leading to a much-improved understanding of EMT itself and its connection to tumor initiation and drug resistance. But of course, new questions have arisen. After surveying the state of the field, this talk will focus on one of those new questions, namely how EMT circuits may couple to epigenetic factors. Specifically, will argue that we epigenetics can play a critical in enabling EMT or its reverse (MET) and that constructing models of these effects must take into global competition for epigenetic modifying enzymes.