

広島統計談話会  
Hiroshima Statistics Study Group

第 289 回談話会を下記のように開催致しますので  
御参集下さいますようご案内申し上げます。

You are cordially invited to the 289<sup>th</sup> meeting as scheduled below.

日 時 : 2015 年 1 月 23 日 (金) 15:00 –  
Date : January 23rd, 2015 (Fri) 15:00 –  
場 所 : 放射線影響研究所 比治山ホール  
Place : RERF Hijiyama Hall  
演 者 : インガ コッホ 博士 (アデレード大学 数理科学研究科 准教授)  
Speaker : Inge Koch, Ph.D.  
Associate Professor  
School of Mathematical Sciences  
The University of Adelaide, Australia  
演 題 : 「プロテオーム質量分析の空間データ解析」  
Title : “Analysis of Spatial Data from Proteomics Imaging Mass Spectrometry”

要 約 :

**Summary:**

Mass spectrometry (MS) has become a versatile and powerful tool in proteomics for the analysis of complex biological systems. Unlike the common MS techniques the more recent imaging mass spectrometry (IMS) preserves the spatial distribution inherent in tissue samples. IMS data consist of tens of thousands of spectra measured over a large range of masses, the variables. Each spectrum arises from a grid point on the surface of a tissue section. Motivated by the requirements in cancer research to differentiate cell populations and tissue types of such data accurately and efficiently, we propose a combined cluster analysis and feature extraction approach and we illustrate this approach on IMS data obtained from tissue sections of patients with ovarian cancer.

The selection of mass variables which distinguish cancer tissue from non-cancerous tissue regions -- or responders from non-responders -- is an important step towards identification of biomarkers. Standard k-means clustering of the raw IMS data does not lead to interpretable cluster maps. We focus on the derived binary mass data and develop a combined cluster analysis and feature extraction approach for these data. Our approach exploits the Difference In ProPortions of occurrence (DIPPS) statistic of subsets of data in the selection and ranking of variables.

We apply these ideas to the cancer and non-cancerous regions of patient tissue sections, and we summarise the variables which best characterise cancer tissue in a single image which has a natural interpretation.

Comparisons of DIPPS maps and their associated ‘cancer’ variables for tissue samples from different cancer patients demonstrates the similarity or diversity of cancer tissue for different patients.