Apply SBGN-AF in the LEGO Project

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What is LEGO Project?

- LEGO is a new development under the Gene Ontology project.
- It is an extension of the existing GO by capturing relationships among various GO terms during the curation of genes.
- Current annotations take a very simple form:
 - Gene_product implied_relation GO_class
 - For MF, relation is has_function
 - For BP, relation is involved in
 - For CC, relation is located_in
- LEGO will enable curators to use the GO to express rich biological statements from the literature
 - Maximize biological knowledge captured by curator
 - Represent complex biology in an accurate, computable manner
 - Prevent
 - "kludges" that use existing terms misleadingly or inconsistently
 - Combinatorial explosion of GO terms

GO annotation 2010

NEDD4

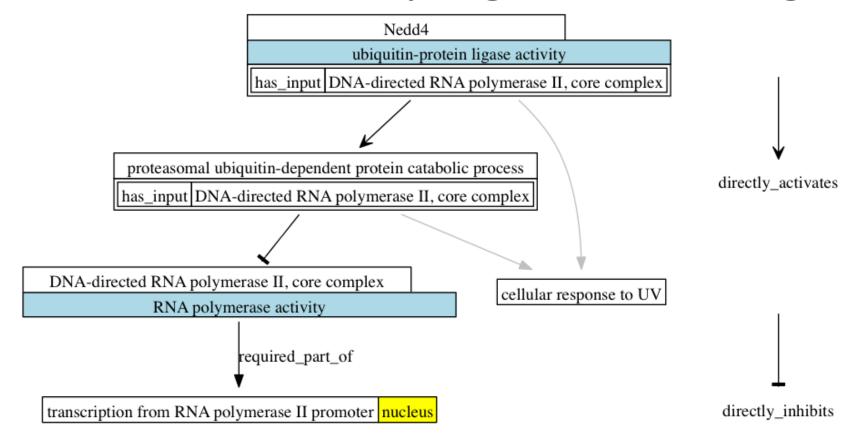
MF

- Ubiquitin-protein ligase activity
- RNA polymerase binding

BP

- Ubiquitin-dependent protein catabolic process
- Cellular response to UV
- Negative regulation of transcription from RNA polymerase II promoter

LEGO viewer plugin for Protege

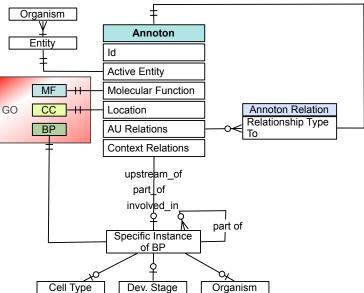


NEDD4 ubiquitin protein ligase activity acting on RNAPII complex involved in positive regulation of proteasomal ubiquitin-dependent catabolic process acting on RNAPII complex involved in negative regulation of RNAPII complex RNA polymerase II activity involved in negative regulation of transcription from RNAPII promoter during cellular response to UV

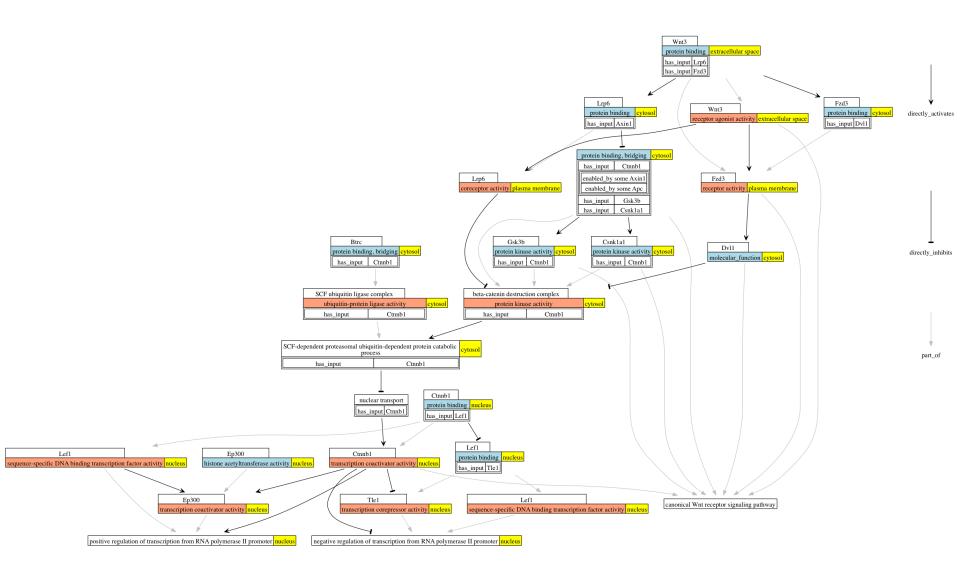
Progress

- Formal spec for construction of LEGO annotation
- Developed plugin for Protégé to enable use as prototype LEGO annotation tool
- Tested with several papers, including review

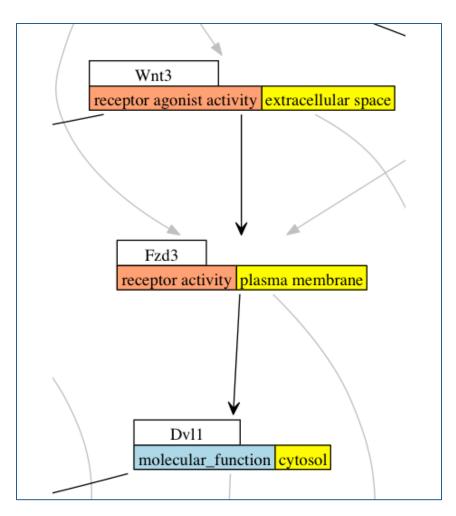
articles on entire pathways

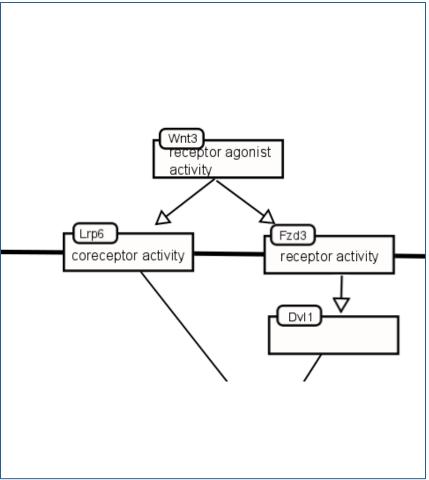


Wnt signaling pathway

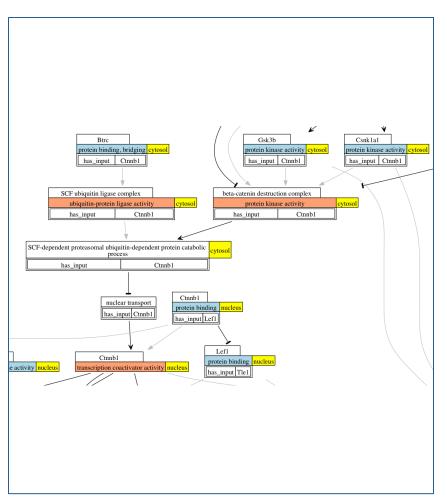


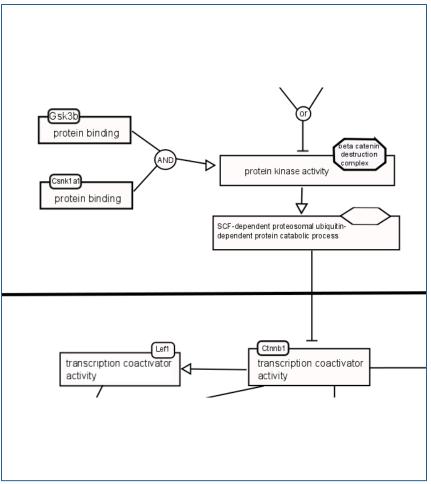
Mapping LEGO to SBGN-AF



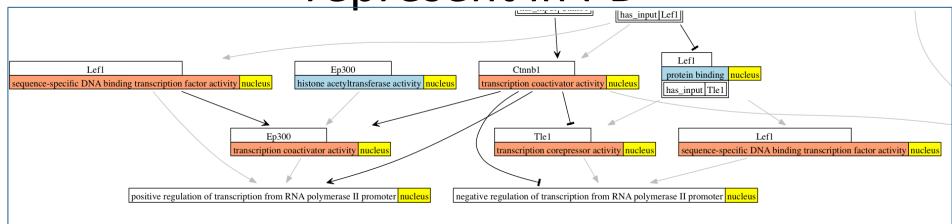


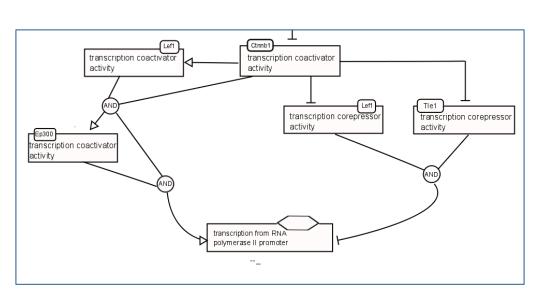
Mapping LEGO to SBGN-AF

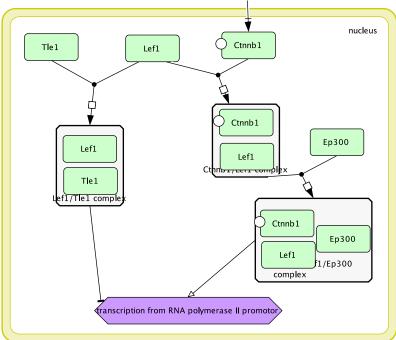




Some part of pathway is easier to represent in PD







Wnt pathway in SBGN-AF

