The author has clear research questions, and convincingly motivates their work, putting it in the context of other Boolean network models and information dynamic research. He should clarify terms like “physically instantiated object” and “architecture” in the context of their research. He does not formally define transfer entropy or active information, and should do so. He gives clear background on the biological processes that motivate the model gene regulatory network. The meaning of the weights of the edges in the network representation, and the states of the nodes in the context of what is being represented biologically is unclear. If on/off means the gene is on/off, and certain edge weights represent activation or inhibition, these should be stated explicitly. The author should motivate his reason for choosing 20 timesteps over which to calculate information dynamics. If this is decided by the longest trajectory in the primary attractor it should be explicitly stated. He motivates his choice of trajectories chosen clearly, as it makes sense to compare a range or biological and abiotic trajectories. The computation of control kernel nodes seems correct, but omits the possibly of having control kernel nodes that are in the same states as nodes in non-primary attractors. These nodes should also be computed as possible control kernels. The plots could be more clear by connecting the scatter points, and consolidated by analysis. There should be a bar plot showing TE vs causal edges. The interpretations of the information dynamics seem reasonable, but are brief, and should be in the results section (either instead of or in addition to the summer/discussion section). Overall, this was a good paper with well-motivated and executed analyses, but needs additional interpretation and clarity in the vocabulary central to the work.