**ABSTRACT INSTRUCTIONS (delete before submitting)**

Head the abstract with the title; authors; and affiliation(s).

Each of these should be on a separate line. **No abstract should exceed 300 words.**

Abstracts should contain a statement of the problem, brief methods, clear results, and a statement of the conclusions or significance of the findings. Abstracts will be reviewed and may be returned to the authors for modification.

**Abstract Title – Bold, font size 14**

**Automatic PCA-based lung lobe segmentation from CT scans**

**Authors – font size 12, with presenting author underlined.**

Zhang, Y.1, Osanlouy, M.1, Clark, A.R.1, Hoffman, E.A.2, Tawhai, M.H1

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**Main text – font size 12, justified, single line spacing**

Human lungs are divided into five distinct anatomical regions, which are called the pulmonary lobes. The left lung consists of the left upper lobe and left lower lobe, while the right lung consists of the right upper lobe, right middle lobe and right lower lobe. The identification of these lobes is of great importance in applications of lung disease assessment and treatment planning. However, to find an effective and time-saving automatic lobe segmentation method is a challenging task because of anatomical variation and incomplete fissures. The current published lung lobe segmentation methods usually heavily rely on anatomic knowledge and largely ignore individual variability. This sometimes lead to a segmentation failure for some pathological lungs which have abnormal anatomic structures and fuzzy appearance of fissure locations.

In this study, we plan to use a statistical shape models (a PCA average model) to help with the lung lobe segmentation. Through deforming the average lobe model, we will be able to predict an approximate fissure locations, this will provide us a ROI of fissures without dependence of other anatomic structures such as airways and vessels. Then, an eigenvalue of Hessian matrix analysis and connected component eigenvector based analysis were used to get a set of candidate fissure points. The results showed the method can

When we genotyped these SNPs in many subjects, no heterozygotes were observed, despite the use of multiple PCR-based methods and several different primer pairs. Experiments with mixing the genomic DNA from different individuals proved that the assays were capable of detecting both alleles simultaneously. This indicates that the observed homozygosity was likely resulting from consistent allelic dropout of one allele in every subject.

It is possible that the DNA (CpG) methylation likely to occur on the imprinted allele could play a role in altering the outcome of genotyping results; however, this phenomenon alone cannot explain the pattern of allelic dropout. Therefore we examined the region containing the three SNPs for evidence of secondary structures that might also be a factor in allelic dropout. The region is GC-rich, and using several prediction algorithms[2](file:///C:\\Users\\jade\\AppData\\Local\\Microsoft\\Windows\\Temporary%20Internet%20Files\\Content.Outlook\\G1ED47IK\\QMBAbstractTemplate2013.doc" \l "_ENREF_2" \o "Huppert, 2005 #8941), [3](file:///C:\\Users\\jade\\AppData\\Local\\Microsoft\\Windows\\Temporary%20Internet%20Files\\Content.Outlook\\G1ED47IK\\QMBAbstractTemplate2013.doc" \l "_ENREF_3" \o "Kikin, 2006 #8943) it appeared likely that it has a propensity for forming G-quadruplex (G4) structures. These arise from the formation of G-tetrads by hydrogen bonding of four G residues, either within or between strands, and the subsequent stacking of these into higher order structures. We hypothesized that DNA methylation may interact to stabilize such secondary structures and block the *Taq* polymerase from actively replicating one template strand.

**Optional references – font size 10, Calibri. Title in Italics**

1. Stuffrein-Roberts, S., *Allelic expression patterns in psychatric candidate genes. PhD Thesis* in *Pathology*. 2008, University of Otago: Christchurch. p. 216.

2. Kikin, O., L. D'Antonio and P.S. Bagga (2006). *QGRS Mapper: a web-based server for predicting G-quadruplexes in nucleotide sequences.* Nucleic acids research. 34: W676-82.