Modelling and simulation of biased agonism dynamics at a G protein-coupled receptor

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Highlights

- A new ordinary differential equation model for biased agonism dynamics at a G protein-coupled receptor (GPCR) is presented.
- The model is general in the number of G proteins and active receptor.
- Numerical simulations reveal new phenomena in active G protein dynamics, including inter-conversion of the observed ligand effect (agonist to inverse agonist).
- The model recapitulates new experimental data for cells and ligands which are believed to exhibit biased agonism.