**Tuesday, 1 November 2005**
**240h**

# Probability Model-Based Analysis of Tumor Vasculature Data

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In a comprehensive study of the microvascular architecture of human primary tumors and their precursor lesions, Konerding and co-workers (2001), obtained data from 3-D scanning electron micrographs of corrosion casts of colorectal adenocarcinomas and normal (control) mucosa. They characterized the vascular network architecture by the following quantities:

• Intervessel distance (microns);

• Interbranch distance (microns);

• Vessel diameter (microns);

• Branching angle (degrees);

each of which admits of a distribution of values for each patient in the study. The complete data set (Konerding, 2004) contains measurements of these quantities for

1. normal colorectal mucosa (as control), and

2. colorectal adenocarcinomas, taken at three different locations within the tumor:

(a) Tumor center

(b) Luminal tumor surface

(c) Tumor periphery

A key objective of the study is to identify and quantify any systematic differences that may exist between normal mucosa vasculature and that of adenocarcinoma at various locations within the tumor. Because each vascular network characteristic variable naturally admits of a distribution of values (an intrinsic physiological property), the observed variability in the data is due to intrinsic physiology far more than to the traditional “measurement” or “process” noise. One must therefore be careful in applying to such data, standard data analysis techniques where observed variability is assumed to be due solely to “measurement” or “process” noise.

In this presentation we discuss a probability model-based approach to the analysis of the data, presenting results for Intervessel distance (IV) data and Branching Angle (BA) data. First we present arguments for why the lognormal probability density function (pdf) is appropriate for IV distance, but the Beta pdf is more appropriate for BA. We confirm the adequacy of these models for normal vasculature data and then develop appropriate models for the corresponding tumor vasculature data. We will show in the presentation how such a probability model-based approach is able to detect differences that are undetectable by standard statistical tests. Specifically we will show how standard tests detect no significant differences in the branching angle data between the individual tumor areas whereas the probability model-based technique shows quite distinctly

the differences that exist.

**References**.

1. M.A. Konerding, E. Fait, and A Gaumann, “3D microvascular architecture of pre-cancerous lesions and invasive carcinomas of the colon,” British Journal of Cancer, 84 (10), 1354–1362, 2001.

2. M.A. Konerding, Personal Communications, June 2004.

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