this is our second effort with a sensitivity analysis. the first approach was quite different: a linear mixed effects model was fit to each species. we then looked at the species for which a model could not be fit (many species were too rare?) to look at the number of species that could detect the 20% change. I think we had a squishy, not great cutoff criteria - I'm trying to avoid that and code the criteria into the code in this effort. when i was describing our approach to a colleague who assisted with our first, related effort, he suggested maybe we did not need to consider each species separately in the gjam context, but maybe see if a 20% change (maybe the mean of all species?) could be detected. I don't want to change given all the work we have done and I like that we are functionally mirroring the initial effort, but does what he describe make sense in the context of gjam?

**ChatGPT said:**

Yes, your colleague’s suggestion **does make some conceptual sense** in the context of GJAM—but your current approach is **more informative**, **better aligned with your previous work**, and **well-justified** given the ecological and statistical goals.

Here’s a detailed breakdown:

**✅ What Your Colleague Suggested**

They’re proposing a **community-level summary**, such as:

“Can we detect a 20% change in the **mean abundance across all species**, rather than for each species individually?”

This would involve comparing the **average prediction across species** for baseline vs. changed years, e.g.:

r

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mean\_baseline <- rowMeans(pred\_array[, "baseline", ])

mean\_changed <- rowMeans(pred\_array[, "changed", ])

Then calculate whether a 20% change in this **community-level mean** is detectable (e.g., using credible intervals or posterior probability that mean\_changed > 1.2 × mean\_baseline).

**Why That Might Seem Appealing:**

* Reduces complexity by aggregating across species
* Potentially more powerful due to pooling
* Easier to summarize for decision-makers

**❗ Why That’s Not Sufficient for Your Sensitivity Analysis**

**1. Loss of Resolution**

GJAM models *joint distributions* of species abundance—yes—but it still estimates **species-specific responses**, which you're leveraging to evaluate **species-level detectability**. Aggregating across species would mask important variation.

For example, dominant species might drive the average, obscuring rare or declining species whose detectability may still matter for management.

**2. Your Sampling Design Targets Species**

You’ve collected data with the intent of monitoring **species-level change**. From that perspective:

* Rare species might be harder to detect, but still ecologically important.
* Managers often care whether we can detect change for *particular species*, not just overall trends.

Your current framework asks:

“How many species (or which species) can reliably detect a 20% change year-to-year, and how does sample size affect that?”

This is **directly useful for guiding plot-level sampling effort.**

**3. Your Current GJAM-Based Approach Mirrors the First Effort**

As you said, your current approach:

* Runs a **single joint model** for all species (unlike the LME-per-species method)
* Then **simulates and evaluates detection per species**, using a more formal and coded threshold.

This makes your results **more reproducible**, and avoids the “squishy” cutoff from before.

**🧠 So, Does a Community-Aggregated Test Make Sense in GJAM?**

Yes—but for a **different purpose**:

* If your goal were to say, “Can we detect any general trend in overall cover at the site level?” then a community-level test could be appropriate.
* If your goal is to assess **how much sampling is needed to detect changes in specific species**, your current approach is better suited.

**🛡 Recommendation**

Stick with your current approach.

Then (optionally), you can *add* a community-level summary to your output for completeness. For instance:

r

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# Community-level posterior difference per draw

community\_diff <- rowMeans(pred\_array[, "changed", ]) - rowMeans(pred\_array[, "baseline", ])

community\_detect\_prob <- mean(community\_diff > 0)

But don’t replace your species-level detectability framework. You’re doing it the right way for the goals you’ve laid out.

Would you like help writing a side analysis like this (e.g., community-level detectability) or formalizing your criteria in code for the species-level summaries?

**You said:**

how similar are the results of our species level aggregations likely to be to a modeling effort where we had run the community-agregated test?

**ChatGPT said:**

Great question — the similarity between **species-level aggregation results** and a **community-level aggregated test** depends on a few key factors. Let's break it down so you can understand when they might be similar, and when they’re likely to diverge.

**🔁 What you're comparing**

You're essentially comparing two approaches to detecting change:

| **Approach** | **What it does** | **Aggregation?** | **Output** |
| --- | --- | --- | --- |
| **Species-level (your current method)** | Simulates posterior predictions *per species* and computes detection probability individually | Aggregated *after* modeling | A distribution of detection probabilities and change metrics for each species |
| **Community-level (your colleague’s suggestion)** | Simulates posterior predictions for the **average** across species directly | Aggregated *before* evaluating change | A single detection probability for overall community change |

**🔍 When they’ll give similar results**

They’ll tend to agree when:

1. **Species responses are highly correlated**:
   * If most species increase/decrease in abundance in the same direction and with similar magnitude, then the **mean abundance reflects the whole community well**.
2. **Dominant species drive most of the signal**:
   * If 1–2 highly abundant species account for most of the variation, then the average response might look like those species.
3. **Rare species have negligible weight**:
   * In a community-level mean, rare species have low influence unless weighted differently.

In these cases, you might see that:

“Most species have high detection probability”  
and  
“The community-level mean also shows a strong signal”

So conclusions about **adequate sample size** might be roughly similar.

**❗ When they’ll diverge**

They will diverge when:

1. **Species respond heterogeneously**:
   * Some increase, some decrease, some show no change.
   * Then the **mean can cancel out signals**, making detection harder at the community level.
2. **Rare species show large changes**:
   * Species-level detection might identify strong changes in less abundant species that are **completely invisible** in a community average.
3. **Non-linear relationships or noise**:
   * Noise in individual species can wash out in a mean, making the community-level signal look smoother (or misleadingly flat).

So you might see:

“A few species had strong detectability of change”  
but  
“The community mean looked unchanged due to canceling trends”

**🧪 Practical similarity?**

Here’s what happens often in real data:

* The **overall trend** may be captured by both approaches (e.g., “things are changing”), but
* The **sensitivity to detecting change in specific species or rare taxa** is **lost in the community-level method**.

That means your **sample size recommendations**, based on species-level detection rates, may **require larger samples** than if you only cared about a community average.

Which is appropriate — you're managing **species**, not a community mean.

**✅ Summary**

| **Question** | **Answer** |
| --- | --- |
| Will species-level and community-level analyses give similar conclusions? | Only if species respond similarly, and dominant species drive trends. |
| Are species-level summaries more conservative and detailed? | **Yes.** They give you insight into *which* species are detectable and *how many*. |
| Is it worth checking both? | Possibly, but only as a complement — your species-level method is the right foundation. |

Would you like to quantify this with a quick code-based comparison using your existing posterior\_list? For example:

* Compare mean\_detect\_prob across species vs.
* A single community\_detect\_prob for each year pair?

I can walk you through that.

**You said:**

please provide a side by side summary of the two approaches with pros and cons of both

**ChatGPT said:**

Here is a **side-by-side summary** of the two approaches — **species-level** vs **community-level** sensitivity analysis — with clearly articulated pros, cons, and use cases.

**🧪 Summary Table: Species-Level vs. Community-Level Sensitivity Analysis**

| **Feature** | **Species-Level Detection (your current GJAM-based method)** | **Community-Level Detection (average response method)** |
| --- | --- | --- |
| **Definition** | Simulate and assess detectability of a 20% change for *each species individually* | Assess detectability of a 20% change in *the mean (or composite) abundance* across all species |
| **Unit of inference** | Each species (taxon) | The whole community (mean or total abundance) |
| **Aggregation** | Detection is computed *per species*, then aggregated | Species responses are aggregated *before* detection is computed |
| **Sensitivity to species differences** | High — captures heterogeneity in species responses | Low — can mask variation by averaging opposing responses |
| **Handles rare species?** | Yes (included, though often harder to detect) | Rare species have minimal effect unless weighted |
| **Detection thresholds** | Applied per species (e.g., >0.8 detection prob) | Applied once to aggregate metric |
| **Output** | Detection probability per species × year pair × sample size | Single detection probability per year pair × sample size |
| **Interpretability** | Richer — species-specific guidance for monitoring | Simpler — easy summary metric for decision-makers |
| **Data requirements** | Higher — requires robust posterior estimates for many species | Lower — focuses on community mean, less sensitive to sparse taxa |
| **Code complexity** | More complex (but implemented and validated) | Simpler (if implemented as posterior mean of community response) |
| **Risk** | May overemphasize noise in rare taxa | May obscure critical signals from rare or divergent species |
| **Best use** | When species-level management or biodiversity is the goal | When managing overall vegetation structure or ecosystem function |

**✅ Pros and Cons**

**Species-Level Detection**

**Pros:**

* Detects heterogeneous responses across species.
* Helps prioritize species for monitoring.
* Aligns well with biodiversity and conservation goals.

**Cons:**

* Interpretation can be complex (e.g., many results).
* Rare species may dominate reporting due to variability.
* Harder to summarize succinctly.

**Community-Level Detection**

**Pros:**

* Easy to interpret and communicate.
* Provides a single metric of change detectability.
* Robust to noisy or rare species.

**Cons:**

* Can **miss important ecological patterns** hidden in species-level variation.
* Averages may **cancel out** meaningful opposing trends.
* Less useful if species-level action is needed.

**🔍 Recommendation**

Since your goals include:

* **Evaluating detectability per species**, and
* **Making decisions about adequate sample sizes** based on species richness and variation,

You are right to stick with the **species-level sensitivity analysis** as your core approach.

However, a **community-level detection probability** could be useful as a **complementary summary** — especially for communicating high-level results to non-technical audiences or as a validation check.

Bottom of Form

More on comparison to first approach:  
  
Yes — I’ve accessed your uploaded report and located the content related to **Objective 2** of your first sensitivity analysis. Here's a side-by-side summary comparing your **previous (LME-based)** approach to your **current (GJAM-based)** approach, including pros and cons of each, to help frame your decision-making.

**Summary of the Two Sensitivity Analysis Approaches**

| **Feature** | **Previous Approach (Objective 2: LME-based)** | **Current Approach (GJAM-based)** |
| --- | --- | --- |
| **Modeling Strategy** | Species-by-species linear mixed-effects (LME) models | Joint species distribution model (GJAM) with full community |
| **Data Structure** | Fit separate LME for each species (with year as fixed effect, plot as random) | Model full species set jointly with predictors (year, land cover) |
| **Handling of Rarity** | Many species excluded due to insufficient data; detection success defined as whether the model converged and had power to detect a 20% effect | Rare species retained due to borrowing strength across species in joint likelihood |
| **Metric for Sensitivity** | Count of species for which a 20% year-to-year change was statistically significant | Posterior detection probability for a 20% simulated change, per species and year-pair |
| **Aggregation** | Summarized by number of species “detectable” (unclear threshold) | Summarized by detection probability per species; allows defining formal threshold (e.g., >0.8) |
| **Decision Framework** | Based on number of species with significant LME coefficients | Based on proportion of species meeting detection probability threshold across subsamples |
| **Statistical Inference** | Frequentist confidence intervals and significance testing | Bayesian posterior distributions and uncertainty propagation |
| **Sensitivity to Sample Size** | Indirectly evaluated by comparing detection counts | Directly modeled by reducing sample size and simulating impact on detectability |
| **Community-level Signal** | Not modeled; each species treated independently | Possible to compute community-level summary, but current focus is species-level sensitivity |
| **Interpretability** | More familiar to ecologists; easy to explain | Requires more statistical nuance to interpret detection probability and modeling structure |
| **Computation** | Fast (per species) but fails on rare taxa | Computationally expensive but more inclusive and robust |

**Pros and Cons**

**✅ LME Approach**

**Pros:**

* Simpler, faster, and easy to explain
* Straightforward interpretation of significant year effects

**Cons:**

* Excludes many species due to convergence issues or data sparsity
* Poor handling of rare species and missing data
* Difficult to define or justify detection thresholds
* Doesn’t simulate effect of sample size reduction

**✅ GJAM Approach**

**Pros:**

* Handles full species set jointly, including rare species
* Posterior draws allow consistent and flexible evaluation of detection probabilities
* Enables direct testing of sampling design changes
* Matches your earlier framework in logic but improves rigor and reproducibility

**Cons:**

* Requires careful model validation and prediction diagnostics
* Interpretation of posterior detection probability may be less familiar
* More computationally intensive

**Does Your Colleague’s Suggestion Make Sense in GJAM Context?**

Yes, but with nuance:

* GJAM **can** be used to simulate a change in a community-aggregated metric (e.g., mean cover across species), and test detectability of a shift in the aggregate.
* However, this sacrifices resolution. GJAM’s joint framework already accounts for shared signal and correlation between species, so **summing posteriors across species isn’t necessarily more informative** — and it **hides which species are driving signals**.
* Your **species-level sensitivity framework** is more robust and transparent, especially when paired with summaries (like rank abundance) to guide decision-making across taxa.

So while a community-aggregated test is statistically possible, it’s **less actionable** and **less biologically informative** for management or monitoring planning.