

Background

1. Recently [1] performed blind whole-cell patch clamp of MCs.
2. Spontaneous and odour-evoked activity were **inversely related**.
3. Cells with high baseline activity were often inhibited by odours.
4. **'Silent cells'** had low baselines while highly excitable by odours.

Model

1. Time discretized into O(1 sec.) bouts $t \in 1 \dots N$.
2. Each bout contains either odour or air.
3. Odours are sparse, high-dimensional.
4. $\text{Odour}_t = \text{unique features } \mathbf{x}_t + \text{common features } \mathbf{c}_t$.
5. Unique features are generated independently per bout.
6. Common features change slowly over bouts.
7. Animal observes dense, low-D receptor activations \mathbf{y}_t .
8. Animal MAP infers unique features from receptor history:
 $\text{argmax}_{\mathbf{x}_t} p(\mathbf{x}_t | \mathbf{y}_1, \dots, \mathbf{y}_t)$.

Key Ideas

1. Common features \mathbf{c}_t are high-D but are *not inferred*.
2. They are accounted for through their effect \mathbf{b}_t on receptors.
3. Projection to low-D receptor space suggests Gaussian dynamics.
4. MC baselines reflect **negative** of expected receptor activations.
5. In odour, baseline removes component due to common features.
6. Unique features remain, inferred by fast MC/GC dynamics à la [2].

