Alexander Bell, PhD

Research Lab Specialist
Department of Radiology
University of Michigan

alejbell@med.umich.edu

Get to know members of the RSF Assembly

Is your research clinical, basic science or translational?
Translational

Tell us about your research?
My background is in Mathematics and Data Science, which I use to develop and utilize advanced methods for feature extraction and analysis to contribute to the understanding and solving of complex problems faced by contemporary clinicians. In my PhD I developed CT image analysis methods to identify distinct phenotypes of asthmatics based on density change gradients in the lung. In the work shown here, I used the elastic principal graph concept, see work by Gorban and Zinovyev[1], with the tool ClinTrajAn[2], to phenotype and model trajectories of patients with chronic obstructive pulmonary disease (COPD).

1 https://arxiv.org/abs/0809.0490
2 https://academic.oup.com/gigascience/article/9/11/giaa128/6006352

Where do you see yourself in 5 years?
I wish to improve our understanding of disease classification beyond arbitrary schemes based on limited measurements. I see myself having published work on, developed and popularized this concept in 5 years.

What do you find is the major benefit of RSF Assembly Membership?
I am grateful to have benefitted from the ATS scholarship award for this work, and the opportunity to advertise myself and this work with the assembly and associated academic community.

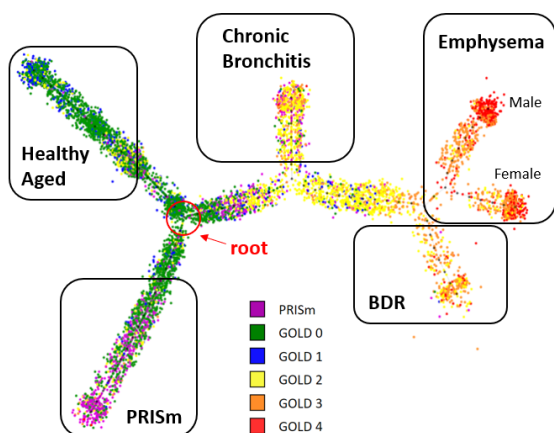**Please follow us on X** @ATS_RSF **and like our Facebook** 📘 **page!**

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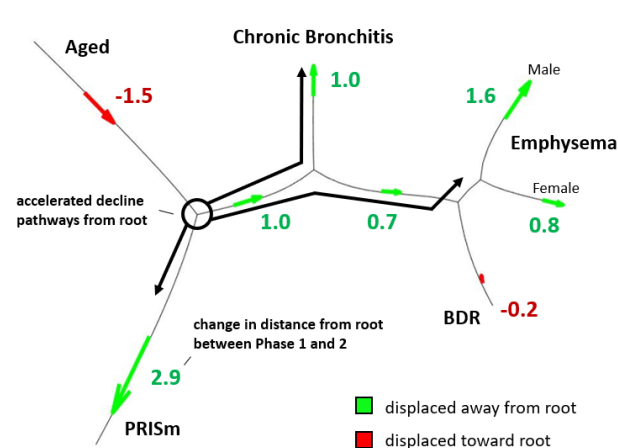
Clinical trajectory analysis with longitudinal validation in COPD: a COPDGene study

Objective: Chronic obstructive pulmonary disease (COPD) is heterogeneous in its clinical phenotypes (e.g. chronic bronchitis, emphysema) and trajectories of disease progression. Clinical trajectory analysis (ClinTrajAn), developed by Zinovyev et al (https://github.com/auranic/ClinTrajan), based on the concept of the branching principal tree, simultaneously phenotypes and determines patient trajectories within cross-sectional clinical data. Our aim was to apply ClinTrajAn to map prominent subtypes and trajectories in a large population of participants, covering the whole range of COPD severity and at-risk profiles, and validate proposed trajectories using longitudinal data.

Methods: Cross-sectional data for 8972 participants from Phase 1 of the COPDGene longitudinal study were utilized for training, with 4585/8972 (51%) of participants having Phase 2 data (≈5 years later). 30 features were selected for training, from demographics, exposure, pulmonary function, and CT imaging. PCA was applied to reduce dimension to six principal components. A bifurcating principal tree fitting this reduced data was computed by averaging over 100 iteratively grown trees fitting random 95% samples.

Results: The averaged tree contained six phenotypic terminal segments and two notable bridging segments (Figure 1 A). Longitudinal analysis showed most participants (69%) stayed on the same segment after 5 years, with segment displacements on average moving away from the root, and a notable increase in displacement for cases with accelerated decline leading to a COPD subtype or PRISm terminal (Figure 1 B).

Conclusion: We applied ClinTrajAn to a large longitudinal study population to model phenotypes and trajectories in COPD, and validated progression pathways through observation of projected displacements over 5 years.

Figure 1

A) simple graph modelling phenotypes and bridges
B) 5-year segmental displacement for accelerated decliners

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