Conclusion: Mean substitution and multiple imputation performed equally well in dealing with missing data generated by TMA. Complete case analysis, the usual default method for statistical software, resulted in the least accurate and least precise estimates. Given the ease of implementing MS or MI, either approach should be preferred to CCA.

doi:10.1016/j.ejcsup.2010.06.020

O-20 RATES OF GROWTH OF BREAST CANCER

R.W. Blamey, G. Ball, I.O. Ellis. *Nottingham City Hospital, Nottingham, UK*

Many estimates of growth rate have been published, mostly theoretical. Here 3 clinically based measurements have been used to produce curves of growth from inception (one cell) to 7 cm diameter for each grade.

1. Screening effect – In a trial of screening an excess of tumours were screen diagnosed by the end of the trial period. Time for excess to present was calculated as G3 3–6 months, G2 1–2 years and G1 5–6 years. The mean sizes by method of detection allowed volume doubling times to be calculated.
2. Occult time for inception to diagnosis – In young women there is an excess of G3's and few G1's. Assuming that inception by age is constant, graphs of actual detection rates at each age and of expected allows calculation of the times for which each grade is occult.
3. Time from primary treatment to death from breast cancer – Plotting times to death gives medians for G3 167 months, G2 98 and G1 50.
4. As tumours enlarge mitoses become concentrated in the outer 2 mm 'shell'.[1]
5. These observations allow curves of volume to be drawn for each grade from single cell inception from which cell doubling is assumed, giving a curve increasing logarithmically. From 10 mm diameter growth begins to slow logarithmically with cell doubling restricted to the outer shell.

Reference:

1. Connor AJM et al. *Breast* 1997;**6**:171–6.

doi:10.1016/j.ejcsup.2010.06.021

O-21 DETECTION AND QUANTIFICATION OF MicroRNAs IN LASER MICRODISSECTED FORMALIN-FIXED PARAFFIN EMBEDDED (FFPE) BREAST CANCER TISSUES

Sarkawt M. Khoshnaw [a], Des G. Powe [a], Jorge S. Reis-Filho [b], Ian O. Ellis [a], Andrew R. Green [a]. [a] *Department of Histopathology, University of Nottingham and Nottingham University Hospitals, Nottingham, UK.* [b] *Breakthrough Breast Cancer Research Centre, Institute of Cancer Research, London, UK*

MicroRNAs (miRNAs) are a class of endogenous non-coding RNAs that target protein coding mRNAs for cleavage or translational repression. Both profiling and functional studies demonstrate deranged miRNA expression in many human cancers including breast tumours. Research in this field is increasing and the potential of miRNAs for being used in clinical settings emphasises the need for sensitive detection techniques.

In this study, techniques for the analysis of miRNA expression in microdissected FFPE breast cancer tissues were developed and optimised. Full face sections from three invasive breast tumour samples and different microdissected areas (1000–10 million $l\mu^2$) and section thickness (10–20 $l\mu$) were analysed. Total RNA was extracted using commercially available RNA extraction kits (miRNeasy FFPE Kit, Qiagen; RecoverAll™ Total Nucleic Acid Isolation Kit for FFPE, Ambion; PureLink FFPE RNA Isolation Kit, Invitrogen). Three miRNAs (miR21: highly expressed, miR-29c: intermediately expressed, and miR-127: low expression in breast cancer) extracted from both gross and microdissected invasive breast cancer tissues were quantified using real-time PCR.

The PureLink kit produced largest quantities of total RNA from FFPE breast tumours. All three miRNA (21, 29c and 127) were successfully detected by real-time PCR and levels of sensitivity were comparable between extraction methods. Our data showed that relative miRNA levels gradually decreased with diminishing amounts of microdissected tissue used but reliable miRNA quantification was obtained using at least 5 million $l\mu^2$ from 20 $l\mu$ thick FFPE breast tissue sections.

In contrast to previously published results, quantity of miRNA detected in breast tissue samples depends on the amount of tissue used, and cannot be performed reliably from one or a few cells.

doi:10.1016/j.ejcsup.2010.06.022

O-22 A NOVEL ARTIFICIAL NEURAL NETWORK BASED ALGORITHM TO ANALYSE THE INTERACTION PATTERNS EXISTING IN GENE MICROARRAYS: AN APPLICATION TO BREAST CANCER GENOMIC DATA

Christophe Lemetre, Lee James Lancashire, Graham Roy Ball. *Nottingham Trent University, UK*

Genomic array technologies, by allowing the assessment of the level of expression of thousands of genes simultaneously in the same experiment, have brought the hope to identify new biomarkers related to particular outcome in disease. The majority of the research conducted to date with gene microarrays has only been focusing on this biomarker discovery. However, these arrays hold the inherent information of gene co-expression patterns and only few groups have focused their attention toward deciphering such network of interactions and regulation.

We present here a novel approach based on Artificial Neural Network technology to further analyse the data extracted from gene array experiments. This approach has been applied to a well-known breast cancer dataset publicly available.[1] The results showed interesting patterns of interactions or gene regulation, and some of them could be confirmed by alternative methods,