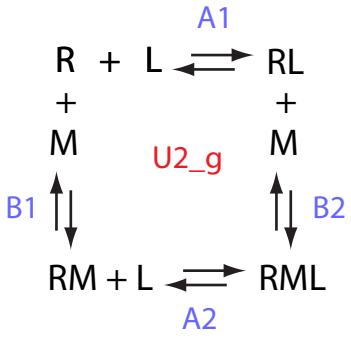
IDAP
Integrative Data Analysis Platform

Model summary - 3

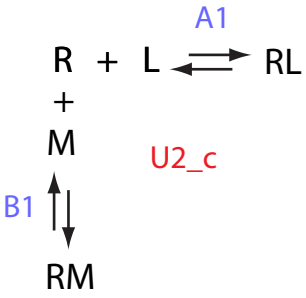
1:1 binding of two different ligands

General model

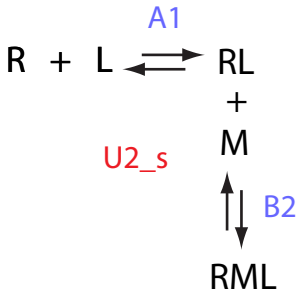


Here we may have different scenarios. (1) M ligand is present with R while L is added. (2) Both M and L are present in the titrant (example: tight-binding L ligand and 'unintended' weak-binding M buffer component, such as DMSO or phosphate, etc.)

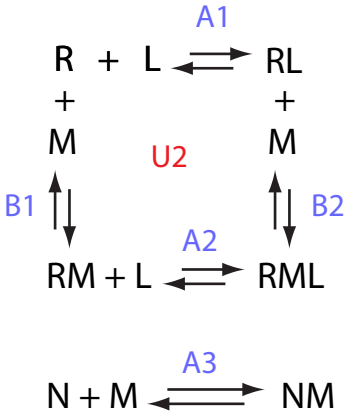
Competitive model



Sequential model



1:1 binding coupled with dissociation



In this scenario, the receptor is comes pre-bound with the M ligand and the mixture of two ligands, L and N, is titrated in. The L ligand directly binds to R, while the N ligand binds free M thus leading to dissociation of M from R. (Example: a ligand solution with a more basic pH---protons will be dissociated from protein histidines when more and more titrant is added (in this case we also need to consider presence of yet another receptor---buffer used for the R solution). Another case: the L ligand in a phosphate buffer (N)---then divalent ions (M) bound to proteins will be progressively dissociated upon titration.