How To Reject A Paper That Uses SEM

1. Is SEM Necessary?

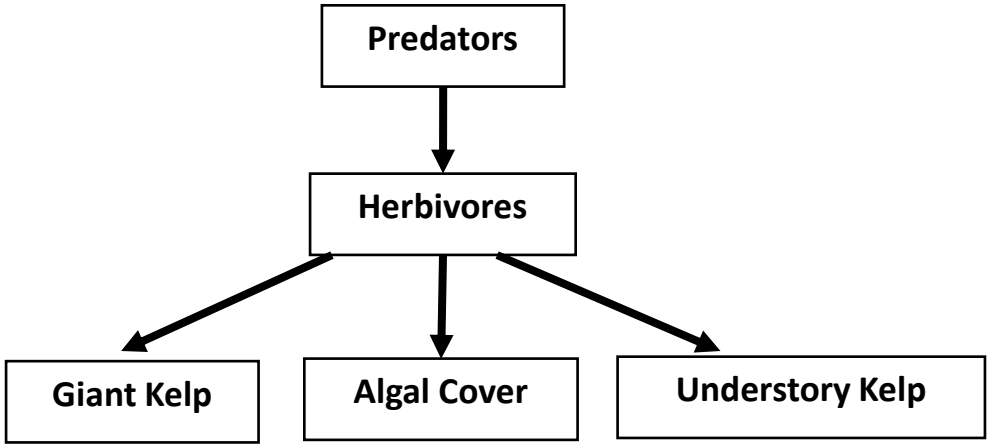
- Is SEM necessary to accomplish the goals of the paper?
- Does the question benefit from a network approach?
- Was the study/experiment designed to accommodate SEM?
  - Replication (power)
  - Identification

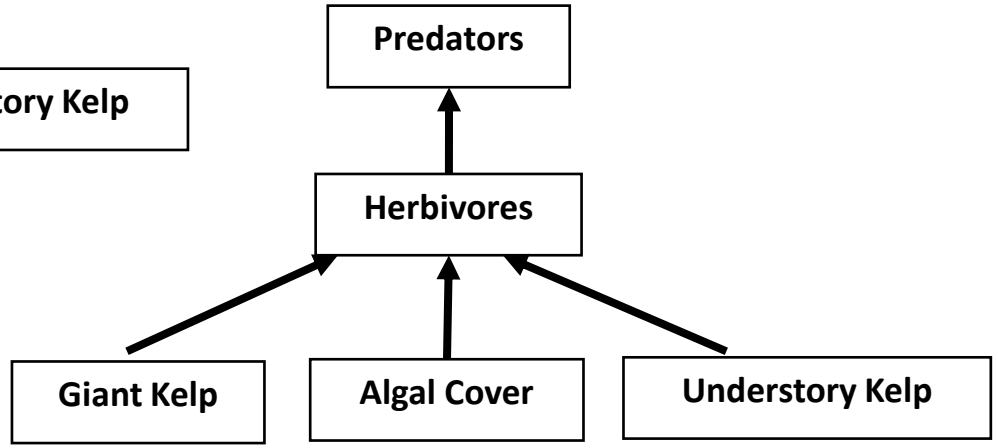
Overview

1. Model specification
2. Checking fit & assumptions
3. Interpretation

1.1 Specification.

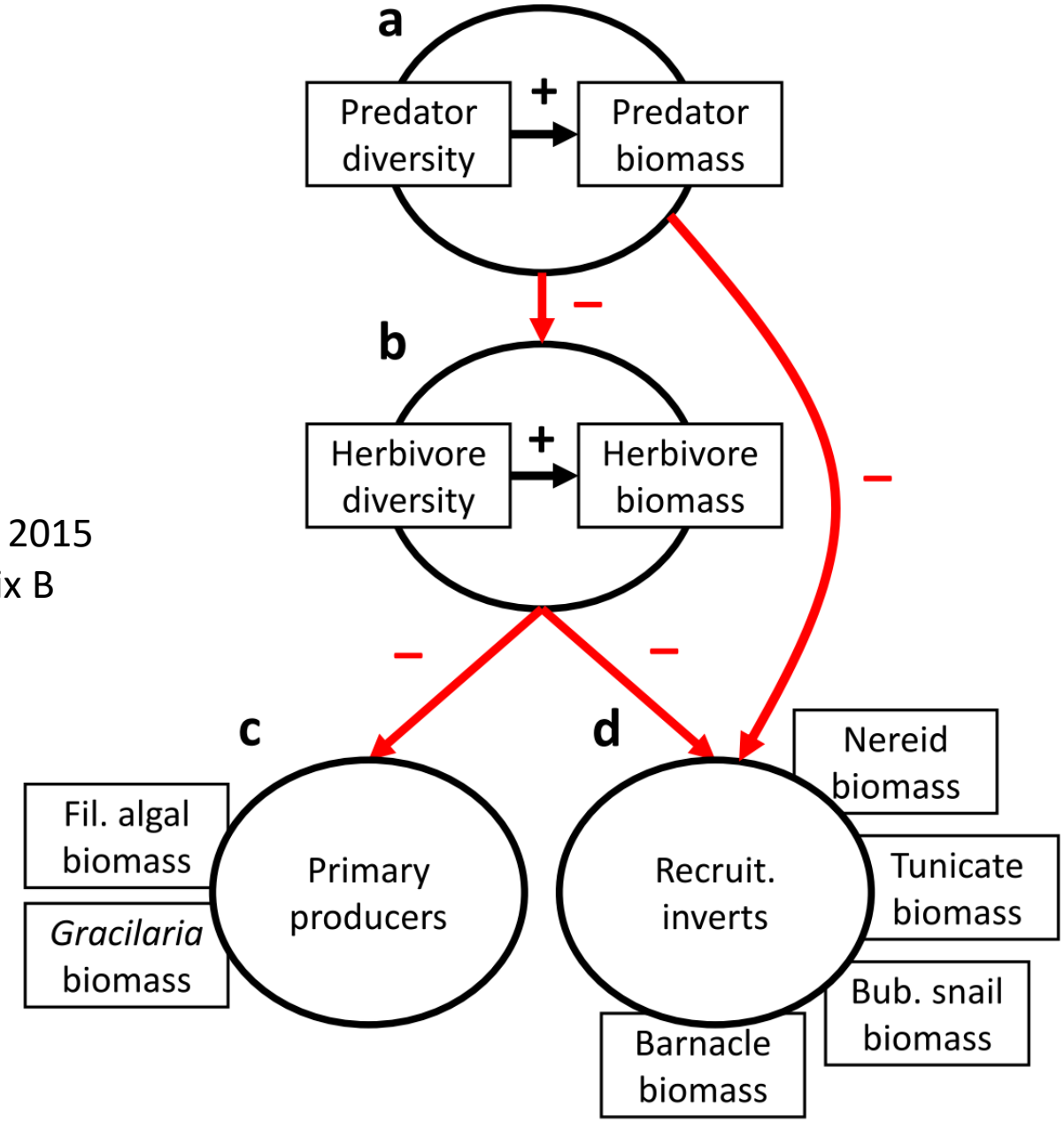
- Justification using a meta-model (rooted in theory)
- Did the authors consider alternate hypotheses?





1.1 Justify your meta-model.

Lefcheck & Duffy 2015
Ecology, Appendix B



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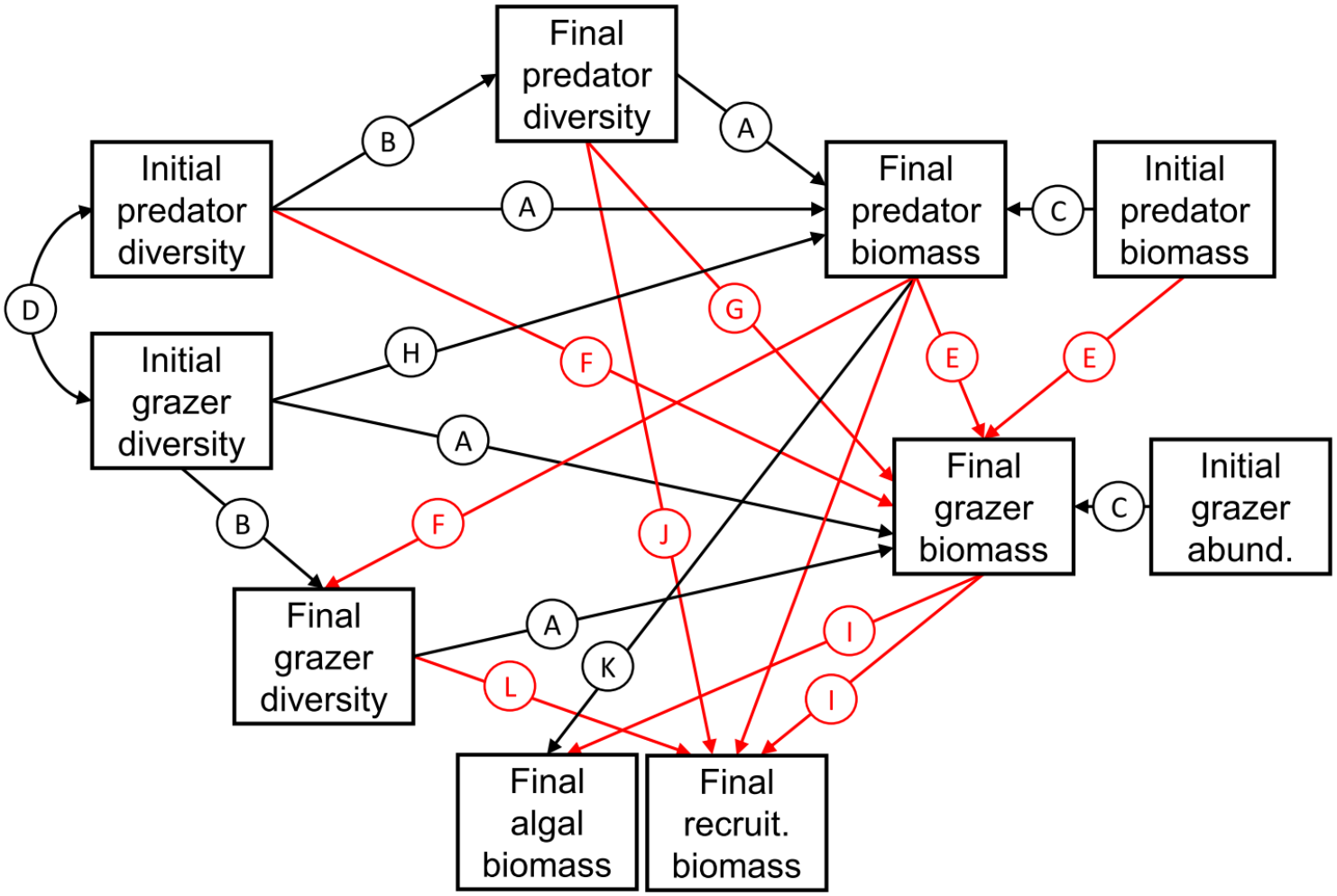

Lefcheck & Duffy 2015
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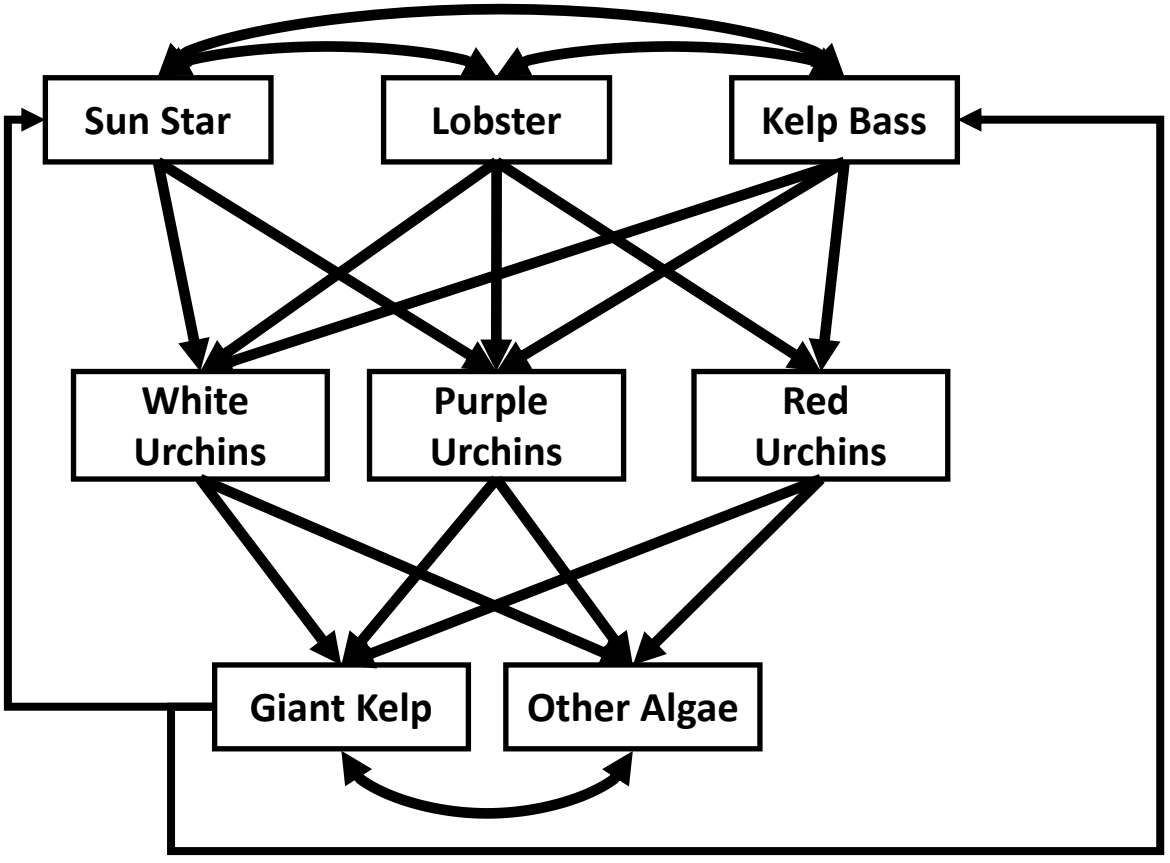
1.1 Specification. Complexity



What will we learn from this model?

How is it being a multivariate model useful?

Would a simpler model better represent processes we can detect given our data?

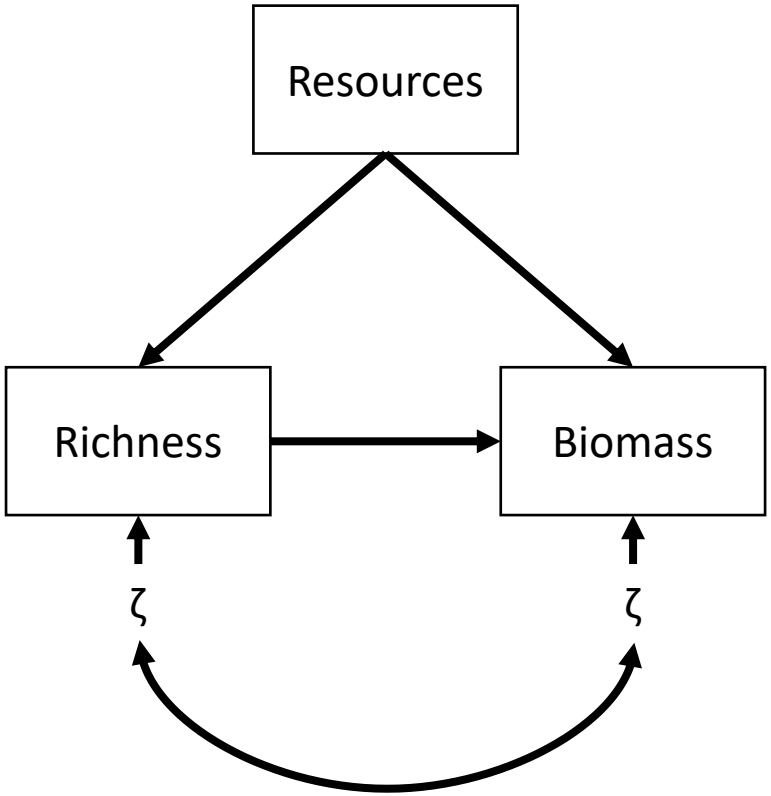
Is this model identifiable?

Will including all of these paths lead to excessive parameter uncertainty?

Can we even estimate the overall fit of the model?*

1.1 Specification. Correlated errors

- Are relationships directional or correlated errors?
- Everything is correlated! Choose wisely…



1.1 Specification. Missing data

- Were any data points missing? Why?
- Were they properly removed from the dataset *before* running the SEM?

1.2 Assumptions. Linearity

- Did the authors check for linearity?
  - Reviewed MS where conceptual figures showed curvilinear relationships, yet the authors fit linear models…

1.2 Assumptions. Normality

- Did the authors check for multivariate normality? (easier said than done)
  - If variables are non-normal, did they transform or fit to a different distribution?
- Did the authors explore residuals from the model output? (Q-Q plots, histograms)
- Did they screen for outliers?

1.2 Assumptions. Correlation

- Did the authors assume data points are independent?
  - Should they be?
- If not, did they correctly test for and address the non-independence?
  - Mixed models
  - Correlation structures
- Is there evidence their estimates could be biased by collinearity?
  - Study design (time, space)
  - Sampling
  - Centering

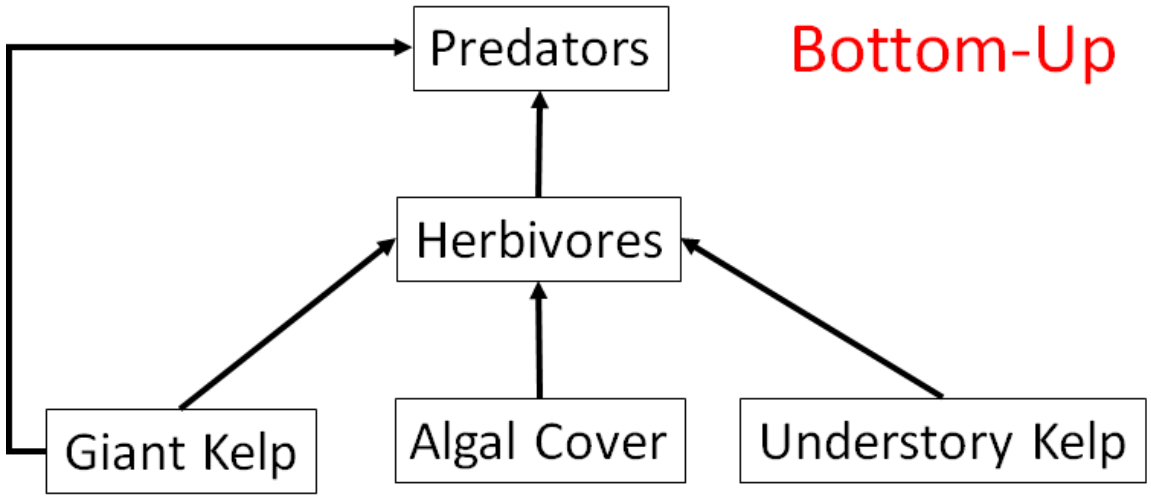
1.2 Assumptions. Model fit

- Did the authors assess model fit?
  - Do they provide a global fit statistic?
  - *Did they interpret it correctly*?? (P > 0.05 is GOOD!)
  - Did they interpret the significance of the path coefficients?

- Did the authors look at the fits of the individual models?
  - R^2
  - Fitted vs. residuals

1.3 Interpretation. Remember biology

- Are estimates biologically relevant?
  - $P < 0.000001$ but $\beta = 1 \times 10^{-18}$
- Do the paths reconcile with the hypothesis & study system?



What if you fit this model, and all paths were significant. You have good model fit. Variables were even well predicted, but…

ALL OF THE PATH COEFFICIENTS WERE NEGATIVE

1.3 Interpretation. Report those coefficients!

- Are both sets of coefficients reported (raw and unstandardized)?
- Are path diagrams properly labeled?
  - Are the size of the arrows based on standardized coefficients?
  - Are non-significant paths distinguished?
  - If non-significant paths are missing from the final model, are they reproduced elsewhere?

1.3 Reproducibility

- Did the authors include data or a script so that their analysis is reproducible?
  - Requirement at most journals now
  - Meta-data, meta-data, for the love of god, META-DATA

Parting Thoughts

Welcome to the SEM Brigade!

9. Think Critically!

- SEM is a tool, it is up to the user to employ it thoughtfully

- Don’t rely on the statistics as much as what you know about biology and ecology
  - If the answer doesn’t make sense, assume the model or test is wrong!

9. Report Bugs

- Software is imperfect
  - Bugs are constantly found and squashed

9. Report Bugs

- Contact the package author
  - `help("piecewiseSEM")`

piecewiseSEM-package {piecewiseSEM} R Documentation

Piecewise Structural Equation Modeling

Description

Fitting and evaluation of piecewise structural equation models, complete with goodness-of-fit tests, estimates of (standardized) path coefficients, and evaluation of individual model fits (e.g., through R-squared values). Compared with traditional variance-covariance based SEM, piecewise SEM allows for fitting of models to different distributions through GLM and/or hierarchical/nested random structures through (G)LMER. Supported model classes include: `lm`, `glm`, `gls`, `pgls`, `sarlm`, `lme`, `glmmPQL`, `lmerMod`, `merModLmerTest`, `glmerMod`.

Details

Package:	piecewiseSEM
Type:	Package
Version:	2.1.0
Date:	2019-03-14
Depends:	R (>= 3.5.0), nlme, pbkrtest
Suggests:	MASS, lme4
License:	MIT

The primary functions in the package are `psem` which unites structural equations in a single model. `summary.psem` can be used on an object of class `psem` to provide various summary statistics for evaluation and interpretation.

Author(s)

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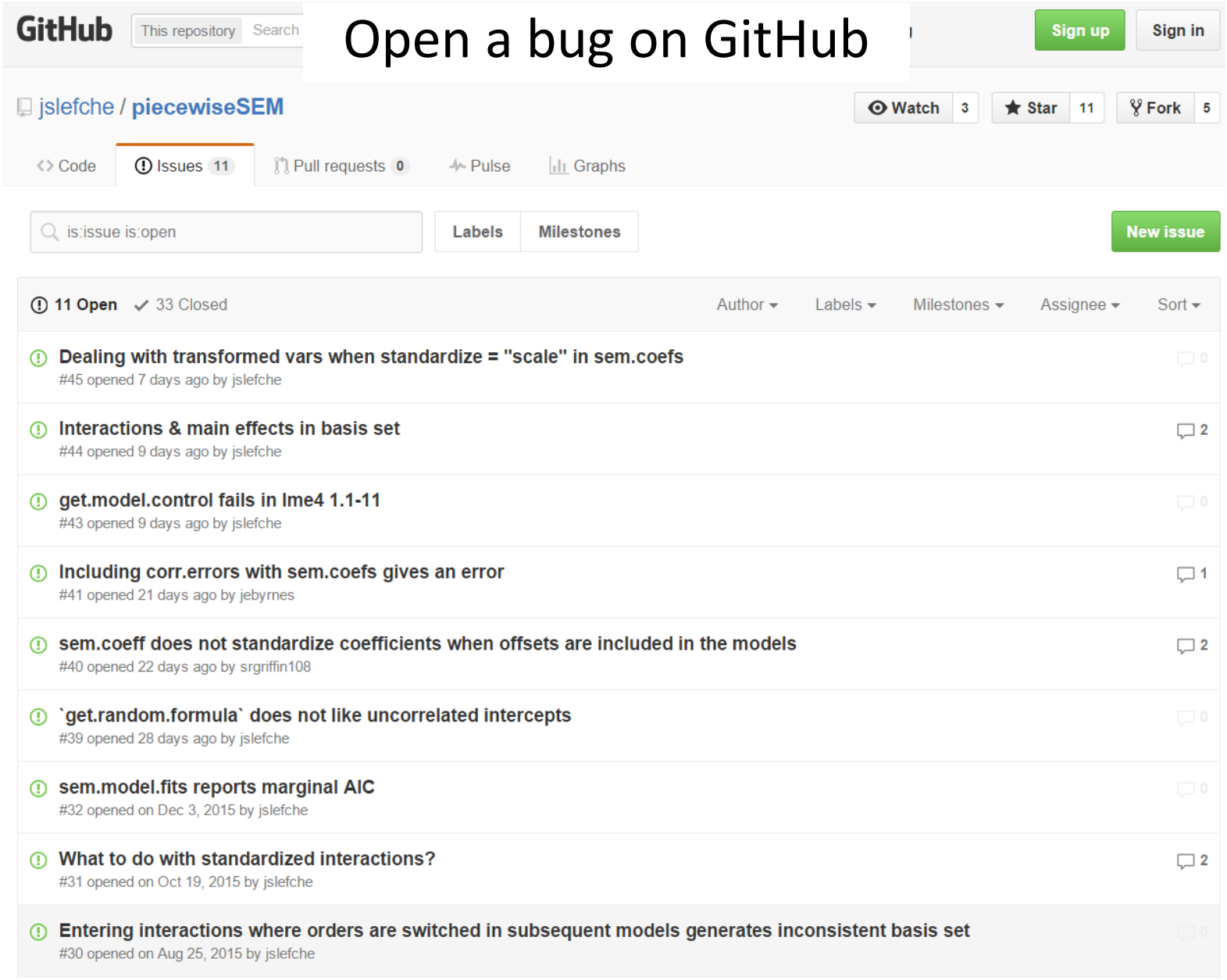
9. Report Bugs

Open a bug on GitHub

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