Date: 10/21/10

To: SG2

From: Noel Cressie

Re: Grain-germ (growth-attrition) model (2 pages) - AN UPDATE

My 8/13/10 memo has been rewritten and extended to be consistent with notation in Cressie (1993), SSD, pp. 753-802. Warning: The notation here is different from the 8/13/10 memo.

Consider $\mathbf{s} \in A$, a spatial domain of interest (e.g., North America) and $t = t_0, t_0 + 1, \ldots$, where t_0 is the start time of the process (e.g., $t_0 = 8402$, the first of a sequence of 3-hourly intervals in 1970). Let $X_t \subset A$ denote the union of all pixels above the thresholds, $\{k(\mathbf{s}): \mathbf{s} \in A\}$. That is, if $Y_t(\mathbf{s})$ is the rainfall in pixel \mathbf{s} at time t, then

$$X_t \equiv \{\mathbf{s} \colon \mathbf{s} \in A \text{ and } I(Y_t(\mathbf{s}) > k(\mathbf{s})) = 1\},$$

where $k(\cdot)$ is given and $I(\cdot)$ is the indicator function. We would initially like to model

$$X_{t+1}$$
 given X_t ,

but later we could also model rainfall amounts in these exceedance regions.

Let $\{\mathbf{x}_{ti}: i=1,2,\ldots,n_t\}$ denote the individual pixels in X_t . That is, $\mathbf{x}_{ti} \in X_t$ iff

$$I(Y_t(\mathbf{x}_{ti}) > k(\mathbf{x}_{ti})) = 1; \quad i = 1, ..., n_t.$$

Let $\{\mathbf{v}_t(\mathbf{s}) \colon \mathbf{s} \in A\}$ denote the velocity vectors (in km/hr) given by NARCCAP at time t. Then

$$\mathbf{u}_t(\mathbf{s}) \equiv 3\mathbf{v}_t(\mathbf{s})$$

is a displacement vector. Define the sets,

$$L_t(\mathbf{s}) \equiv \{c\mathbf{u}_t(\mathbf{s}) \oplus \mathbf{s} : -1 < c < 1\}; \quad \mathbf{s} \in A,$$

and

$$M_t \equiv \bigcup \{L_t(\mathbf{x}_{ti}) \colon i = 1, \dots, n_t\}.$$

Alternatively, M_t could be defined by using some fraction, f, of the threshold:

$$M_t \equiv \{ \boldsymbol{\omega} : \boldsymbol{\omega} \in A \text{ and } I(Y_t(\omega) > f \cdot k(\boldsymbol{\omega})) \}; \quad 0 \le f < 1.$$

Now use "Bernoulli thinning" on M_t . After thinning, denote the resulting set as D_t ; that is, each pixel is or is not in D_t according to iid Bernoulli random variables with probability p_t ; $t = t_0, t_0 + 1, \ldots$ Denote

$$D_t \equiv \{\mathbf{s}_{t,j} \colon j = 1, \dots, |D_t|\},\,$$

where $\{\mathbf{s}_{t,j}\}$ are the "germs" (foci of growth). The "grains," $\{Z_{t,j}\}$, are iid random sets (here, they are random vectors centered at $\mathbf{0}$ with random length and random orientation). That is,

$$\{Z_{t,j}: j=1,\ldots,|D_t|\}$$
 are iid as Z_t .

Finally,

$$X_{t+1} \equiv \bigcup \{Z_{t,j} \oplus \mathbf{s}_{t,j} \colon j = 1, \dots, |D_t|\},$$

which we can write as $X_{t+1} \equiv \{\mathbf{x}_{t+1,i} \colon i = 1, \dots, n_{t+1}\}$. (Define $A \oplus B \equiv \{\mathbf{a} + \mathbf{b} \colon \mathbf{a} \in A, \ \mathbf{b} \in B\}$.)

Hence, attrition can occur if p_t is small and $|Z_t|$ is small. Growth can occur if $|Z_t|$ is large. Notice that M_t expands the set of possible pixels, and then the thinning field is used to randomly delete some of these pixels. This describes a type of "birth and death" process.

Notes

- 1. Data are the sequence, $X_{t_0}, X_{t_0+1}, \ldots$
- 2. Given the dynamical nature of the model, we should be able to estimate p_t , $E(|Z_t|)$, and $var(|Z_t|)$ from the pair (X_t, X_{t+1}) ; $t = t_0, t_0 + 1, \ldots$
- A reference for this type of model in a cancer-cell-growth context is:
 Cressie, N. and Hulting, F.L. (1992). A spatial statistical analysis of tumor growth.
 Journal of the American Statistical Association, 87, 272-283.
 More details can be found in Cressie, N. (1993). Statistics for Spatial Data, rev. edn.,
 Wiley, NY, pp. 753-802.
- 4. The hitting function is given by (9.7.4) on p. 777 of Cressie (1993). Choice of K in that formula is determined by whether a closed-form calculation of (9.7.4) is possible. I suggest starting with K equal to a vector of length ℓ and orientation θ . Then $\check{Z} \oplus K$ will be parallelogram.