Computational and experimental approaches in neuronal morphogenesis and network formation

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Introduction

- Modeling dendritic morphological complexity
- Development of synaptic connectivity
- Spontaneous bioelectric activity in developing neuronal networks in vitro
- Balance of excitation and inhibition

Nervous system

- neurons
- synaptic connections
- neuronal networks

Cortical organization

- Cell bodies
- Dendrites and axons
- Synaptic connections
- Layers
- Excitation Inhibition



Neuronal morphological diversity



Cat deep layer Superior Colliculus neuron Schierwagen, J. Hirnforsch. 27 (1985) 670 Rat cerebellar Purkinje cell - Berry and Bradley Brain Res. 112 (1976) 1-35.

Shape parameters of dendritic branching patterns

- Number of segments
- Length of segments
- Diameter of segments
- Topological structure
- Curvature of segments
- 3D embedding



Cat deep layer superior colliculus neuron A. Schierwagen J. Hirnf. 27 (1986) 679 Modeling dendritic morphological complexity using principles of neuronal development

Quantification of dendritic morphological variability Source of morphological variability Morphological differences between cell types 'Design rules' of dendritic morphology Functional implications of dendritic shape characteristics

Axonal and dendritic outgrowth through growth cone elongation, branching, and retraction



Modeling dendritic morphological complexity

find minimal phenomenological rules for reproducing dendritic morphological complexity



Random selection of segment for branching



$$p_i \approx 2^{-S\gamma_i} / C$$

Selection probability of a terminal segment for branching depends on its centrifugal order

Topological variation due to random branching

S=0 p_i =1/n equal selection probabilities



Tree-type probabilities depend on mode of branching

Trees with 8 terminal segments



Branching in continuous time



Branching probability per unit of time of a tip:

- E: "competition parameter"
- S: modulation of order dependency

C: normalization factor

 $p_b(t) = D(t) \cdot n(t)^{-E} \cdot \left\{ 2^{-S\gamma} / C \right\}$

D(t): baseline branching rate $B(t) = \int_{0}^{t} D(s) ds$

Random branching sequences

E = 0 (no competition) \Leftrightarrow B = 3 D = B / 10 = 0.3 / day (constant)



Unrestricted proliferation of the number of terminal segments

Competition parameter E determines shape of terminal segment number distribution



Variation in terminal segment number

Matching between distributions of observed and model trees



Optimized branching parameters B and E



Growth function n(t) - influence of baseline branching rate function D(t)

$$\frac{dn(t)}{dt} = D(t)n(t)^{1-E} \qquad n(t) = [1+EB(t)]^{1/E} \qquad B(t) = \int_{0}^{t} D(s)ds$$
$$n(t \mid E = 0) = e^{B(t)} \qquad B(t) = \int_{0}^{t} D(s)ds$$



Growth curve for the number of tips n(t)

Rat multipolar nonpyramidal dendritic trees (Parnavelas, Uylings)

Growth function n(t) for

(a) constant basal branching rate D = 0.049

(b) exponential basal branching rate

 $D(t) = 0.3e^{-(t-1)/3.7}$



Segment length distributions

"Segment lengths determined by both neurite branching and elongation" Model approach: step 1: optimize branching process step 2: include elongation into mode

Model optimized on S1rat layer 2/3 pyramidal basal dendrites

> Branching: B = 3.85 E = 0.74 S = 0.87

Elongation: V_{be} = 0.22 µm/h V_{e} = 0.51 µm/h CV = 0.28

Empirical: $T_0 = -24 h$ $T_{be} = 240 h$ $T_e = 432 h$

This example for constant D

Growth of a model tree



Initial length after branching event

After branching event: S1-rat layer 2/3 Pyramidal basal dendrites 152-Lrequency branching 38 Daughter segments 72 24 48 96 0 start with zero length

Intermediate segments Terminal segments 44 33 22 11 80 160 240 320 400 120 0 Segment length



Daughter segments start with *initial* length



S1-rat layer 2/3 Pyramidal basal dendrites

Branching: B = 2.52 E = 0.73 S = 0.5

Elongation: $I_{in} = 6 \mu m$ $\sigma(I_{in}) = 5$ $v_{be} = 0.22 \mu m/h$ $v_{e} = 0.51 \mu m/h$ cv = 0.28

Empirical: $T_0 = 24 h$ $T_{be} = 240 h$ $T_e = 432 h$



Modeling guinea pig cerebellar Purkinje cell dendritic trees



Branching:		Observed trees		Model trees		
B = 95	Shape parameter	Mean	Sd	Mean	Sd	
E = 0.69	Degree	436	31.8	436	32	
S = -0.14	Asymmetry index	0.5		0.49		
	Centrifugal order	13.7	5.1	13.8	5.9	
Elongation:	Total length	9577	1105	9265	683	
α(l _{in}) = 0.7 μm	Terminal length	11.3	8.8	10.6	7.5	
l _{in} = 10.63 μm	Intermediate length	10.6	7.5	10.6	7.6	
σ(l _{in}) = 7.53	Path lenth	189.3	64.1	166	66	



Elongation by polymerization of tubulin



Tubulin model



$$\frac{dL_i}{dt} = a_i C_i - b_i$$

$$\frac{dC_i}{dt} = b_i - a_i C_i + \frac{D}{L_i + k} (C_0 - C_i) + fC_0 - gC_i$$

$$\frac{dC_0}{dt} = s - \sum_{i=1}^n \frac{D}{L_i + k} (C_0 - C_i) - \sum_{i=1}^n fC_0 - gC_0$$

Competition for tubulin



Competitive interactions among axonal terminal branc



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Development of synaptic connectivity

Developing neuronal networks show an overshoot in number of synaptic connections







Van Ooyen & Willshaw's model

"competition for target-derived neurotrophins"

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$$\frac{dC_i}{dt} = (k_{a,i}LR_i - k_{d,i}C_i) - \rho_i C_i$$
$$\frac{dR_i}{dt} = \varphi_i - \gamma_i R_i - (k_{a,i}LR_i - k_{d,i}C_i)$$
$$\frac{dL}{dt} = \sigma - \delta L - \sum_{i=1}^n (k_{a,i}LR_i - k_{d,i}C_i) / v$$

Effects of neurotrophins



Arjen van Oo

Innervation patterns



Arjen van Oo







Arjen van Oo

Spontaneous bioelectric activity in developing neuronal networks in vitro

Multi-electrode array





Long-term longitudinal recording of firing activity

Dissociated rat cortical culture on a multi-electrode array



mmin Pr P electrode number 5, man Mar mo All Time (days in vitro)

iling (#spikes / 4 hour)

sca

18 DIV

Active / quiescent phases and network bursts



Probabilistic structure of network bursts



Developmental changes in network bursts



Balance of excitation and inhibition

Chronic silencing of spontaneous activity induces disinhibition



Chronic suppression of spontaneous activity increases the excitation / inhibition ratio



Working hypothesis: activity-dependent regulation of excitatory and inhibitory network development

