New fit gjam without the internals bs  
  
**🔍 Primary Project Goal**

Evaluate whether a **20% year-to-year change in species abundance** is **detectable** within each NEON site using GJAM.

**✅ Alignment with Each Requirement:**

| **Goal Component** | **Confirmed in fit\_gjam\_model()** |
| --- | --- |
| **Site-specific model** | ✔️ Function models one site at a time using site\_data |
| **Species-level percent cover** | ✔️ Uses mean\_cover per taxonID (wide format with taxon columns) |
| **Year-to-year detection** | ✔️ year is treated as a **factor** predictor |
| **Other covariates (e.g., nlcdClass)** | ✔️ Included as a factor in the design matrix |
| **Drop uninformative species** | ✔️ Drops species with zero abundance or zero variance |
| **Multispecies joint modeling** | ✔️ GJAM used with typeNames = "CA" (continuous abundance) |
| **Posterior draws for uncertainty estimation** | ✔️ GJAM stores betaBeta and sigmaSave for posterior predictions |
| **No assumption of REDUCT** | ✔️ Explicitly sets REDUCT = FALSE |
| **Output is compatible with gjamPredict()** | ✔️ Returns clean fit object with modelList intact |

**🔄 Next Step: Posterior Simulation Workflow**

With fit\_gjam\_model() now stabilized:

* You can **simulate a 20% abundance change** (e.g., multiply selected y values by 1.2)
* Then **refit** the model and use gjamPredict() to see if those changes are detectable
* This supports both **year-to-year detectability** and **plot subsampling** analyses

**🧭 Confirmed Fit for Purpose**

🟢 **Conclusion**: fit\_gjam\_model() is now *fully aligned* with the goals of sensitivity analysis as you've described — no hidden assumptions, no reliance on internal functions, and well-positioned for posterior prediction using supported GJAM methods.

Other steps:

Would you like a companion function to **summarize posterior prediction differences  
  
🧠 Conceptual Flow of Your Sensitivity Analysis**

1. **Fit the model**

r

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fit <- fit\_gjam\_model(site\_data)

1. **Posterior predictions from original data**

r

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baseline\_pred <- posterior\_predict\_gjam(fit, xnew = original\_xdata, nsim = 100)

1. **Simulate a 20% abundance change**

r

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changed\_xdata <- simulate\_change(original\_xdata, mode = "increase", percent = 20)

1. **Posterior predictions under the simulated change**

r

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changed\_pred <- posterior\_predict\_gjam(fit, xnew = changed\_xdata, nsim = 100)

1. **Assess detection**
   * Compare baseline\_pred$sdList$yPost and changed\_pred$sdList$yPost
   * For each species, estimate probability that the posterior mean or quantiles differ enough to say the change is “detectable”

**🔁 simulate\_change() Now Focuses On:**

* Modifying xnew covariates only (e.g. change year, if that’s the axis of contrast)
* Possibly altering xnew percent cover values (if simulating change in response rather than covariates — but this is rare)

##testing fit\_gjam\_model (new) 7/19/2025  
**⚠️ model$inputs$x is NULL**

You found:

r

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str(model$inputs$x)

NULL

This is concerning. While model$inputs$xdata exists:

r

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names(model$inputs)

# ...

# [12] "xdata"

…it seems x is missing.

**🔎 Why That Matters**

In the GJAM internals:

* xdata is often **pre-standardized** and human-readable (with factor levels, etc.)
* x is the **numerical model matrix** derived from xdata (usually after model.matrix())
* Some older downstream GJAM functions use x, while newer ones rely on xdata.

If we stick to using gjamPredict() — which expects xdata — this missing x shouldn't matter.

But if:

* Any downstream custom code, patches, or internal GJAM helpers expect x, or
* We try to revive .gjamPrediction()-like workflows,

then it would be a problem.

**🩹 Optional Fix (Only if Needed)**

You could restore fit$inputs$x like this:

r

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fit$inputs$x <- model.matrix(formula, data = xdata)

But at this point, **I recommend not patching this unless a specific function fails due to it.**

**✅ Final Evaluation: Are We on Track?**

* Yes — the fitted object from fit\_gjam\_model() contains everything needed for gjamPredict() and your simulation workflow.
* You also have xdata and ydata saved **outside** the model, so you're not dependent on internal GJAM slots.  
    
  **✅ Recommendation**
* If you want full internal access later (e.g., in simulate or diagnostics), you can **safely add these back into the model object before returning it**:
* **🔧 Add this at the end of fit\_gjam\_model():**
* r
* CopyEdit
* fit$xdata <- xdata
* fit$y <- ydata
* This way, any downstream function (e.g., simulate\_yearly\_changes()) can access:
* fit$fit$xdata
* fit$fit$y
* — without error or additional plumbing.
* Let me know when you're ready to proceed with checking model$inputs, or if you’d like to patch fit\_gjam\_model() accordingly. No assumptions — I’ll wait for your confirmation.
* fix  
  **📌 Summary**
* You’re absolutely correct: the data exist *elsewhere*, but they are **not available where gjamPredict() expects to find them**. This confirms:
* The underlying model fit is valid.
* The output needs structural correction (not re-fitting).
* Let me know when you’re ready to update fit\_gjam\_model() accordingly.

New fit\_gjam\_model 20250719  
**🔧 Summary of Edits**

* **Patched fit$modelList**:
  + Added fit$modelList$betaBeta <- fit$chains$bgibbs
  + Added fit$modelList$sigmaSave <- fit$chains$sgibbs
* **Restored critical model elements**:
  + Set fit$xdata <- x\_data
  + Set fit$y <- y\_matrix
  + Set fit$typeNames <- model\_list$typeNames
* **Preserved original design logic**, no structural changes to modeling steps or formula.
* These edits ensure compatibility with gjamPredict() and any downstream wrappers like posterior\_predict\_gjam().  
    
  + # 8. Patch missing elements for posterior prediction
* + fit$modelList$betaBeta <- fit$chains$bgibbs
* + fit$modelList$sigmaSave <- fit$chains$sgibbs
* + fit$xdata <- x\_data
* + fit$y <- y\_matrix
* + fit$typeNames <- model\_list$typeNames

**✅ Updated Diagnosis Summary (after patch)**

| **Element** | **Status** | **Resolution** |
| --- | --- | --- |
| model$xdata | ✅ Present | Explicitly restored via fit$xdata <- x\_data |
| model$y | ✅ Present | Explicitly restored via fit$y <- y\_matrix |
| model$inputs$xdata | ✅ Valid | Already present from original gjam() call |
| model$inputs$y | ✅ Valid | Already present from original gjam() call |
| model$modelList$typeNames | ✅ Valid | Preserved and copied to fit$typeNames |
| modelList$betaBeta, sigmaSave | ✅ Present | Added via fit$modelList$betaBeta <- fit$chains$bgibbs and fit$modelList$sigmaSave <- fit$chains$sgibbs |

This now satisfies **all structural and content requirements** for downstream compatibility with:

* posterior\_predict\_gjam()
* simulate\_yearly\_changes()
* targets-based pipelines