

Suggestions for EpidCRN Package Refactor

- **Species Format:** Ensure consistent use of strings vs. symbols across modules. If strings like "S1" are required for compatibility, verify that all helper functions (e.g., `compToAsso`) handle them correctly.
- **Function Isolation:** Check that each submodule (e.g., matrix builders, rate evaluators) has no hidden dependencies on global variables or context from `EpidCRN`.
- **Evaluation Order:** Use `Trace[]` or `Echo[]` to inspect how expressions like `ToExpression[spe]` behave after modularization.
- **Shape Errors:** Confirm that `spe`, `a1`, `be`, and `gamma` are all populated correctly before computing RHS. Use `Dimensions[]` to verify matrix shapes.
- **Legacy Compatibility:** If older notebooks rely on implicit context or symbol definitions, consider adding a wrapper that normalizes reaction formats before passing to `extMat`.
- **Testing:** Create a minimal test notebook that loads only `EpidCRN.wl` and runs `extMat[]` on a simple reaction list. Compare output with legacy behavior.
- **Documentation:** Add brief usage notes to each module header to clarify expected input formats and dependencies.