* Mycobacterium avium complex (MAC)
* Disproportionately affects middle-aged and elderly, resistant to treatment
* Can develop in preexisting abnormal lungs (bronchiectasis or emphysema) or normal lung tissue
  + Bronchiectasis - a chronic lung condition where the walls of your airways (bronchi) widen and are thickened from inflammation and infection
  + Emphysema – lung disease that damages the alveoli in your lungs
* Fibrocavitary disease – severe form of NTM infection that occurs when the MAC bacteria creates a cavity or hole in the lung tissue (this is the “classic” NTM infection, described principally as upper lobe fibrocavitary disease with underlying emphysema)
* However in last three decades, nodular-bronchiectasis pattern (“non-classic infection”) has been increasingly observed. Occurs in any lobe, but more severe in right middle lobe (RML) and lingula, and possibly right upper lobe, manifesting as advanced bronchiectasis and atelectasis
* In studies, NTM lung disease appears to be more severe in RML and lingula
  + The reason for this is not known
* Acquisition:
  + Inhalation of NTM-contaminated water, biofilm, or soil aerosols
  + Microaspiration (from above – swallowing dysfunction, or below-GE reflux)
* Why more apparent on right?
  + In adults, right mainstem bronchus makes a less acute angle at its takeoff from the trachea, and is shorter than the left mainstem bronchus (2.5cm vs 5cm on average)
  + About equal in children, however
  + Secretions traveling down are more likely to go into these areas?
  + RML bronchus is more narrow, might be harder to clear airway with forced exhalation
  + RML and lingula are near the heart, the constant beating might cause microatelectasis (small passages are blocked or pressure is applied to outside of lung), might set up a nidus of infection (place in which bacteria have multiplied) that can spread
  + The “tapping” from the heart beat might skew macrophages in those areas to other types of macrophages (without other underlying causes, might not be super convincing, since these would be present in everyone
* People with primary ciliary dyskinesia (genetic mutations that affect the tiny hairline cilia in the lungs, nose and ears, impairing their ability to remove germs and pollutants, and allowing mucus buildup and infection) more predisposed to bronchiectasis and NTM lung disease

Notes from meeting

* Drug resistant TB
* NTM
* Look for disease in lungs
  + Large nodules, ground glass opacities
* To account for 6 measures per subject, add random intercepts
  + For thesis, try other types of correlation
  + Maybe ways to play with correlation structure
  + Can do comparison between lobes
* Scoring 0, 1, 2, 3
  + 0
  + 1: <25%
  + 2: 25-50%
  + 3: >50%
  + Take into account all radiologists (2 people scoring, 3 if tiebreak needed)
* Ordinal logistic regression: basic approach assumes proportional odds (this is a big assumption)
* Ordinal logistic regression
  + 3 intercepts
  + Treat CT findings as separate outcomes (separate model)
  + Repeated findings are the different lobes
* ICC: variance between raters
* 2 raters and ways to account for repeated measures: this will be the difference between preliminary data and my project

2025 – re-reading notes

* Matt’s work had 71 subjects, mine might have up to 164
* Model each lung pattern separately
* GLMM, random intercept
* Other ways to account for repeated measures
* Would make sense to do AR1 if (?) over time
* Spatial correlation?
* Easiest is a random intercept (correlation would be same
* Need to account for correlation in some way
* Right df
* Two part model (0 + continuous)
* Steps
  + Refit
  + Any other ways to account for correlation other than random intercept
  + 2-part model (0+continuous)
* Cumulative logit: odds interpretation
  + Odds of having higher score for particular lobe compared to other is…
* Proportional odds assumption (should maybe test for when it doesn’t hold either
  + Odds interpretations are valid across all levels of covariates
* When i fit model, go in and interpret each of the estimates
* ICC -> these models not fitting error term, not really able to do this
* If you use pseudolikelihood, we could? (another approach, he uses quadrature, not pseudolikelihood)

Before meeting on 1/14

* Repeated measures: 6 lobes scored (within subject repeated measures)
* Also the 2 (or 3) raters
* Random intercept?
* Consider partial proportional odds if proportional odds fails

From my meeting on 1/14

* Nothing formal to present for March, just getting together; PPT slides, can make simple paragraphs, where I’m at and what our plan is, can mention data analyzed for previous abstract
* Doing definitive analysis and more data
  + Multiple raters
  + Comparing SAS and R
  + Ordinal logistic regression
  + Playing with different correlation structures
  + Testing proportional odds assumption (test with a more complex model that doesn’t require this assumption)

Help

Fit the simplest model (no other fixed effects yet):

r

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library(ordinal)

simple\_mod <- clmm(Value ~ 1 + (1|newID) + (1|rater), data = tib)

summary(simple\_mod)

Add fixed effects or correlation structures incrementally, e.g.:

r

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next\_mod <- clmm(Value ~ Attribute + (1|newID) + (1|rater),

data = tib)

or if you want to specify a correlation structure (which can be tricky):

r

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next\_mod\_corr <- clmm(Value ~ Attribute,

random = newID,

data = tib,

correlation = corAR1(form = ~ lobeIndex | newID))

That said, specifying correlation + random intercepts can lead to convergence issues, so proceed carefully.  
  
Checking proportional odds assumption: standard PO model: fit\_PO <- clmm( Value ~ x1 + x2 + (1 | subject) + (1 | rater), data = your\_data, link = "logit" ) nominal version in which at least one predictor is allowed to violate PO: fit\_nominal <- clmm( Value ~ x1 + x2 + (1 | subject) + (1 | rater), nominal = ~ x2, # allow x2 to have category-specific effects data = your\_data, link = "logit" )