



RamAn – not as delicious,
but at least as versatile



Raman Spectroscopy for label-free cell type identification

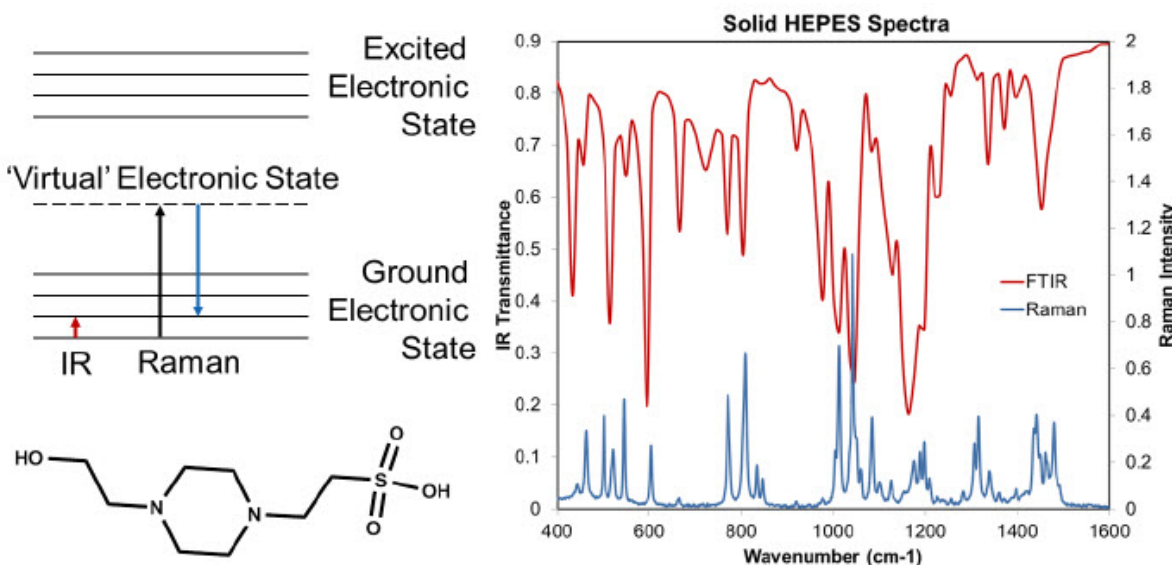
Johanna Schaffenrath

Technical Journal Club

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What is Raman scatter?

- Raman = indirect measure of the vibrational spectrum (FTIR = direct vibrational absorbance)
- Raman spectroscopy exposes the sample to monochromatic light → some of the scattered light is shifted to a lower energy, since some molecules in the sample got a higher vibrational state.
- Raman scattering increases with light energy (but more background)



How is the data collected and analyzed?

Components:

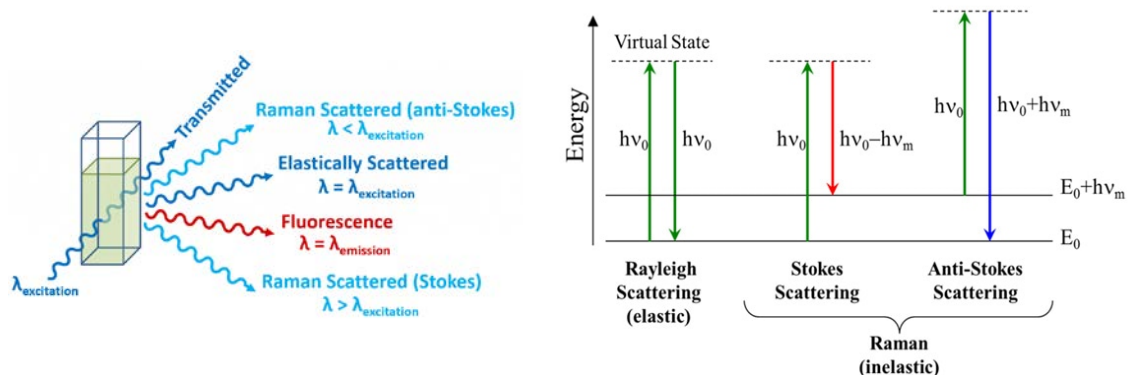
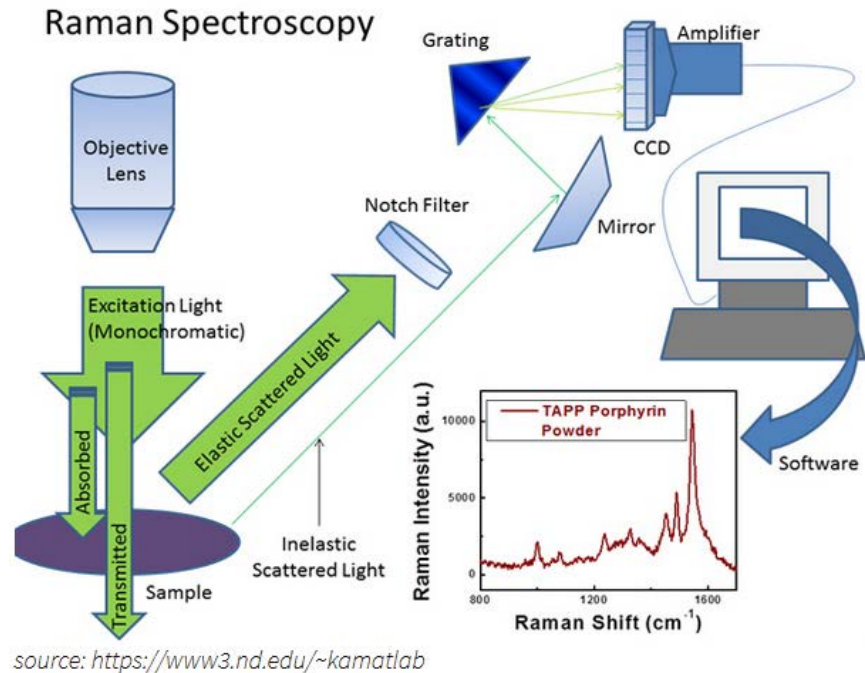
- laser
- sampling interface
- spectrometer

Laser characteristics:

- small form factor
- low power consumption
- narrow linewidth
- stable power output
- stable wavelength output

Setup characteristics:

- TE cooled spectrometer to collect weak signal with reduced noise
- Thinned CCD camera for higher sensitivity
- High resolution spectrometer to resolve closely spaced peaks (standard lasers: 785nm, 532nm)

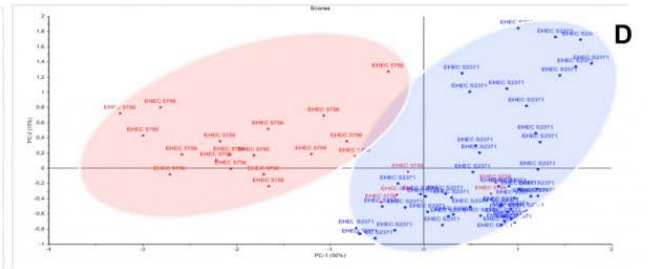
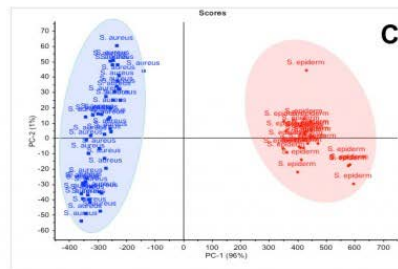
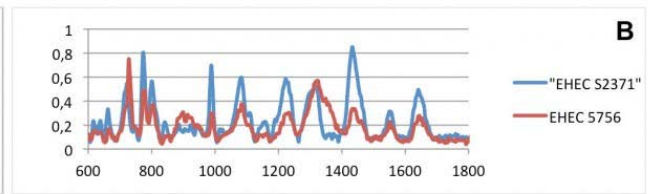
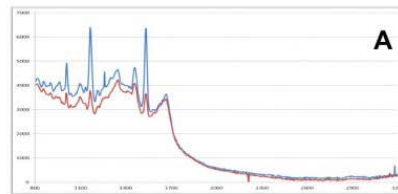


How is the data collected and analyzed?

Data analysis:

- preprocessing stage: reducing the effect of unwanted signals

- cell media,
- glass substrate,
- fluorescence,
- detector noise,
- calibration errors,
- cosmic rays,
- laser power fluctuations



- Multivariate data analysis

- Unsupervised methods
- Supervised methods

- Classification models

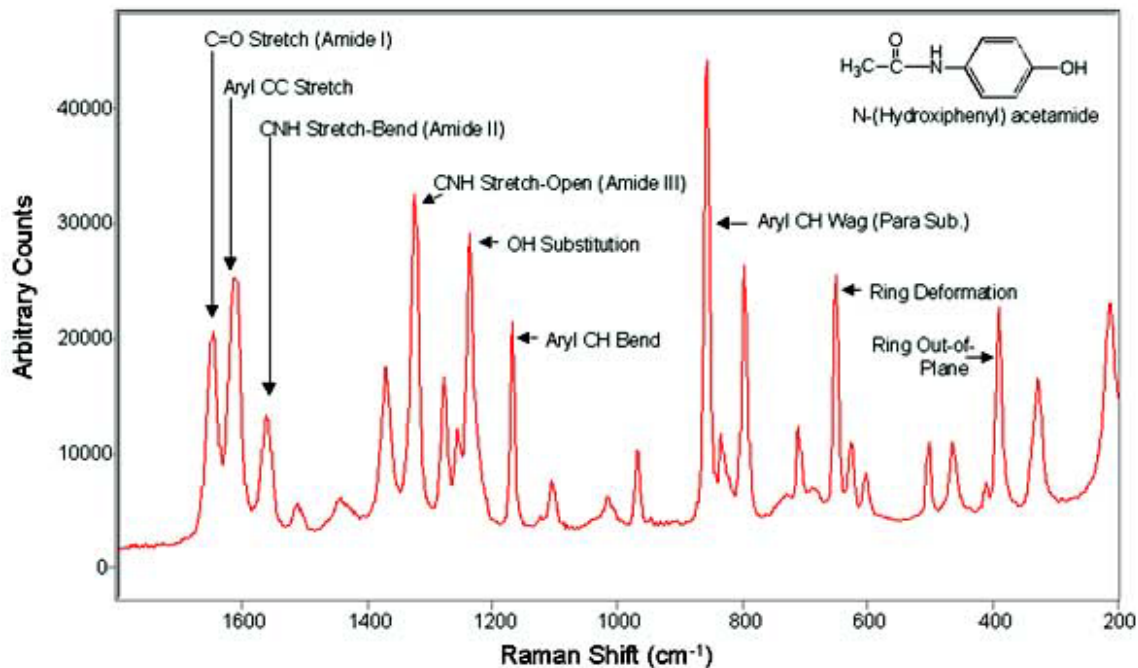
- Linear Discriminant Analysis (LDA)
- Soft Independent Modeling of Class Analogy (SIMCA)
- Artificial Neural Networks (ANN)
- Support Vector Machines (SVM)

- Statistics

How to interpret a Raman spectrum?

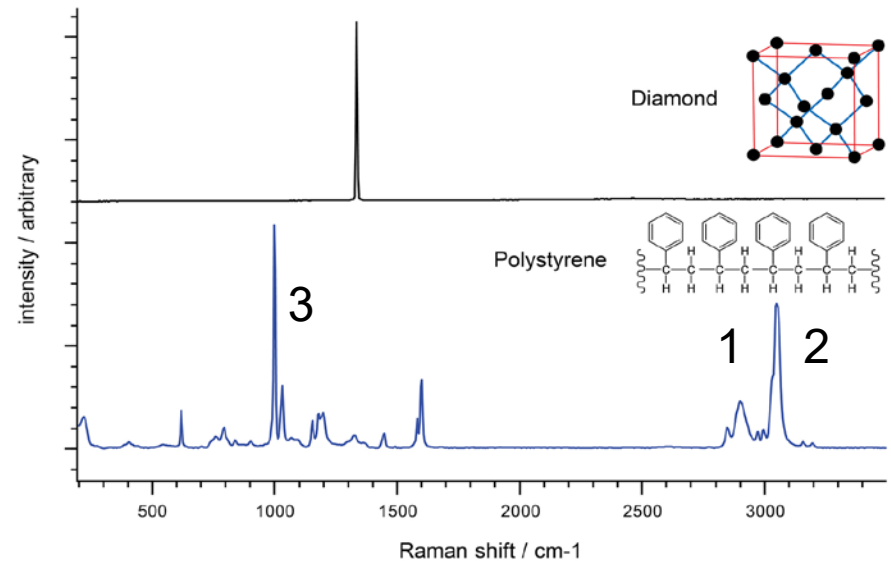
- Photons are forced to leave their straight path by interaction with sample
- Laser light interacts with molecular vibration causing up/downshift of laser energy
- Bonds in the sample can be identified by analyzing the energy shift
- Spectrum is unique to a material → good for identification of compounds

Functional group	Region
C—C	~600-1300 cm^{-1}
C=C	~1600 cm^{-1}
C≡C	~2100-2300 cm^{-1}
C—H	~2700-3100 cm^{-1}



How to interpret a Raman spectrum?

- Polystyrene: less symmetric molecule with hydrogen and carbon & different bond types – vibration frequencies depend on atom mass and bond strength:
 - heavy atoms, weak bonds = low Raman shift
 - Light atoms, strong bonds = high Raman shiftC-H vibration $\sim 3000\text{ cm}^{-1}$ and C-C $\sim 800\text{ cm}^{-1}$, C=C $\sim 1600\text{ cm}^{-1}$,
- strength of bonds affects vibration
 - C-H vibrations 2900 cm^{-1} : aliphatic carbon chains (1)
 - C-H vibrations 3050 cm^{-1} : aromatic carbon rings (2)
 - Vibrations at 1000 cm^{-1} : whole aromatic carbon ring vibration (3)
- Diamond: crystals with regular identical atoms in same configurations



How can Raman spectroscopy be used?

Fields:

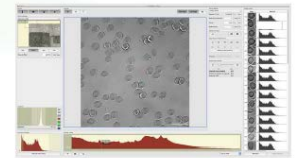
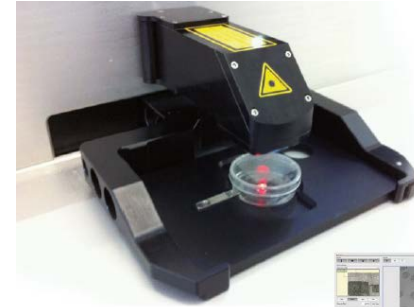
- material science
- food industry
- medicine
- analytical chemistry
- Forensics etc.

Analysis of:

- different cell states (e.g. cancer research)
- rare cell analysis
- interactions (cell-compound)
- toxicology
- questioned documents
- biological samples
- trace analysis
- explosives and GSRs etc.

Advantages for life science:

- Stable/good cell viability
- no changes applied e.g. cells for therapies can be sorted without alterations
- Cultured tissue can be analyzed without disruption
- Small sample volume
- rare cells identification
- 785nm laser for biological samples → no cell damage, minimally absorbed by aqueous solutions



Graft from autologous cartilage biopsy material

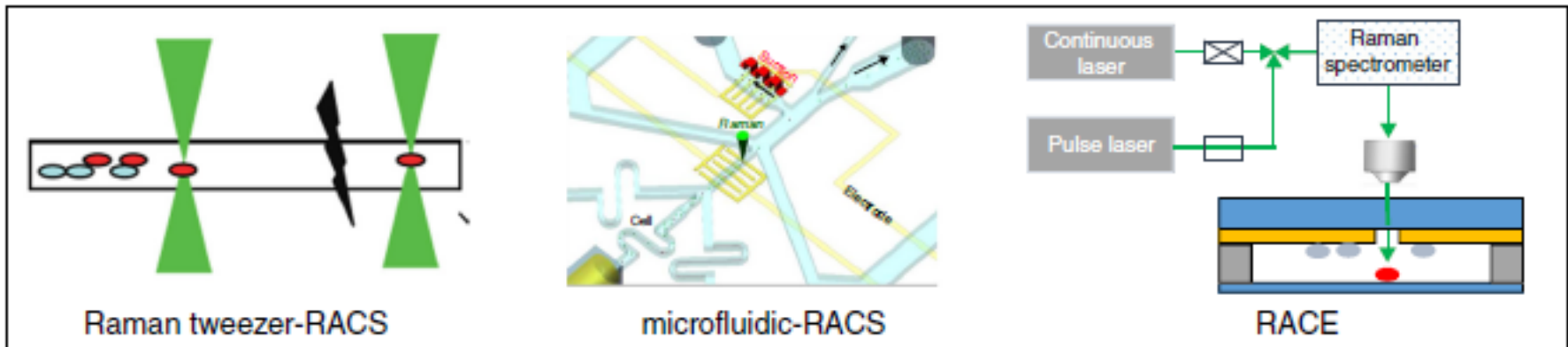


Raman based cell sorting

Raman-activated cell sorting (**RACS**):

- No need for external labelling
- Consists of single cell Raman spectra analyzer (SCRS) & a cell isolation system
 - in solution (Raman tweezers)
 - in flow (microfluidic based RACS)
 - on a surface (Raman activated cell ejection — RACE)

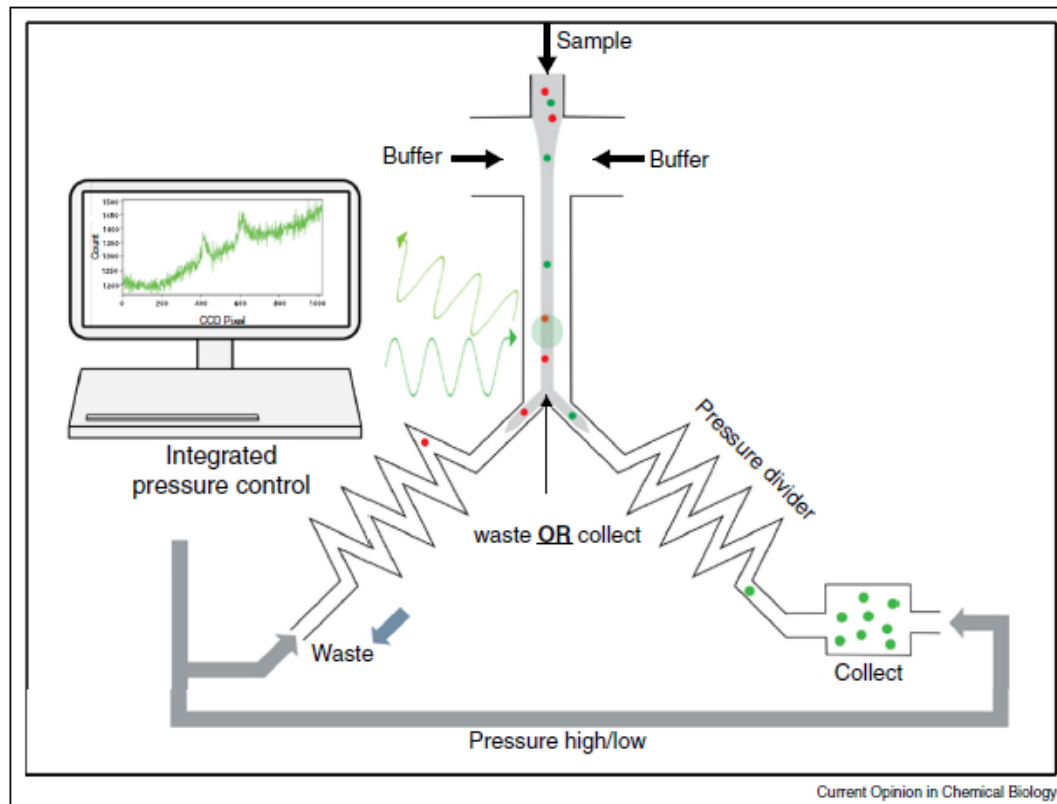
RACS in solution: Optical tweezers - highly focused laser beam gives attractive or repulsive force to hold and move neutral objects



Raman based cell sorting

trap-free RACS in flow (microfluidic based):

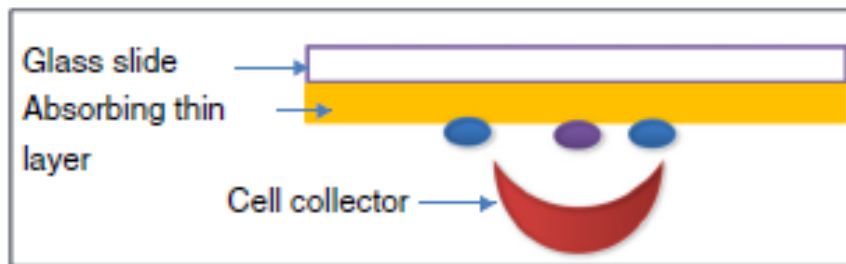
- simple hydrodynamic focusing
- pressure switch mechanism to sort individual cells based on Raman signals



Raman based cell sorting

On a surface: Raman activated cell ejection (RACE)

- to maintain spatial organization of cells & to understand interactions and functions
- RACE can isolate cells of interest in their biological niches
- 337 nm pulsed laser used to isolate single cells by laser induced forward transfer (LIFT)
- Cells are mounted on specific slide coated with laser absorbing material & can be ejected using LIFT



Fluorescence vs. Raman activated cell sorting

FACS:

- External labelling – requires previous knowledge of the sample
- Information restricted (Abs, lasers, physical parameters)
- Cells in suspension
- Fast (up to 5000 cells/s)

Raman tweezer RACS:

- External label free (maybe intrinsic stable isotope labelling) – no pre-knowledge needed
- Information about biochemical and metabolic features (lipids, proteins, carbohydrates, nucleic acids..)
- Cells in suspension
- Slow (~3min/cell)

Microfluidic RACS:

- Slow (5-100 cells/s)

RACE:

- Cells in suspension, tissue, attached to solid surface
- 1cell/s

(Coherent anti-Stokes Raman spectroscopy (CARS) and stimulated Raman scattering (SRS) overcome naturally weak signal of spontaneous Raman scattering and significantly shortening Raman acquisition time)

Raman spectroscopy for cell identification

Meso-Raman approach for rapid yeast cells identification

Martina Alunni Cardinali^a, Debora Casagrande Pierantoni^b, Silvia Caponi^{c,*}, Laura Corte^b,
Daniele Fioretto^{a,d}, Gianluigi Cardinali^{b,d}

^a Department of Physics and Geology, University of Perugia, via Pascoli, I-06123 Perugia, Italy

^b Department of Pharmaceutical Sciences, University of Perugia, via del Liceo 1, I-06123 Perugia, Italy

^c Institute of Materials, National Research Council (IOM-CNR), Unit of Perugia, c/o Department of Physics and Geology, University of Perugia, Via A. Pascoli, I-06123 Perugia, Italy

^d CEMIN-Excellence Research Center, University of Perugia, via Pascoli, I-06123 Perugia, Italy



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Raman micro-spectroscopy for accurate identification of primary human bronchial epithelial cells

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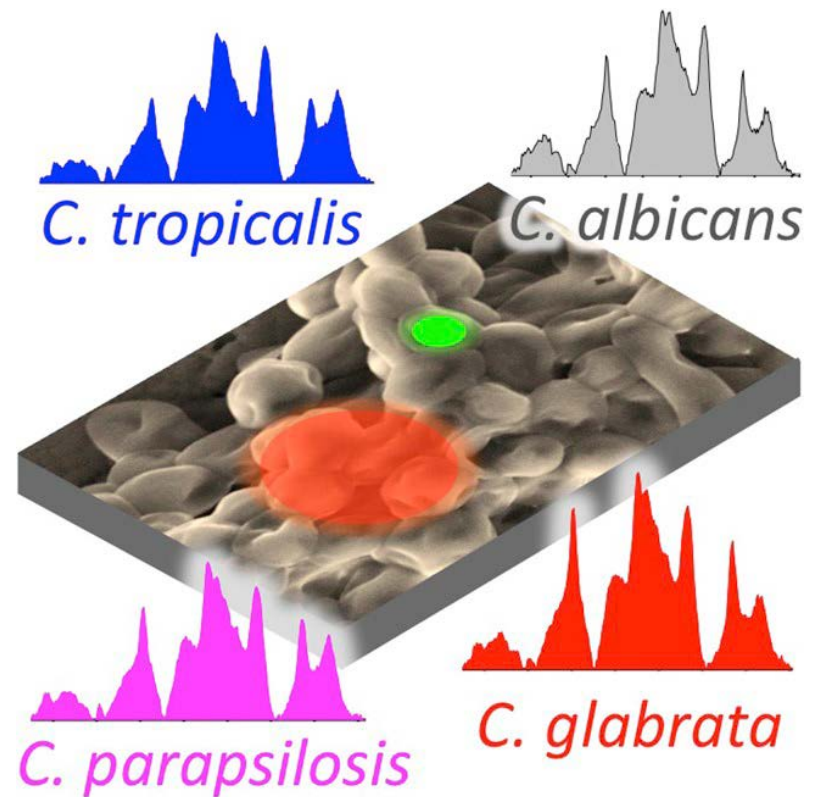
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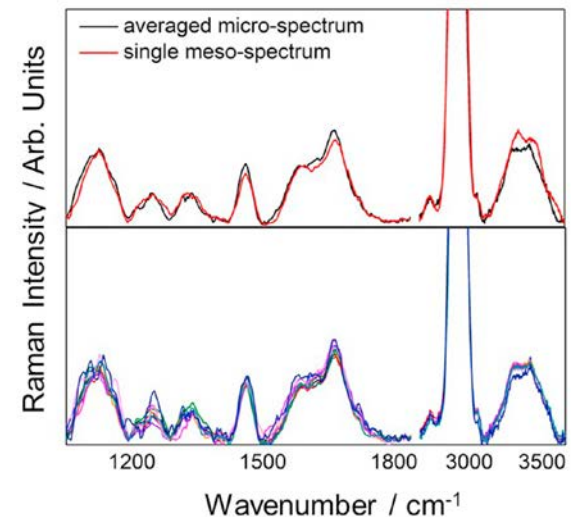
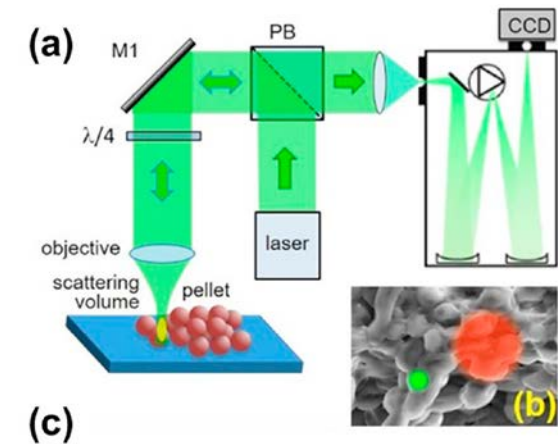
Meso-Raman approach for rapid yeast cells identification

- A meso-Raman approach for yeast cell identification
- Unpolarized and Depolarized Raman Spectra for PCA analysis
- Future efficient and reliable protocol for medical diagnosis in clinics



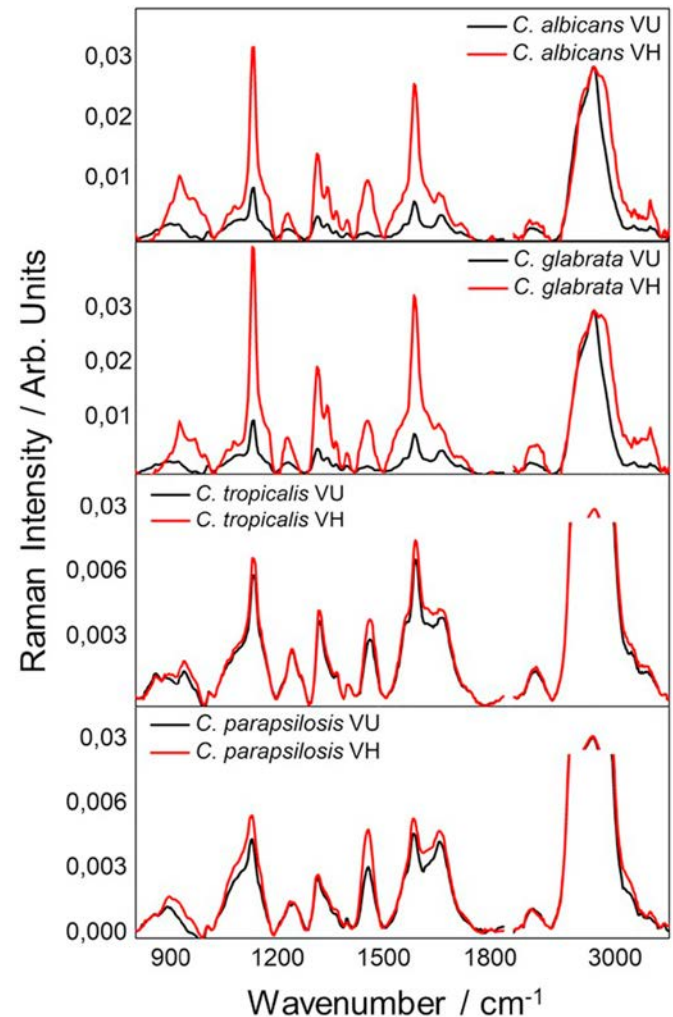
Setup and comparison of micro- and meso Raman spectra

- Schematic of the Raman spectroscopy setup
 - 532nm laser
 - Spectra in unpolarized (VU) and depolarized (VH) configurations
- SEM micrograph of the *C. albicans* film
 - Green dot: 2 μm spot of the 20mm lens
 - Red dot: 8 μm spot of the 30mm lens
- Lower panel: ten spectra a yeast cells film using the 20mm objective lens
- Higher panel: comparison between average of ten spectra and single spectrum collected by the 30mm lens



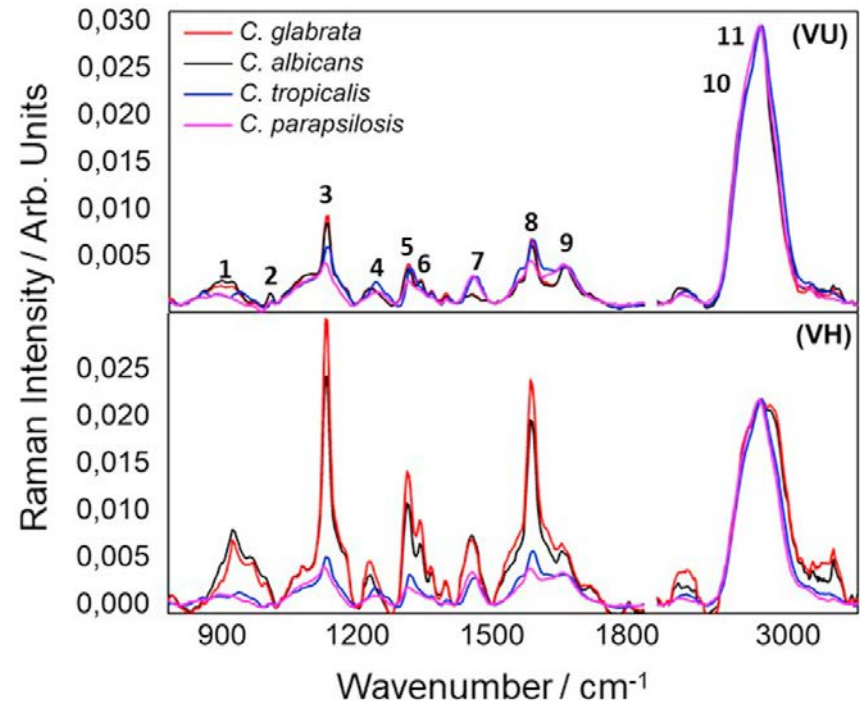
Different symmetry of vibrational modes induce different peak intensities in unpolarized vs. depolarized mode

- Raman averaged spectra of *Candida* films after fluorescent background subtraction and normalization to high frequency
- CH₂-CH₃ stretching bands recorded using the depolarized and unpolarized configurations
- Different symmetry of vibrational modes of biomolecules (caused by different interactions with local environment) differ in de- and unpolarized configuration



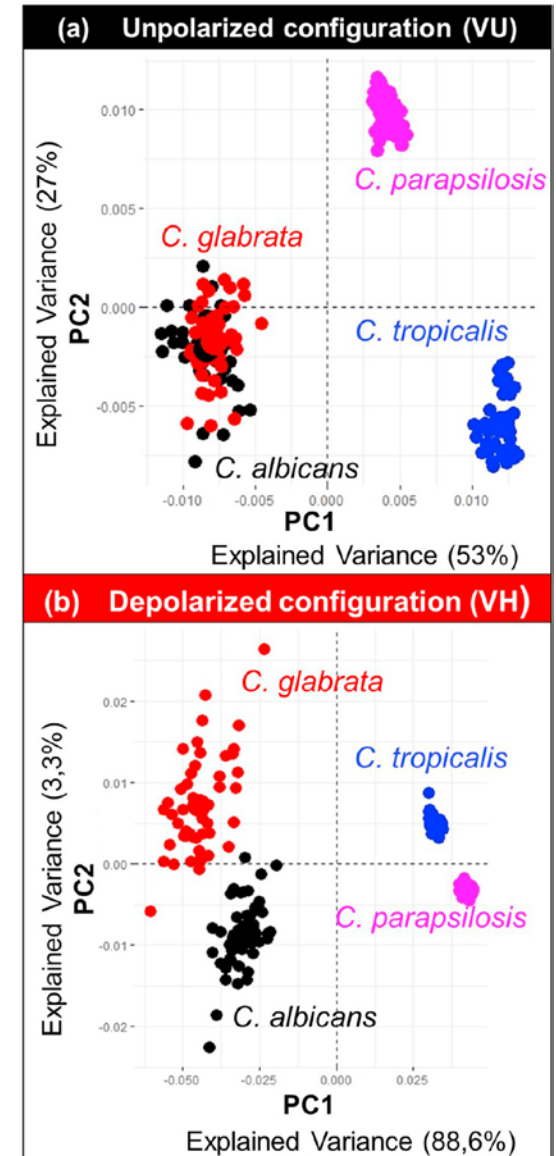
Comparison of averaged Raman spectra in depolarized and unpolarized configuration

- Average of 50 spectra in de-and unpolarized mode
- 800 - 3100cm⁻¹ investigated
 - Except “silent region” 1780-2640 cm⁻¹
- depolarized (upper panel)
- unpolarized (lower panel)



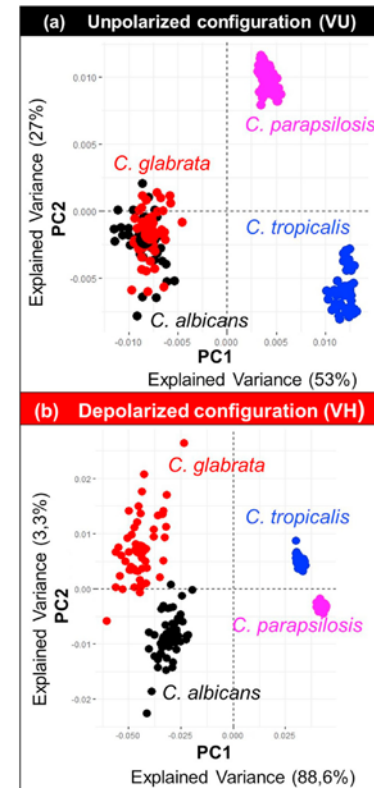
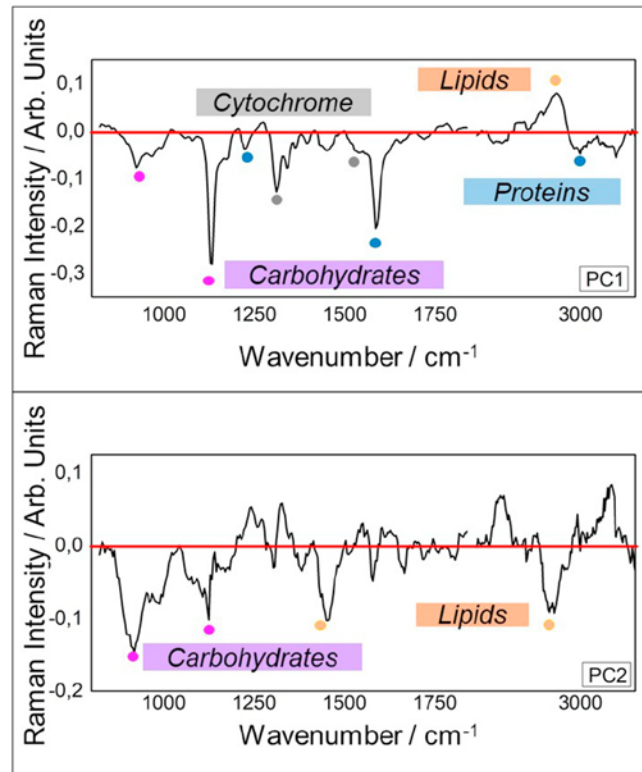
PCA analysis on VU & VH spectra shows value of VH configuration

- PCA plot obtained from VU spectra and from VH spectra of four different pellets:
 - *C. tropicalis*
 - *C. parapsilosis*
 - *C. albicans*
 - *C. glabrata*
- Clear discrimination of only 3 groups using VU spectra
- Using VH spectra, samples can be divided into 4 groups
 - Baseline subtraction may play a major role in distinguishing *C. albicans* and *C. glabrata*
- Spectroscopic data in different polarization helps identifying these species
- Candida samples are highly luminescent - baseline subtraction is important



Shape analysis of PC1 & PC2 gives further information

- Projection of the loadings plot on the PC1 & PC2
- PC1 can distinguish **C. tropicalis** and **C. parapsilosis** from **C. albicans** and **C. glabrata** due to different relative protein and lipid content (high frequency CH stretching band profile)
- PC2 distinguishes **C. glabrata** and **C. tropicalis** from **C. albicans** and **C. parapsilosis**. Frequencies assignable to carbohydrates (glucose, glycogen) and frequencies characteristic of lipid components mostly present on **C. albicans** and **C. tropicalis** spectra.



Conclusions & Significance

- Established a possible procedure for Raman phenotypical identification of yeast cells using meso-Raman approach
 - Meso-Raman records averages of tens of cells → reduced acquisition time and facilitated data processing
 - Reduced spectral variability (metabolic states, colony architecture, cellular portions)
 - Most common *Candida* species could be distinguished using PCA analysis including depolarized spectra
 - Large scale microbial identification possible, since no selection of cell portion for analysis is needed
- Low price, low biomass needed (short incubation times)

Raman spectroscopy for cell identification

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Raman micro-spectroscopy for accurate identification of primary human bronchial epithelial cells

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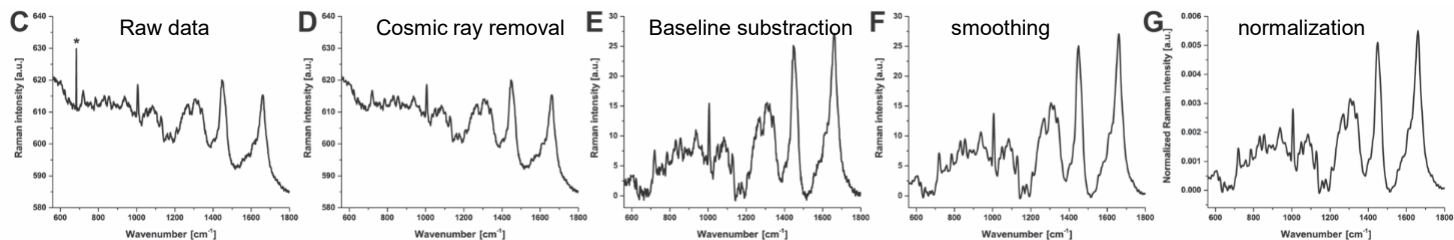
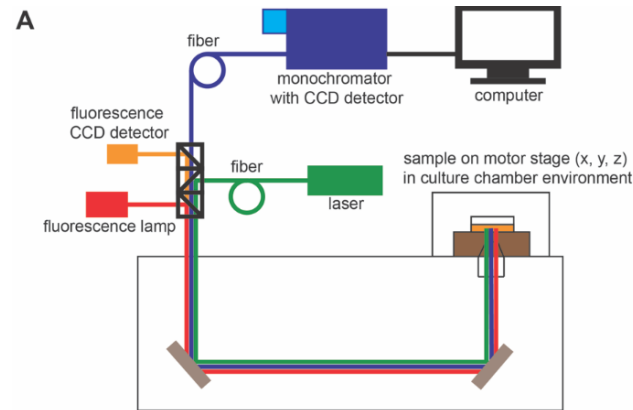
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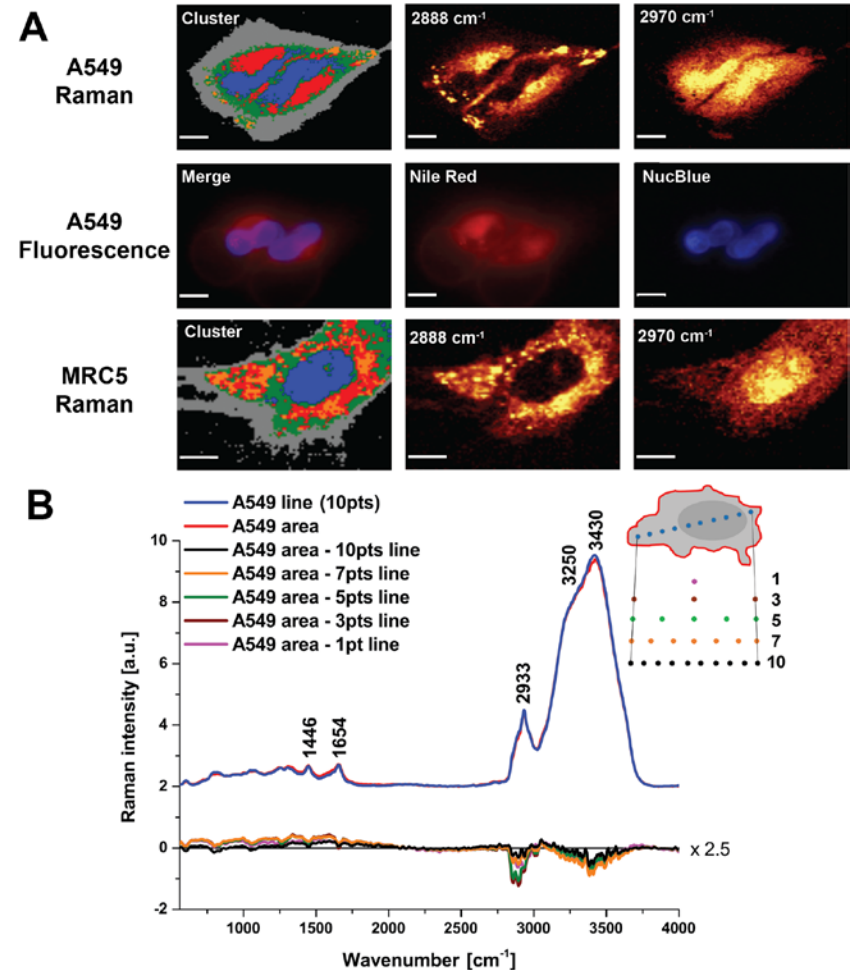
Raman micro-spectroscopy for accurate identification of primary human bronchial epithelial cells

- Development and application of optimized protocol for confocal Raman micro-spectroscopy to identify different living human lung cell lines in culture
- Delineation of immortalized human cell lines derived from lung cancer (A549), fibroblasts (MRC5) and 3 primary human bronchial epithelial cell (HBEC) lines based on lipid composition, lipid droplets and differences in DNA content



Comparison of line scan data acquisition from A549 and MRC5 cells

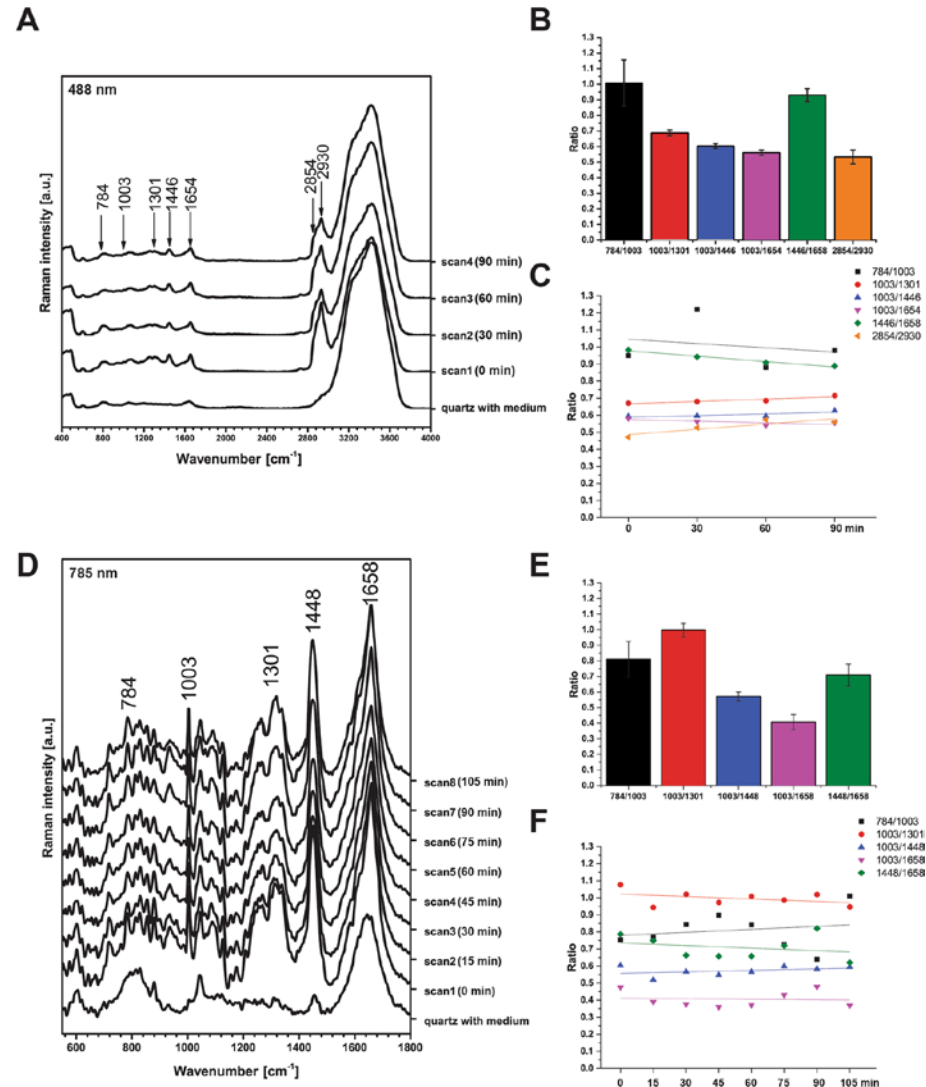
- Comparison line scan vs. Area scan to increase the analysis speed
- Comparison of Raman vs. Fluorescence
 - MRC5 cells could not be compared to fluorescence: migratory cells
- Area scans using 488 & 785 nm, combined with quartz substrate used
- Area scan (488nm) with image production using k-means clustering and sum filters to optimize the procedure
- Fluorescence images to compare lipid rich regions & nuclei
 - NucBlue for nucleus
 - NileRed for lipids
- Averaging spectra from line spanning a single cell – using 10 points could recapitulate the area spectrum in short time



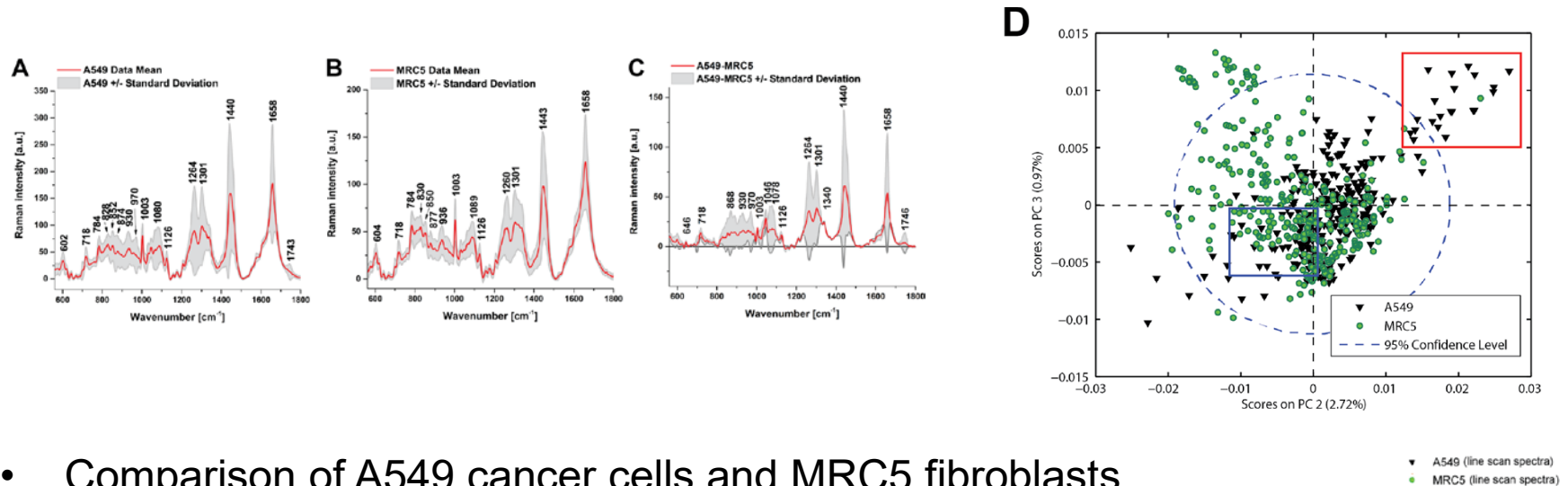
Impact of longitudinal line-scan data acquisition at multiple time points on live cell spectra

Testing the impact of line scan acquisition on the cell's biochemistry

- Repeated scan of same cell over 2 hours with 488 & 785 nm
- No significant change of peak intensity ratios, but trend to be altered after 2 hours using 488 nm
- For 785 nm intensity ratios seem unaltered after 2 hours repeated measurement → preferred illumination for repeatedly analyzing the same cell



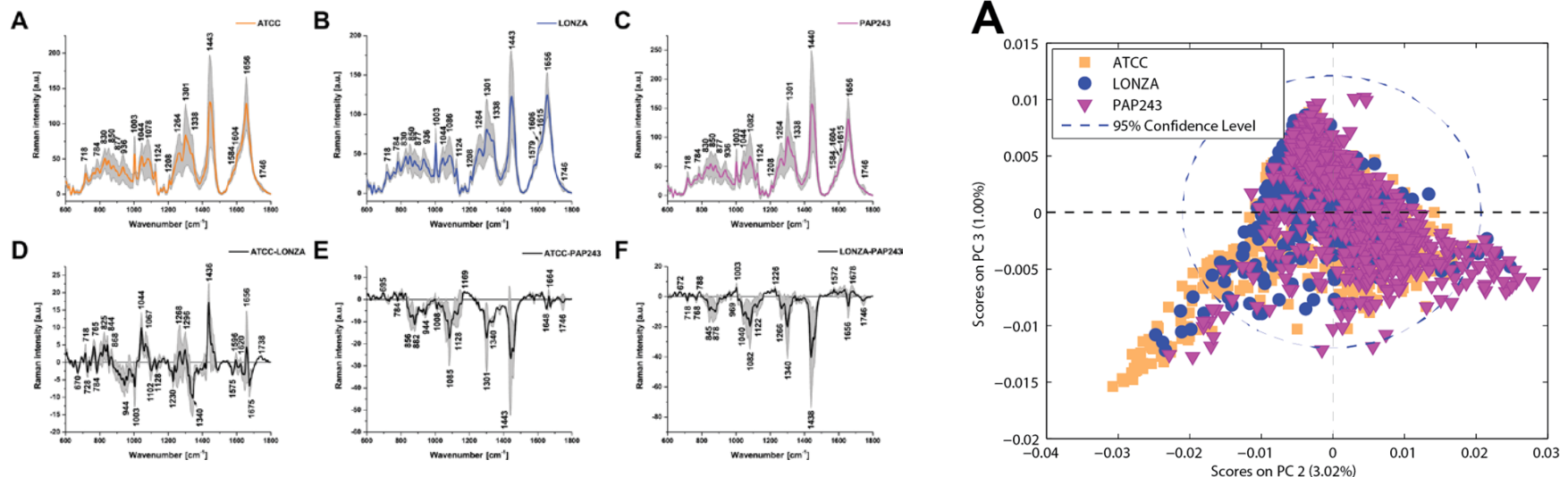
Analysis of live human immortalized lung cell lines



- Comparison of A549 cancer cells and MRC5 fibroblasts
 - 10 point line scan experiments over 30 cells each
- Variability within lines is sufficiently low to detect differences between lines (DNA band, lipids and proteins)
- PCA analysis reveals presence of lipid droplets as distinguishing factor (PC3 higher in A549 cells)

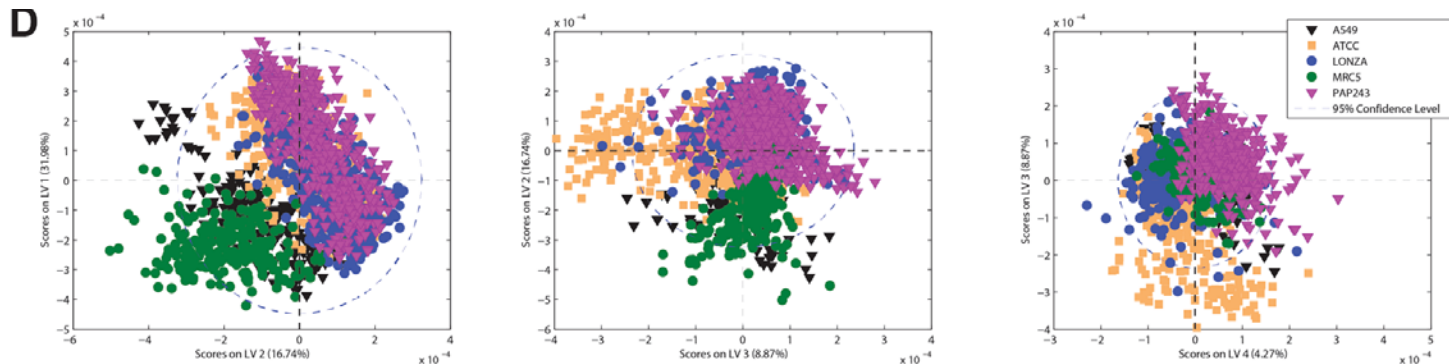
Identification of primary human bronchial epithelial cells in culture

- 10 point line scan experiments over 30 cells for 3 different primary HBEC lines
 - in house, patient derived (never smoker, carcinoid diagnosed)
 - Smoker, non-cancer (ATCC)
 - Never-smoker, non-cancer (LONZA)
- Assessing the ability to distinguish the cultures by comparing mean spectra, difference spectra and PCA (key differences from DNA, Lipids and proteins)
- Patient derived culture shows greater difference to the commercial cultures



Testing the classification potential for HBEC & immortalized cell line cultures

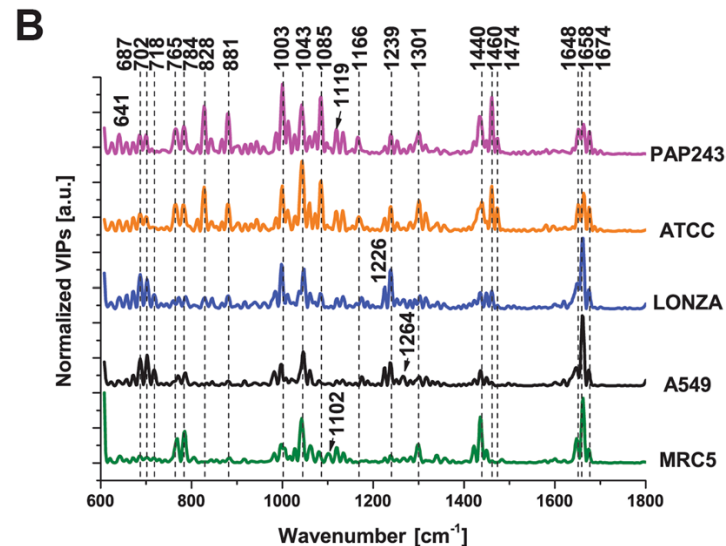
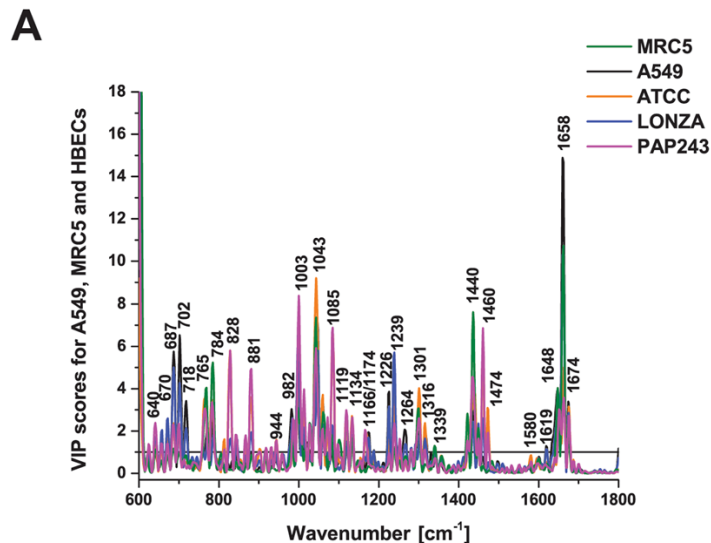
- Partial least squares discriminant analysis (PLS-DA) – a chemometric technique widely used to optimize separation between different sample groups
 - Up to 4 latent variables show good discrimination
- Classification of average line-scan spectra: sensitivity, specificity, area under the curve
- Further performance confirmation using
 - root mean square error of calibration,
 - - of cross-validation and
 - – of prediction
 - → good validity criteria using PLS-DA



Cell line	Sensitivity	Specificity	AUC	RMSEC	RMSECV	RMSEP
MRC5	100%	98.2%	0.9897	0.1328	0.1462	0.1614
A549	100%	94.6%	0.9732	0.1352	0.1474	0.1631
HBEC PCS-300-010 (LONZA)	93.8%	91.7%	0.9648	0.2210	0.2450	0.2628
HBEC CC-2440 (ATCC)	93.8%	97.9%	0.9767	0.2064	0.2294	0.2138
HBEC PAP243	93.8%	93.8%	0.9831	0.2282	0.2454	0.2426

Variable Importance in Projection (VIP) scores for PLS-DA model of all Raman data

- To identify most discriminatory spectral regions for immortalized cancer cells, fibroblasts and HBECS
 - Lipids: 718, 1264, 1301, 1440, 1658
 - Proteins: 641, 1003, 1166/1174, 1239, 1580, 1658, 1674
 - Nucleic acids: 784, 828, 1316, 1458
 - Carbohydrates: 881, 944, 1034, 1085



Conclusions & Significance

- Development and application of an optimized protocol for Raman micro-spectroscopy of different living human lung cell lines in culture
- Successful delineation of immortalized cell lines mainly based on differences in lipid composition
- PLS-DA model performance of all 5 cell types investigated
 - Highly relevant Raman bands: lipids, proteins, nucleic acids and carbohydrates
 - high average sensitivity of 96.3% and specificity of 95.2%
- Raman features associated with lipids might be useful as biomarkers for monitoring cancer progression
- Probably useful in identifying different primary HBEC cultures to identify different lung cell types in co-cultures and study early carcinogenesis



Thank you for your interest!