Spatial Statistics for Langerhans Cells



Fig. 7. Variation over time of Langerhans cells within an incubated epidermal sheet in MEM (stained with fluorescent-labeled monoclonal antibody for CD1a). N, r2 and HSI indicate the cell number, mean of nearest neighbors, and Hopkins-Skellam index, respectively. Each map is a 250-µm square. A revised figure, cited from Numahara *et al.* (1994b).



Fig. 8. Voronoi tessellations for the pattern of ATPase-stained epidermal Langerhans cells (guinea pigs). Each rectangle has an area of $400 \times 250 \mu m$. A revised figure, cited from Numahara *et al.* (2001).

adjust the position of their territorial centers until a stable set of boundaries is obtained.

(II) Random packing model of territory: a new individual arrives after the former occupants have established their territories; in asynchronous settlement, adjustment of the centers does not occur.

(III) Poisson model: a set of points distributed at random. Tanemura and Hasegawa (1980) also investigated distributions of the number of edges of the Voronoi polygons in the three models.

Numahara *et al.* (2001) counted and compared the number of edges of the 315 Voronoi polygons on the five epidermal Langerhans cell maps (Fig. 8) with the models. We chose the random packing model for the process of spatial distribution by statistical tests. Langerhans cells begin to appear in the epidermis by 7 weeks of gestation. Through pattern formation, a new Langerhans cell may arrive after the former Langerhans cells have established their coordinates. The natural course also reinforces the selected model. **2.6 Repulsive potential function**

The main aim of point process statistics is to understand and describe the short-range interaction among the points (Illian *et al.*, 2008). Ogata and Tanemura (1984) discussed a class of repulsive potential functions, and provided an approximation method.

The model functions are:

(i) very-soft-core potential (V-S-C),

$$\Phi\sigma(r) = -\log[1 - \exp(r/\sigma)^2],$$