Analysis of dDNP NMR metabolic data from cancer cells (- poster)

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Analysis of dDNP NMR metabolic data from cancer cells


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To prevent unnecessary and expensive treatment of benign prostate cancer, more sensitive tools are needed. Metabolomics combined with datamining have shown great potential for locating motifs and biomarkers for prostate cancer. [1]

The aim of this project is to use metabolic data to distinguish between aggressive and benign prostate cancer cell lines. Four cell lines are analysed: PC3 and DU145 (aggressive), and Ln-Cap and PNT1a (non-aggressive).

Cells were incubated for 30 minutes with 13C6-d7 isotope labeled glucose, before metabolites were harvested and hyperpolarized with dissolution Dynamic Nuclear Polarization (dDNP). This technique has been shown to be quantitative and reproducible. [2] From the resulting spectra, integrals of peaks were measured and two dataset were generated. One with standardized peak values for each peak outside the glucose area (peak data) and one where these peaks were collected to metabolites (met. data).

Random Forest Feature Extraction

Random Forest (RF) analysis was used to examine what features are important for differentiating between the cell lines. Results are shown in fig. 3 below.

Biomarkers and classification

Random Forest (RF) analysis was used to examine what features are important for differentiating between the cell lines. Results are shown in fig. 3 below.

These results show a great potential for classification of aggressiveness in prostate cancer by a PC-DFA model trained on dDNP NMR metabolomics data. RF can be used to identify biomarkers through feature extraction, and feature extraction can additionally be used for limiting the number of features used for training the PC-DFA model, possibly making a it more predictive and less likely to overfit. Future work could be to obtain metabolic fingerprints from prostate cells taken from biopsies on cancer patients, to investigate if the model also works on non-lab cell strains.

References: