Resampling beech bark disease severity over time in a chronosequence

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What is beech bark disease?

- Insect-fungus complex
  - <u>Insect</u>: Cryptococcus fagisuga
  - <u>Fungi</u>: Neonectria ditissima, faginata
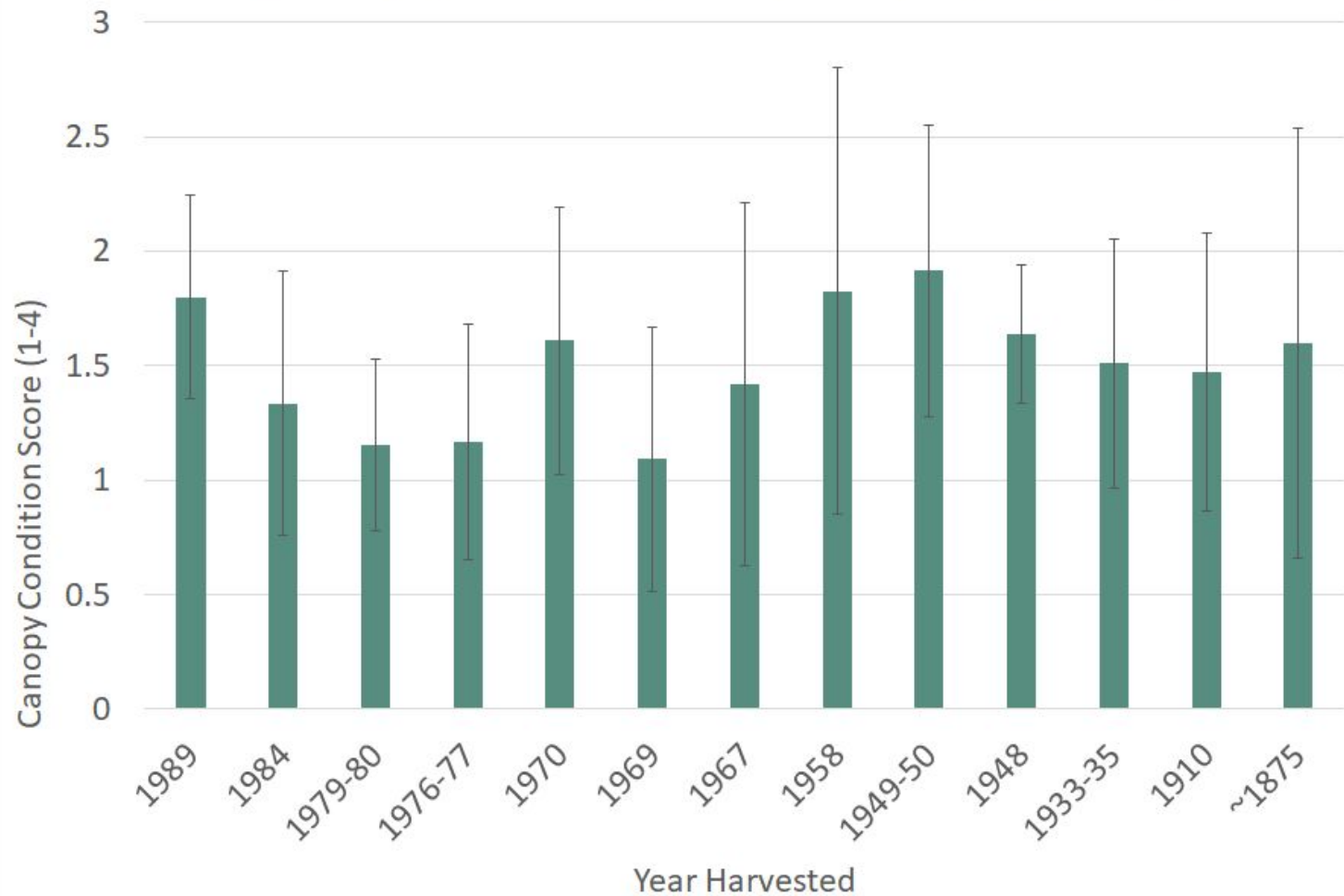- Canker disease
  - Causes girdling

Methodology

- 5 transects, 13 chronosequence stands
- DBH measurement
- John Cale BBD Scoring System
  - Wax secretion cover
  - *Neonectria* fungus presence
  - Tree condition
- Data Analysis
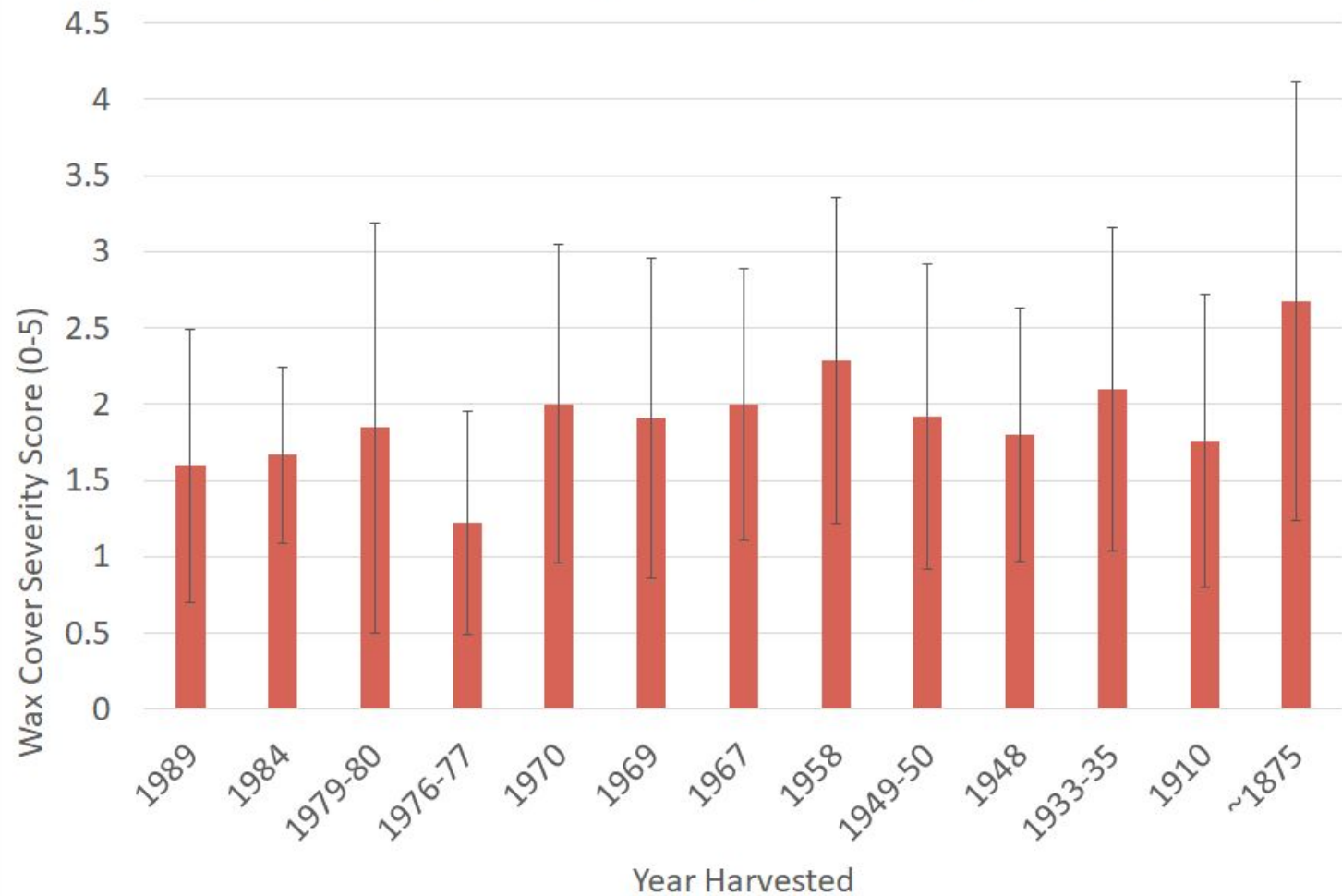 - Simple Linear Regression
  - Two-way ANOVA
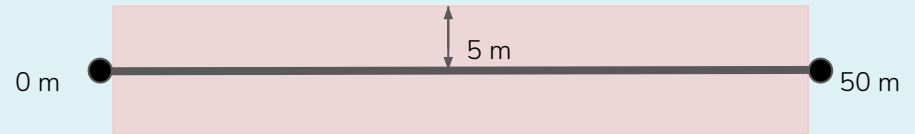
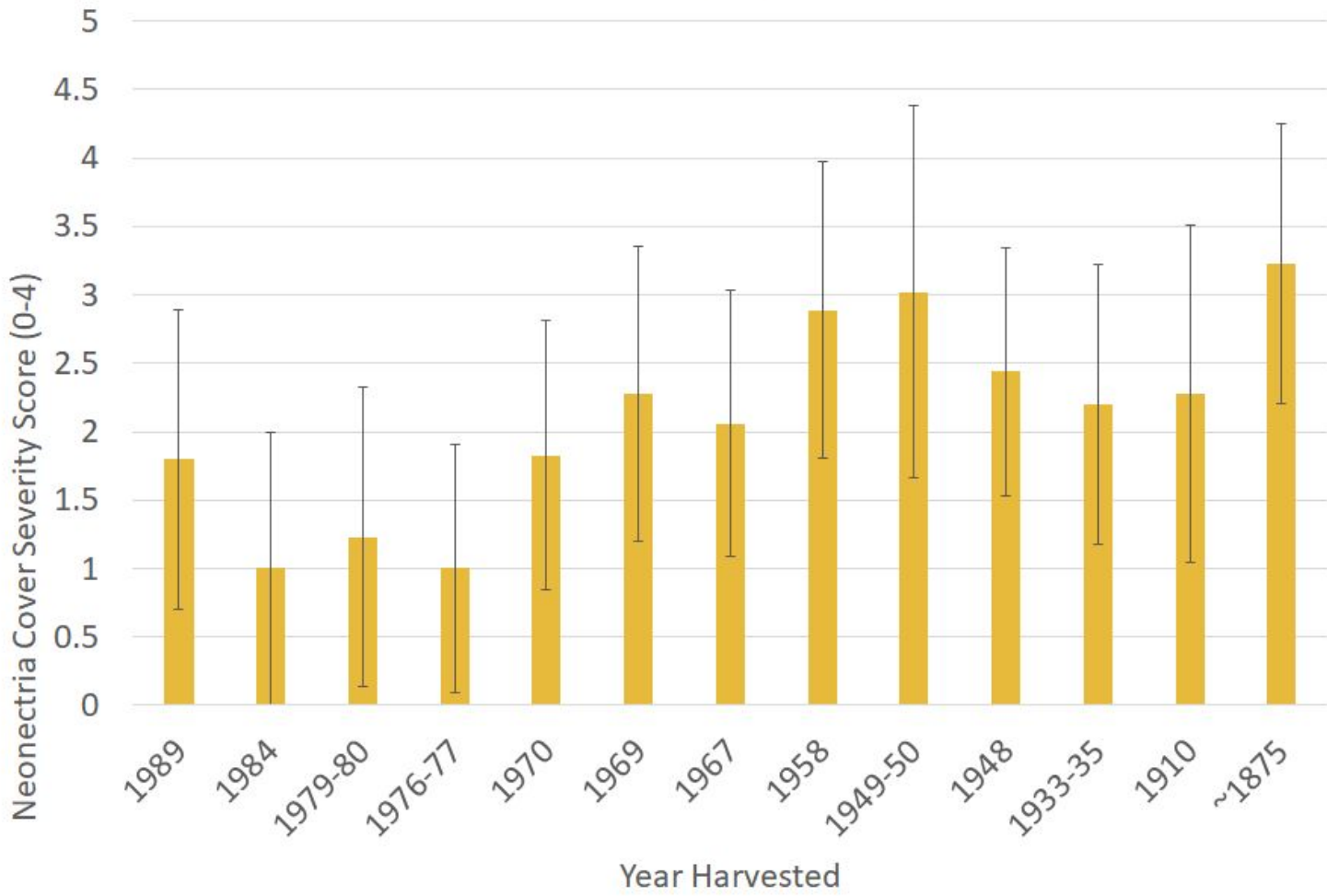*Standard transect layout (2012, 2021)*

Average Canopy Condition Ratings From 2012 at Different Stand Ages

Average Wax Cover Ratings from 2012 at Different Stand Ages

Average Neonectria Cover Ratings From 2012 at Different Stand Ages

What am I doing?

- Re-sampling to assess progression
- Has severity increased?
- Stand age effect?

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