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Commentary on viewpoint submitted to JAP, Guilhem Collier, Felix Horn and Jim Wild. University of Sheffield,

“Could lobar flow sequencing account for convection-dependent ventilation heterogeneity in normal man ?”

Authors: Verbanck and Paiva

Based on 4DCT imaging (3), this viewpoint (5) investigates how lobar flow sequencing can contribute to generate a positive phase III slope. Results suggest that inter lobar differences in expansion and deflation during the respiratory cycle contribute partly to Scond. We agree that further imaging measurements, such as measurement of 1D flow profiles in the main bronchi with hyperpolarized gas MRI (1) can provide added regional insight into lobar flow asynchrony. From our experience, measurement of such flow profiles at the entrance of each lobe is feasible but technically challenging in airways below the main bronchi due to the background signal from gas in the lungs outside of the airway of interest.

We also believe that the regional detail of the CT imaging data could be further put to use by looking at the sub-lobar nonlinearity and hysteresis of lung deformation. After all, much of the heterogeneity in specific ventilation occurs at smaller length scales than the lobes. It would be interesting to see if normal Curv and Scond values could be simulated by feeding an idealized airways tree (such as (4)) with localized ventilation imaging data eg from dynamic CT or HP gas MRI (2).

Ultimately lung ventilation cannot be fully modeled from elementary consideration of diffusion-convection equations of mass transfer in a simple branching model of the lungs alone and anatomically specific information from functional imaging like this can help inform these models and add to our understanding of global lung function tests in this way.

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