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.