This is what I propose:

1. Fit end-inspiratory shape model for each subject at each time point [ADDITIONAL TIME-POINT DATA COMING FROM DAVE MILNE FOR SOME OF OUR EARLIER SUBJECTS!]. We will need end-expiratory shape models at a later date.
   1. For each subject+time, calculate the mode weightings for the normal model (will need to use the most recent model from Mayhar). Test whether shape is different in IPF subjects, if it changes over time, and if it is associated with lung function measurements.
2. Convert CALIPER files to an exdata field file, where a data point is a region of interest of specified size with spatial coordinates and a tag for tissue classification (e.g. 1=normal, 2=honeycomb…)
   1. For each subject+time, calculate the volume of each tissue type in each lobe. Test whether shape (and lung function) is associated with the amount of tissue abnormality.
   2. For each subject, calculate the change in volume and location of abnormal tissue over time. Test whether this is associated with change in lung function.
3. Convert the vascular file (that we have to this point ignored) into something readable. Image mask? Brian mentioned in an email that this is included in the CALIPER data.
   1. Identify the blood vessels that have cross-sectional area <= 5 mm^2.
   2. Calculate PVV5 for whole lung (i.e. the volume of all blood vessels that have x-sec area <= 5mm^2)
   3. Calculate PVV5 for each lobe
   4. For each subject, test whether PVV5 by lung or lobe is associated with regional tissue abnormality and/or lung function and/or outcome.
4. Create a vascular tree model for each subject (and at each time-point, by registration between time-point shape models).
   1. Forward simulation of perfusion and vascular distension (i.e. PVV5) for a model with subject-specific tissue abnormalities