Pharmechanics Measuring biased agonism with a kinetic analysis Montana Molecular platform for real time data from fluorescent biosensors

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kTau = C

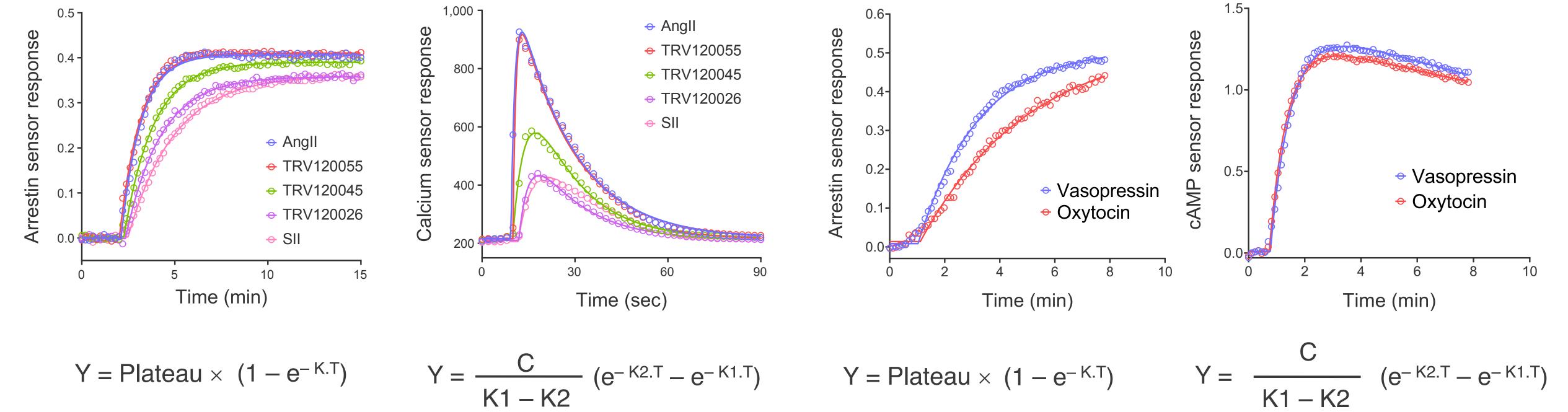
Overview

- Presently, biased agonism analysis requires specialist expertise.
- Here a new simpler method is described based on signaling kinetics (the initial rate).
- Robust biosensors from Montana Molecular provide biochemical-quality real-time signaling data in live cells.
- The model is applied to these data to measure biased agonism for angiotensin A1 and vasopressin V2 receptors.

Angiotensin AT1 receptor

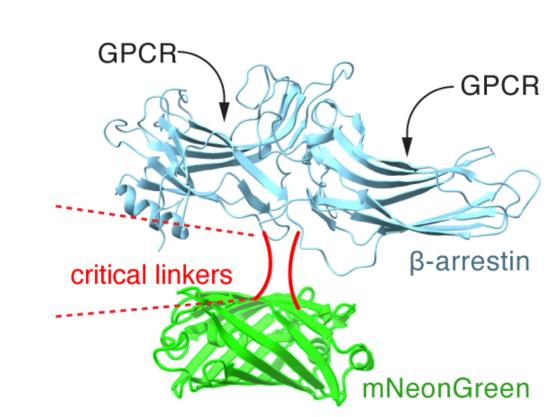
V2 Vasopressin receptor

kTau = C



Data analysis

- The initial rate of signaling is a measure of ligand efficacy. This parameter is called kTau¹.
- kTau is a direct measure of efficacy¹.
 Consequently, bias can be quantified by dividing kTau for one pathway by kTau for another.
- Equations are applied to biosensor time course data to measure kTau. This is done for a maximally-stimulating agonist concentration¹.



kTau arrestin	kTau Ca ²⁺	Bias ratio		
100	100	1.0		
99	120	0.8		
66	21	3.1		
50	15	3.3		
38	10	3.8		
	arrestin 100 99 66 50	arrestin Ca ²⁺ 100 100 99 120 66 21 50 15		

Bias ratio – kTau arrestin / kTau Ca²⁺

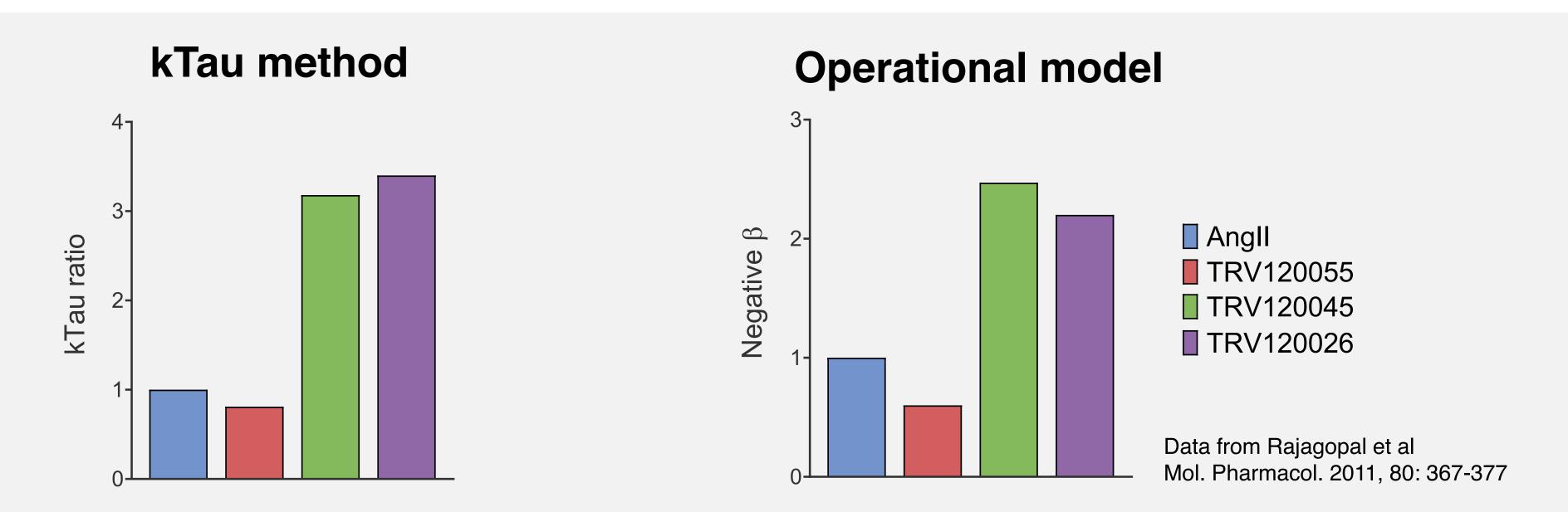
 $kTau = Plateau \times K$





	kTau arrestin	kTau cAMP	Bias ratio
Vasopressin	100	100	1.0
Oxytocin	57	109	0.5

kTau values – % of vasopressin Bias ratio – kTau arrestin / kTau cAMP



Biosensors

- Genetically-encoded fluorescent sensors (Montana Molecular) were used to measure arrestin recruitment, Ca²⁺ signaling (Red GECO)² and cAMP generation (RedcADDis)^{3,4}.
- The BioTek Synergy MX plate reader was used to obtain high temporal resolution data for the arrestin signal. Short read times were enabled by the brightness (high quantum yield) of the sensors.

References

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 PLOS One 2012, 7: e42791
 SLAS Discovery 2016, 21: 298-305
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Conclusions

- Quantifying biased agonism can be complex.
- We have developed a new simpler method based on initial rates (kTau).
- Robust biosensors enable the analysis platform to be applied.
- The new analysis gives similar estimates of bias to existing methods.
- This approach will improve the efficiency of biased agonism drug discovery.