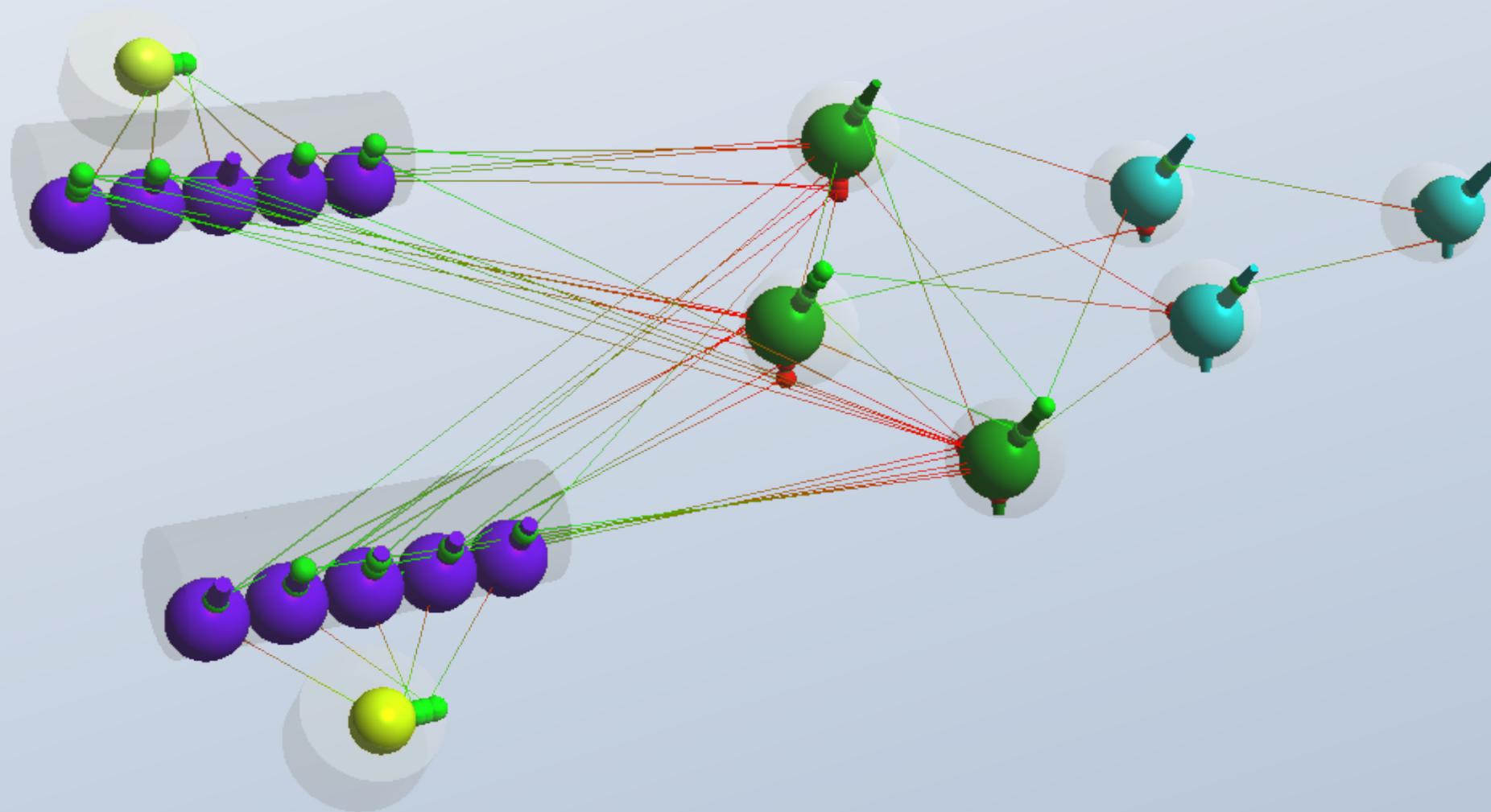


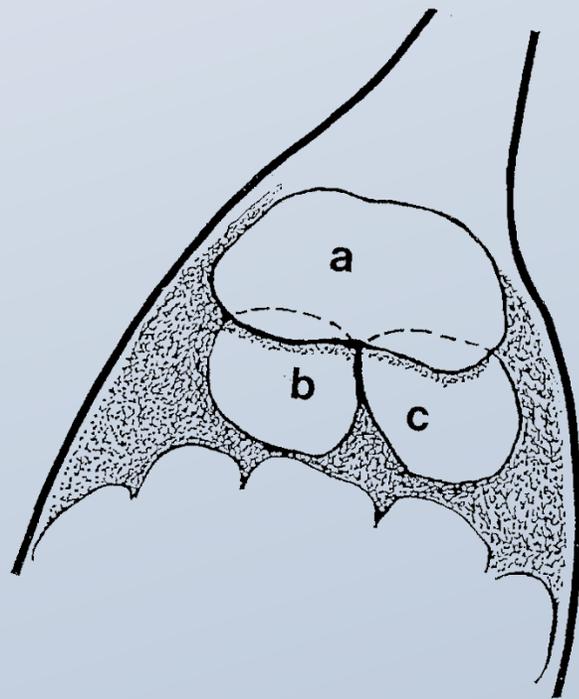
Constructing an in silico model of the pheromone system of the moth

Recognition of the correct ratio of components

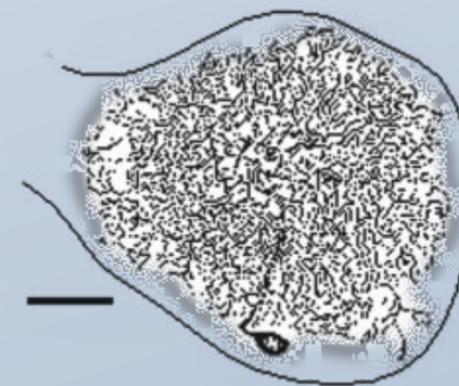


Relevant facts about (*S. littoralis*) MGC

- Three glomeruli, two ORN types, two pheromone components;
- Profuse arborisations between LNs in glomeruli;
- Connections between LNs are mostly inhibitory, as well as those between LNs and PNs;
- (Synchronised) self-sustained oscillations.

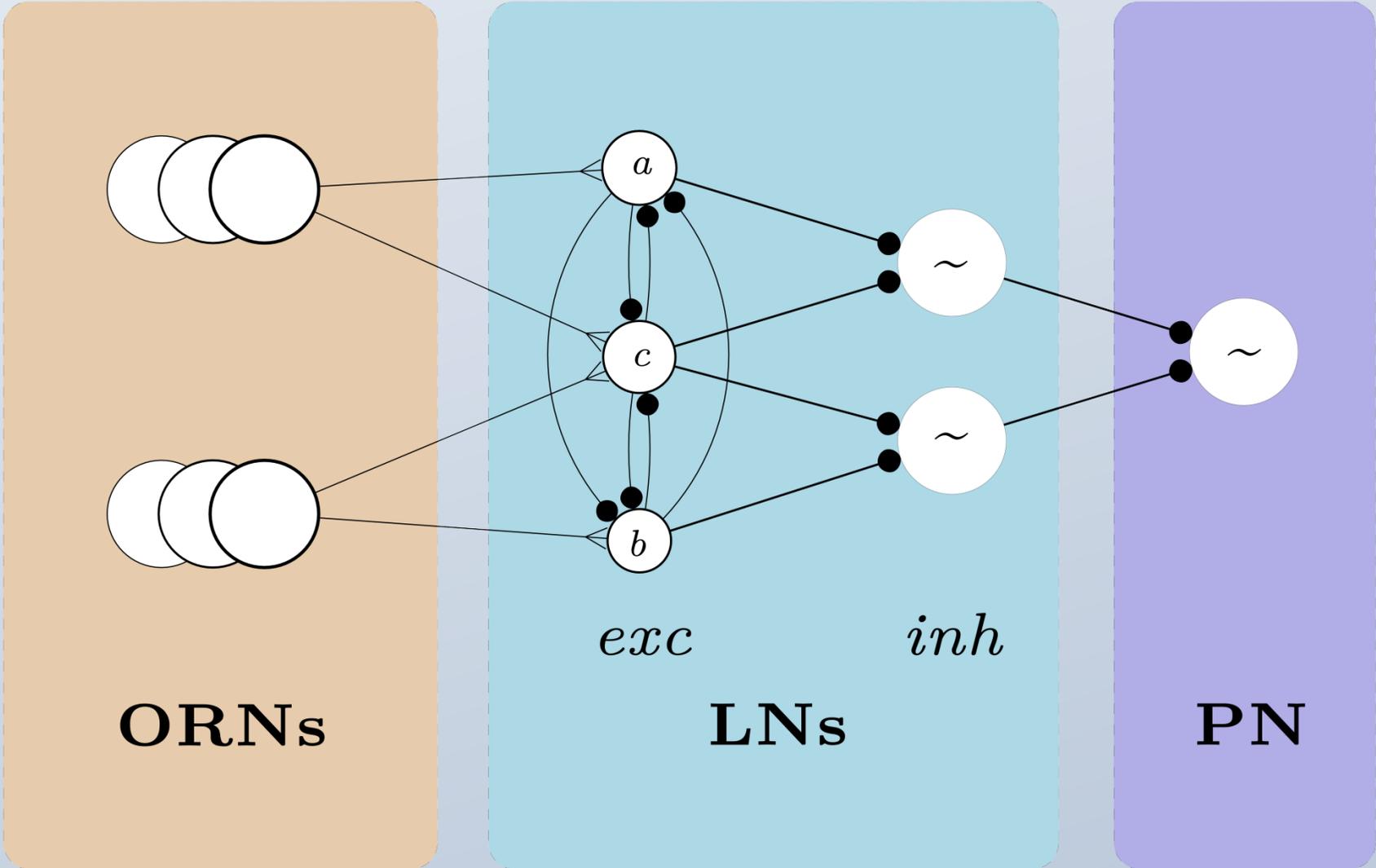


Ochieng SA, Anderson P, Hansson BS. *Tissue & Cell*, 1995, 27(2):221–32.



Hansson BS & Anton S. *Annu. Rev. Entomol.*, 2000, 45:203–31.
Christensen TA et al. *BioSystems*, 2001, 61:143–53.

Model structure: Topology & Individual components



Inhibition at PN from LN_{inh} effective only with LNs firing simultaneously

Model implementation: Neurons and Synapses

LN_s, PN_s

g_{Na}	=	7.15
E_{Na}	=	50
g_{K}	=	1.43
E_{K}	=	-95
g_{l}	=	0.021
E_{l}	=	-55
C_{mem}	=	0.143
g_{Kl}	=	0.00572
E_{Kl}	=	-95

Destexhe A, Mainen ZF, Sejnowski TJ. J Comput Neurosci. 1994 Aug;1(3):195-230.

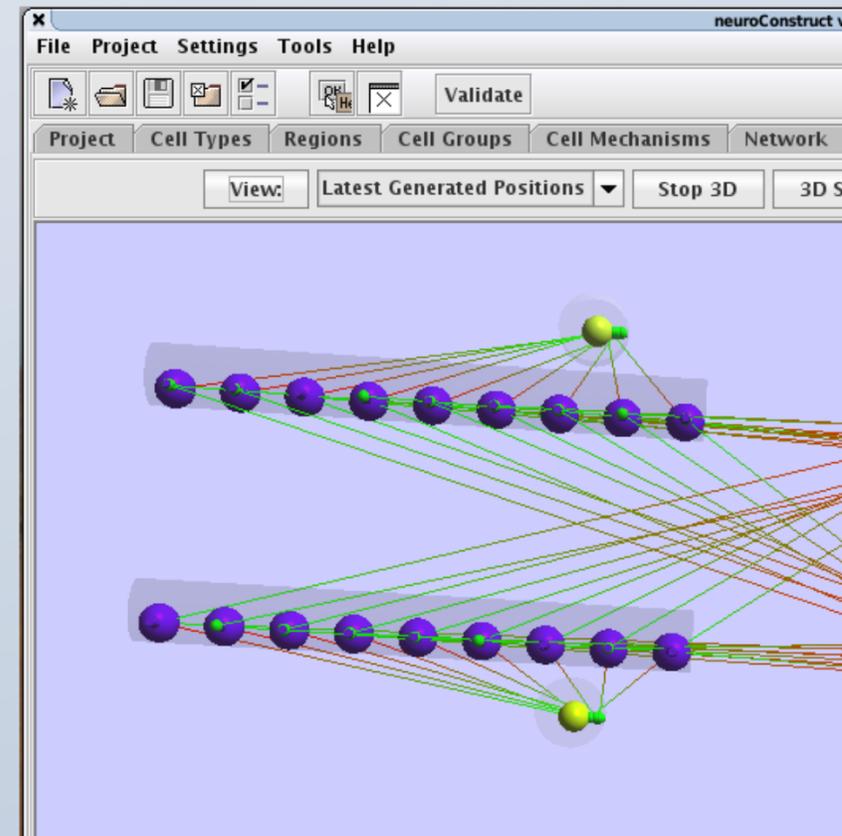
Traub RD, Miles R et al (several sources).

ORN_s

- Irregularly spontaneously firing, 2 ms 20 mV rectangular impulses + 10 ms refractory period;
- Rate follows a Poisson distribution with variable ;
- ORNs formed into battery to produce smoother stimulation.

Model implementation: Technical details

- Using 5-6th order Runge-Kutta integration algorithm;
- Model topology built in neuroConstruct and exported in NeuroML;
- Model runner written in C++;
- ~1:5 model time:execution time (2.4 GHz Core 2 Quad CPU) for the presented model;
- Use of map neurons planned.



```

Snesdhar 1.0
~/Projects/Ptherosys/...
~/libCN/src/
queue
+ Makefile
+ Makefile.in
+ cn-runner.cc
+ cnlib-integrate-base.
+ cnlib-integrate-k85.
+ cnlib-integrate-k85.
+ cnlib-model-cycle.cc
+ cnlib-model-export.cc
+ cnlib-model-import.cc
+ cnlib-model-struct.cc
+ cnlib-model.h
+ cnlib-neuron.cc
+ cnlib-neuron.h
+ cnlib-neuron_time.cc
+ cnlib-neuron_time.h
+ cnlib-oscillator.cc
+ cnlib-oscillator.h
+ cnlib-reader-tape.cc
+ cnlib-reader-tape.h
+ cnlib-synapse.cc
+ cnlib-synapse.h
+ cnlib-types.cc
+ cnlib-types.h
+ cnlib-unit.cc
+ cnlib-unit.h

const double __CN_Params_NeuronHH[] = {
    120.0, // gNa: Na conductance in 1/(nOhms * cm^2)
    55.0, // ENa: Na equi potential in mV
    36.0, // gK: K conductance in 1/(nOhms * cm^2)
    -72.0, // EK: K equi potential in mV
    0.3, // gL: Leak conductance in 1/(nOhms * cm^2)
    -50.0, // EL: Leak equi potential in mV
    1.0, // Cmem: membr. capacity density in muF/cm^2
    0, // Externally applied constant current
};

const char* const __CN_ParamNames_NeuronHH[] = {
    "Na conductance, 1/(n\316\251 * cm\302\262)",
    "Na equi potential, mV",
    "K conductance, 1/(n\316\251 * cm\302\262)",
    "K equi potential in mV",
    "Leak conductance, 1/(n\316\251 * cm\302\262)",
    "Leak equi potential, mV",
    "Membrane capacity density in \302\265F/cm\302\262",
    "Externally applied constant current",
};

const char* const __CN_ParamSvms_NeuronHH[] = {
    "gNa",
    "ENa",
    "gK",
    "EK",
    "gL",
    "EL",
    "Cmem",
    "Icc",
};

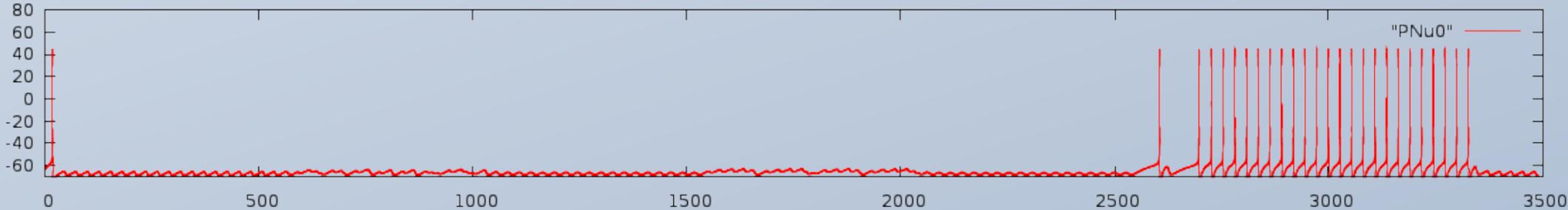
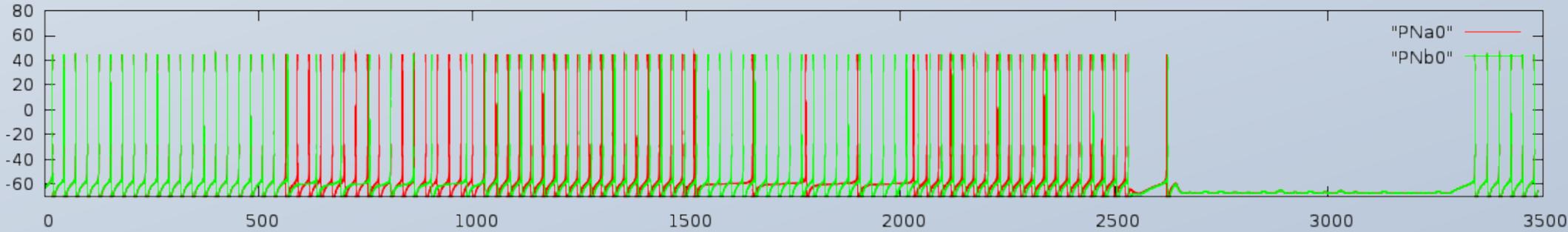
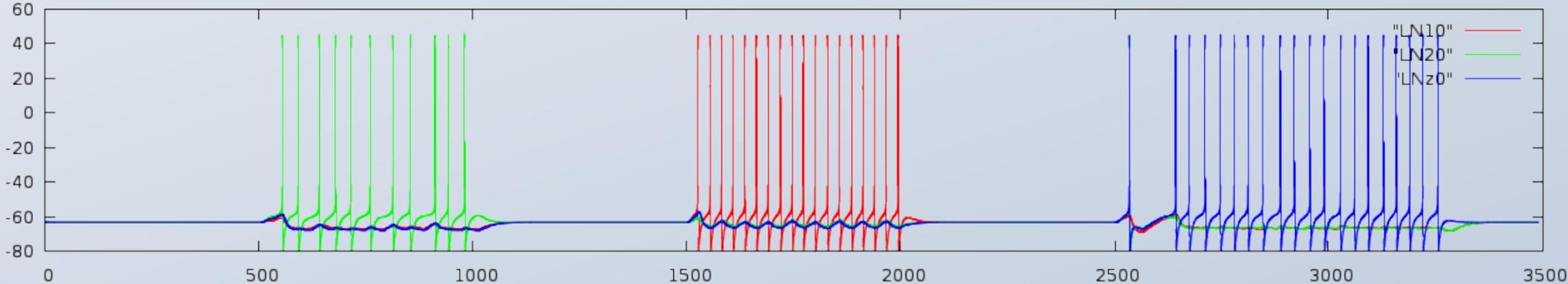
```

Detection of a 1:1 ratio

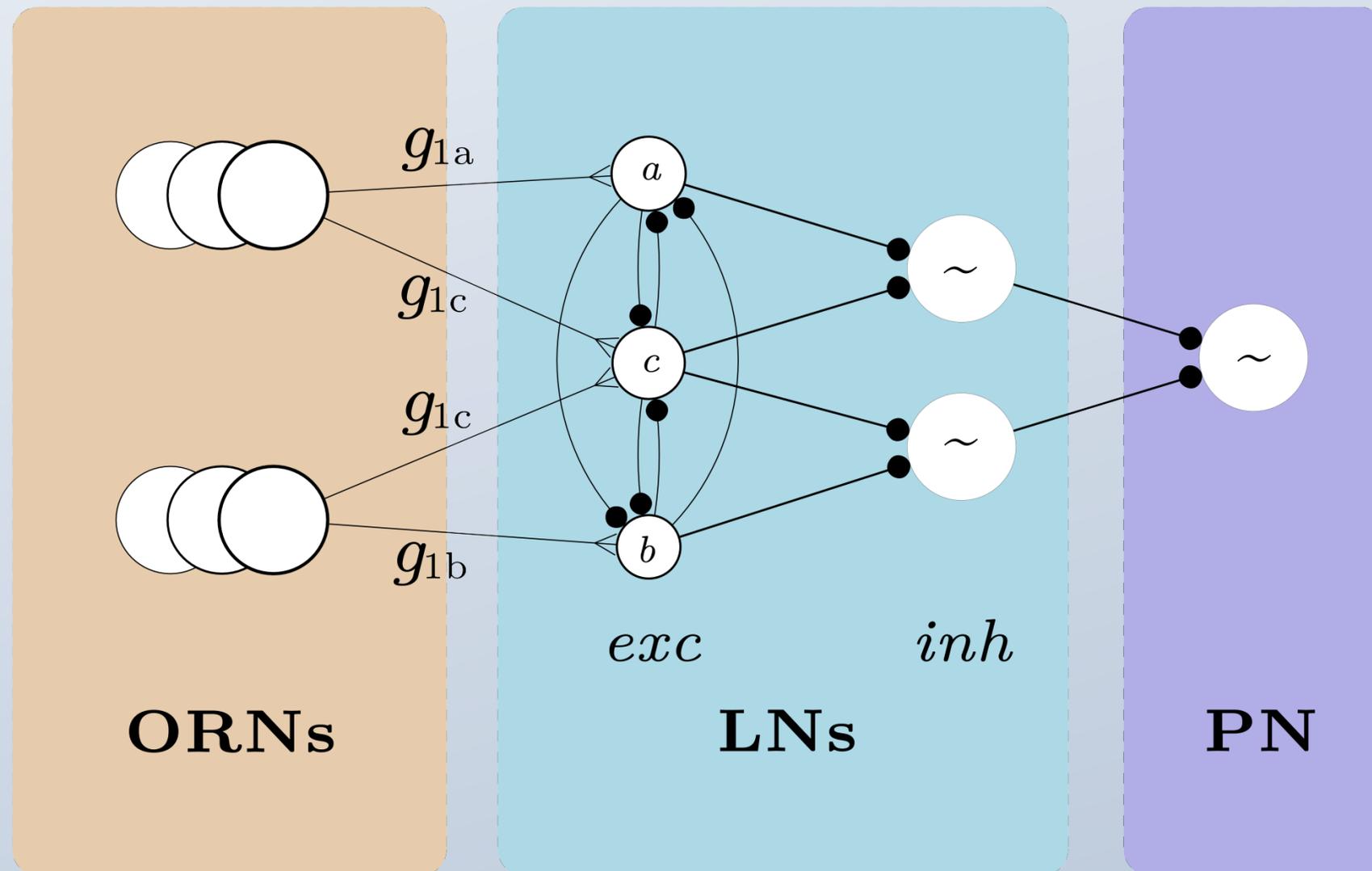
$$\begin{matrix} a \\ b \end{matrix} = \begin{matrix} 0.02 \\ 0.08 \end{matrix}$$

$$\begin{matrix} a \\ b \end{matrix} = \begin{matrix} 2.0 \\ 0.08 \end{matrix}$$

$$\begin{matrix} a \\ b \end{matrix} = \begin{matrix} 0.08 \\ 0.08 \end{matrix}$$



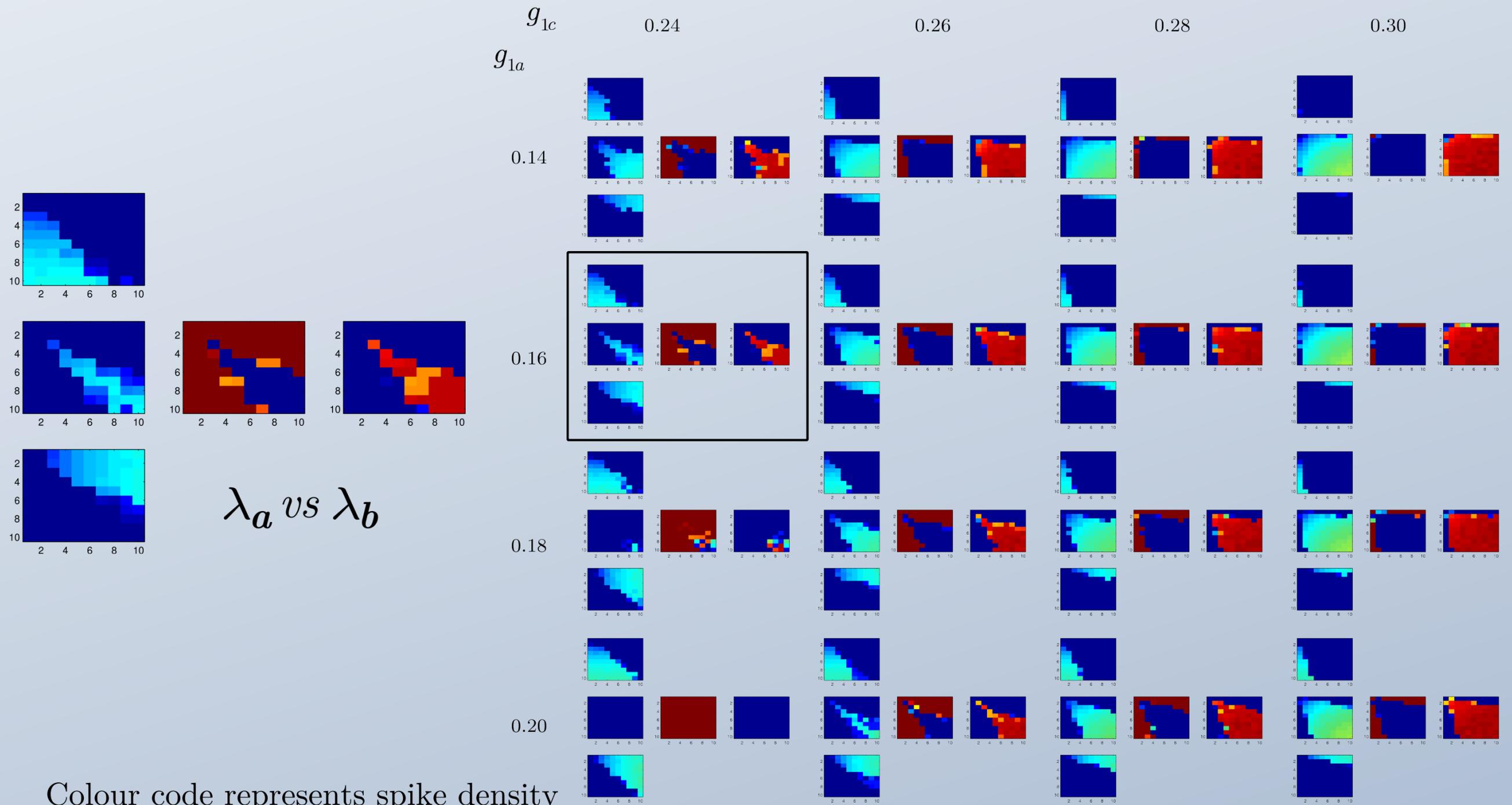
Optimal balance of synaptic strength between ORNs and LNs



$$(g_{1a} + g_{1b}) : g_{1c} = \sim 4:3$$

$$g_{2a} = g_{2b} \ll g_{2c} \quad (\text{can do with a single inhibitory LN})$$

Running the simulation & Search for optimal parameters (with 200 ORNs)

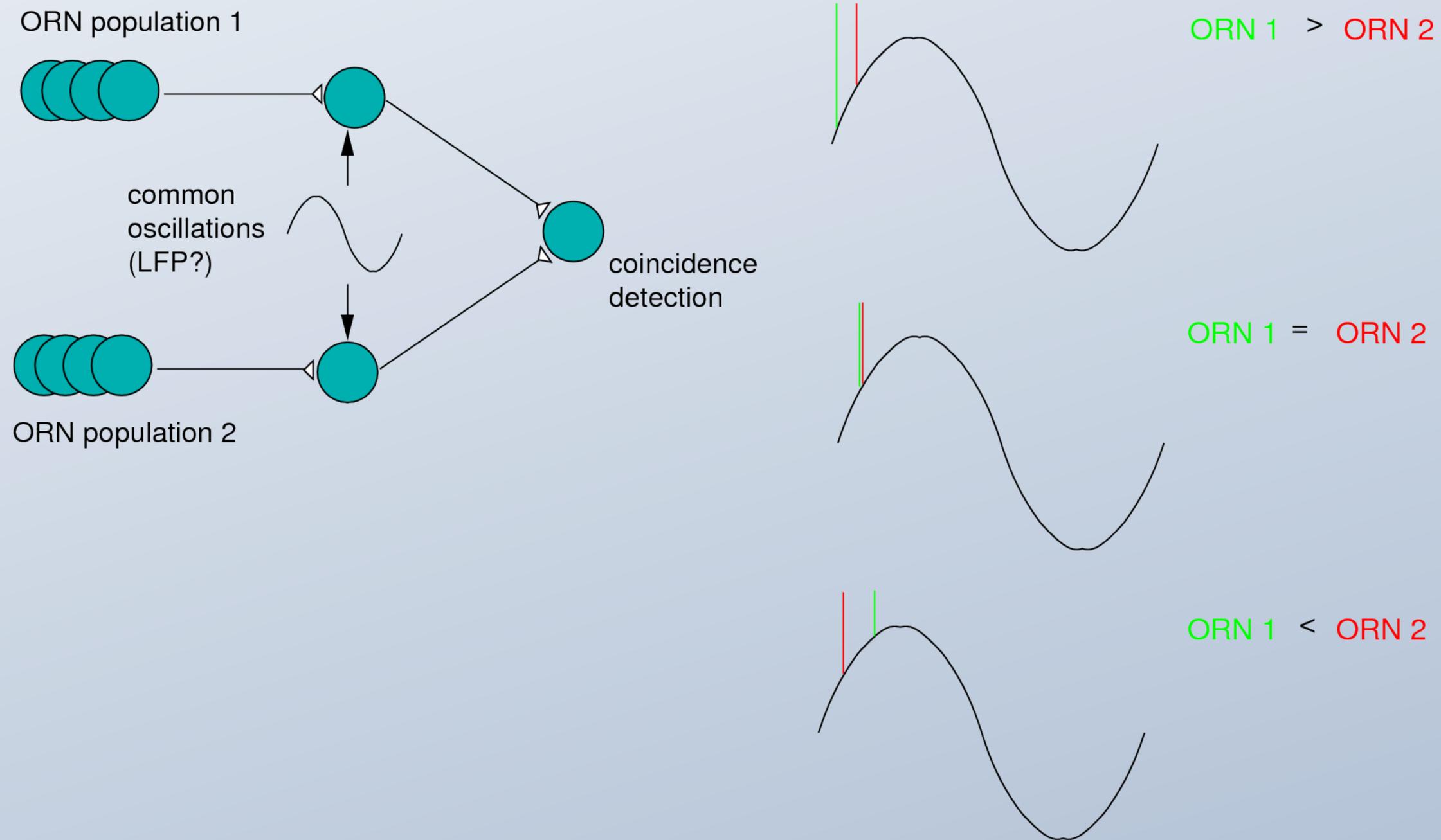


Colour code represents spike density
(blue = no spiking, red = spiking at max rate)

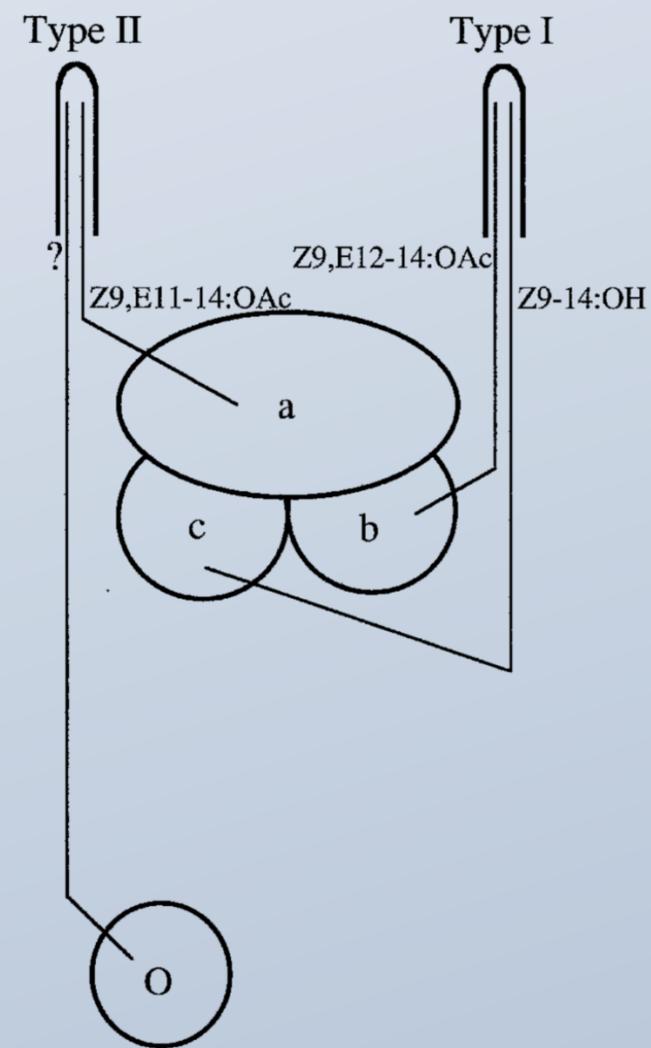
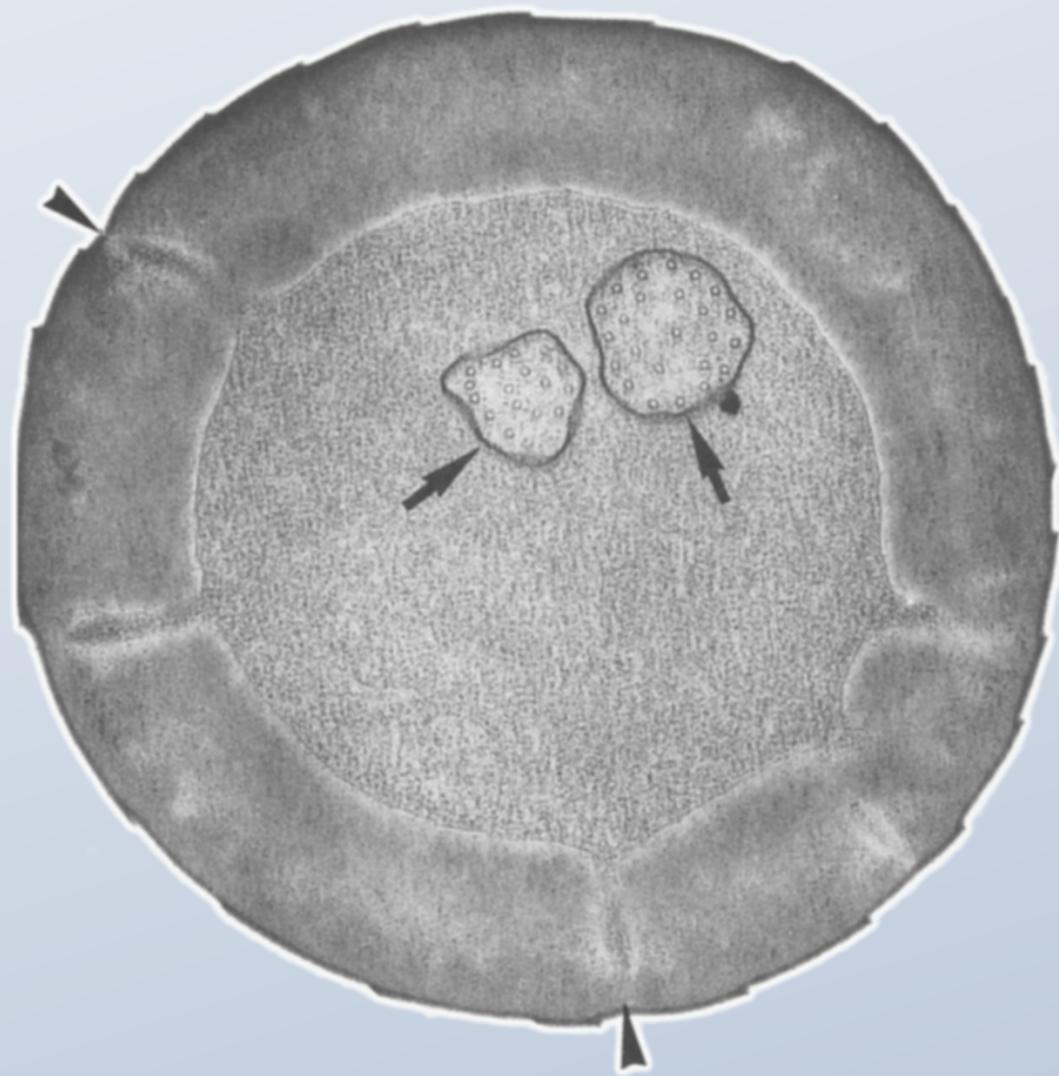
Extending the model

- Adaptable for different ratios: to what extent?
- How to extend it for more than two pheromone components?

An alternative model, based on subthreshold oscillations and coincidence detection



Adaptation for the wide dynamic range of pheromone concentrations



Ochieng SA, Anderson P, Hansson BS. *Tissue & Cell*, 1995, 27(2):221–32.

Thanks!