

**Why Risk it, When You Can {rix} it: A Tutorial for Computational Reproducibility Focused
on Simulation Studies**

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Abstract

Reproducibility remains limited in psychology, in part because reproducibility exists on a spectrum – from sharing isolated code fragments to providing fully executable pipelines that ensure identical results. This article introduces Nix and the {rix} R package as a way to provide a comprehensive solution for achieving full computational reproducibility in simulation studies.

Building on this, we also demonstrate a tutorial on how to use {rix} to obtain a reproducible manuscript using the apaquarto extension.

Keywords: reproducibility, Nix, simulation studies, R, computational methods

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Psychological science is in the midst of a credibility revolution, which has prompted substantial progress in how research is conducted and evaluated (Vazire, 2018). Yet, despite notable progress, a key cornerstone of science, reproducibility (i.e., the ability to precisely reproduce the results of a study or studies based on provided data, code, materials, and software/hardware) remains limited (Hardwicke et al., 2020). ~~As a result, ensuring reproducibility~~ This remains an open and pressing challenge for psychological science.

Addressing this gap is complicated by the fact that reproducibility is not a binary feature but instead exists along a continuum (Peng, 2011). At the lower end, researchers may share only their manuscript. Further along the spectrum, they might provide partial code, full analysis scripts, or publicly accessible datasets. At the highest level, researchers document a fully specified computational environment that allows others to recreate identical results—from raw data to final manuscript output—with minimal friction. Open-science initiatives have made considerable progress along this continuum. Journal incentives such as open-science badges (Kidwell et al., 2016), together with platforms like GitHub and the Open Science Framework, have made data and code sharing increasingly routine (Levenstein & Lyle, 2018). However, these efforts largely occupy the lower and middle portions of the spectrum, focusing on *what* is shared rather than *how* shared materials can be executed in practice. Data and code are never self-sufficient; they depend on a hierarchy of software components known collectively as dependencies, including the version of the programming language, the set of packages used by the analysis, and the system libraries that those packages require in order to function correctly. When these dependencies differ from those used in the original analysis, code may fail, behave differently across machines, or yield conflicting numerical results (Baker et al., 2024; Glatard et al., 2015; Hodges et al., 2023; Nosek et al., 2022).

These issues are particularly acute for simulation studies, which rely on complex codebases, versioned dependencies, and intricate software configurations (Luijken et al., 2024;

Siepe et al., 2024). To make this concrete, we use *computational environment* to refer to the complete software context required for an analysis to run successfully—the programming language version, package versions, system libraries, and operating system (Rodrigues, 2023; Rodrigues & Baumann, 2026). We define *computational environment reproducibility* as the ability to reconstruct this entire software stack on any machine and at any future time, such that executing the same code yields the same numerical results. Empirical assessments show that current practice falls short of this ideal. Siepe et al. (2024) report that nearly two-thirds of simulation studies in psychology provide no accompanying code, and among those that do, documentation of the computational environment is rarely included. This gap is consequential: simulation studies inform methodological recommendations, meaning that insufficient reproducibility undermines confidence in those recommendations (Luijken et al., 2024; White et al., 2024).

Arguably, these challenges persist because researchers must navigate a fragmented landscape of solutions, each addressing only part of the problem. Package-level managers such as {renv} (Ushey, 2024) and {groundhog} (Simonsohn, 2020) stabilize R package versions but do not manage the R interpreter itself or the system-level libraries those packages depend on. Workflow orchestration tools such as {targets} (Landau, 2021) and Make (Feldman, 1979) support reproducibility in a different sense: they specify the structure of an analysis by formalizing the order in which steps should run and by tracking dependencies among intermediate results. These tools clarify *how* an analysis proceeds, but they assume that the software stack required to run each step is already stable. Containerization tools such as Docker, including R-focused implementations like Rocker [Isnt rocker a R instance of Docker? JG] (Boettiger, 2015; Boettiger & Eddelbuettel, 2017) offer a more comprehensive approach by bundling the full environment—operating system, system libraries, interpreter versions, and packages—into a single executable image. Yet their use requires familiarity with Linux system administration, and even containerization may suffer from temporal drift when Dockerfiles rely on mutable upstream repositories (Malka et al., 2024). For a detailed comparison of these tools and their limitations, see Rodrigues and Baumann (2026). Researchers thus face a difficult choice between solutions

that are accessible but incomplete or approaches that are powerful but demand substantial technical expertise.

In this article, therefore, we focus specifically on computational environment reproducibility as the foundation upon which other reproducibility practices depend. For that, we introduce Nix ([Dolstra et al., 2004](#)), a functional package manager designed to make software installation deterministic, and `{rix}` ([Rodrigues & Baumann, 2025](#)), an R interface that allows researchers to use Nix without needing deep knowledge of its underlying language or infrastructure. Our objective is not to introduce a specific workflow orchestration system or to prescribe a particular analytic structure. Instead, we aim to show how Nix and `{rix}` can establish a stable, cross-platform environment within which any analysis—whether organized in simple, documented script sequences (e.g., .R files that `source()` others), through more formal orchestration tools (e.g., targets) or embedded as code chunks in .Rmd or .qmd—can be executed reliably.

We illustrate these ideas through a reproducible simulation study conducted in R, culminating in an automated APA-formatted manuscript generated with `apaquarto` ([Schneider, 2024](#)). Although the example centers on R because of its prominence in psychological methodology, the principles underlying environment reproducibility apply equally to other languages, including Python and Julia, and to different development environments such as RStudio, VS Code, Emacs, or Positron. Later in the article, we briefly comment on rixpress ([Rodrigues, 2025](#)), which extends Nix-based reproducibility to workflows spanning multiple languages. Throughout, our emphasis remains squarely on the reproducibility of computational environments as the essential basis for transparent, reliable, and durable scientific workflows.

A Practical Example: Setting up a Reproducible Simulation Study with `{rix}`

Before proceeding with the technical implementation and tutorial, we refer readers to the Appendix A, which presents a simulation study scenario designed to ground the subsequent

discussion in a concrete example¹. The scenario mimics a typical methods manuscript, describing both the statistical design and the computational details one might encounter in practice. While the example is illustrative rather than substantive—~~readers can follow the tutorial without engaging with the specifics of the simulation~~—we include it to anchor the discussion in something more tangible.

Simulation studies typically structure code into multiple component files, each handling a distinct analytical phase. We provide our implementation in this conventional format, organized into five sequential files²: data generation (`01_data_generation.R`), statistical model specification (`02_models.R`), simulation execution (`03_run_simulation.R`), performance metric calculation (`04_performance_metrics.R`), and results visualization (`05_plots.R`). However, because our focus is on the reproducibility of the complete manuscript, we embed all simulation code directly within this manuscript as executable code chunks in the `.qmd` file. When this document is rendered, the simulation runs in its entirety (i.e., from data generation through final visualizations). This is not needed and, in fact, most simulation studies are too long to be included in the manuscript compilation. We will come back to this later in the tutorial.

Notably, the workflow depends on several R packages (see Appendix A)³. Thus, let's pretend a researcher wants to reproduce our simulation and results reported in the article. What might prevent them from obtaining identical results? The most immediate concern may involve package versions. A researcher installing packages today may encounter errors if functions have been renamed or deprecated, or may obtain results that differ subtly due to changes in computational defaults. Beyond package versions, some R packages depend on system-level libraries that must be installed separately from R itself. Our simulation illustrates this directly: the

¹ Note that the rationale, programming-related choices, and results should not be used for substantial interpretation. For instance, the usage of `{rvinecopulib}` and the parallel set-up may be considered an overhead.

² Readers can find the files for these simulations here: <https://github.com/felipelfv/Why-risk-it-when-you-can-rix-it>

³ For instance, in this context, we use parallel processing which requires specifying the amount of cores to be used. This type of information should be mentioned.

{rvinecopulib} package provides an interface to a C++ library and links against Boost, Eigen, and RcppThread (Nagler & Vatter, 2025). Moreover, the R language itself introduces version dependencies. Code written with R 4.3 may use syntax or functions unavailable in R 4.0 [** % vs. |>?JG**]. More subtly, R’s random number generator has changed across major versions, meaning that identical code with identical seeds can produce different random sequences depending on the R version. For simulation studies where reproducibility of specific random draws matters, this version sensitivity is consequential. Moreover, if one also employs literate programming for the manuscript as in our case, additional dependencies arise: R Markdown or Quarto documents require pandoc, and PDF output requires a LaTeX distribution—each with its own versioning and platform-specific installation.

Nix and {rix}: A Comprehensive Solution

A potential solution to the above issue is Nix (Dolstra et al., 2004). Nix is a package manager [**Bruno you once used the analogy of Nix like the apple application store. I kind of like this because it is more than a package manger. (JG)**] built around declarative, isolated environments rather than ad hoc system-level installations. Unlike familiar tools such as `install.packages()` in R or `apt-get` on Linux, Nix manages language versions, package versions, system dependencies, and cross-platform consistency through a single framework (Rodrigues & Baumann, 2025). Rather than modifying shared directories, Nix builds each environment as an explicit, self-contained specification. This addresses the fragmented landscape described before: where researchers currently must coordinate separate tools for package management, interpreter versions, and system dependencies, Nix handles all three within a unified declarative model.

Core Principles

Rather than installing software into global directories (e.g., `/usr/lib`), Nix places every package in its own directory under `/nix/store`. Each package path contains a cryptographic hash representing its precise inputs—source code, dependencies, and build instructions. Because these paths are content-addressed, multiple versions of the same software can coexist without

conflict. A researcher can, for example, maintain projects requiring R 4.1.0 and R 4.3.3 side by side, or use different package versions across analyses, switching between them seamlessly ([Rodrigues & Baumann, 2025](#)).

The Nix ecosystem is built around nixpkgs, a version-controlled repository comprising more than 120,000 packages, including nearly all of CRAN and Bioconductor. By pinning a specific commit or date, researchers freeze the entire software stack—R itself, R packages, and all system libraries—at that point in time. This eliminates the system-dependency problems that tools like {renv} cannot address ([Rodrigues & Baumann, 2025](#)).

This architecture also ensures stability over time. Empirical work has shown strong rebuildability and reproducibility rates for historical nixpkgs snapshots ([Rodrigues & Baumann, 2026](#)). Combined with binary caches, which often allow environments to materialize in seconds, Nix becomes practical for interactive research workflows ([Rodrigues & Baumann, 2025](#)).

The {rix} Package: R Interface to Nix

Nix expressions are written in a dedicated functional language unfamiliar to most researchers. The {rix} package removes this barrier by providing an R-native interface. A single call to `rix()` generates complete Nix configurations from standard R syntax, specifying R versions, CRAN packages, system libraries, and even Python or Julia components when required. Users never need to read or write Nix code directly, as {rix} performs the translation automatically ([Rodrigues & Baumann, 2025](#)).

A key feature of {rix} is its integration with rstats-on-nix, a community-maintained fork offering daily CRAN snapshots and weekly tested environments on Linux and macOS. Researchers can request, for example, `rix(date = "2024-12-14")` to obtain a validated and reproducible environment without manually assessing compatibility. After the configuration is generated, `nix_build()` instantiates the environment, and binary caches typically allow this to complete within seconds ([Rodrigues & Baumann, 2025](#)).

Although Nix is capable of replacing tools like Docker for isolation or {renv} for package management, it does not require an all-or-nothing transition. Researchers can adopt it gradually

and use it alongside familiar tooling. For instance, by building Docker images with Nix, converting existing {renv} lockfiles, or running {targets} pipelines within a Nix-defined environment (Rodrigues & Baumann, 2025). This allows Nix to strengthen reproducibility while preserving established workflows. For projects requiring more sophisticated pipeline management, {rixpress} extends Nix’s guarantees to workflow orchestration, enabling step-level isolation across languages, though such capabilities lie beyond the present focus on environment reproducibility. We will come back to this after the tutorial.

Step I: Installing Nix and {rix}

Before proceeding, both Nix and the {rix} R package need to be installed. Installation procedures differ across operating systems (Windows via WSL2, Linux, and macOS), and detailed, up-to-date instructions are maintained in the official {rix} documentation:

- **Linux and Windows (WSL2):** <https://docs.ropensci.org/rix/articles/b1-setting-up-and-using-rix-on-linux-and-windows.html>
- **macOS:** <https://docs.ropensci.org/rix/articles/b2-setting-up-and-using-rix-on-macos.html>

Once Nix is installed, {rix} can be installed from CRAN using `install.packages("rix")`, or directly through Nix without requiring a pre-existing R installation (see the documentation links above for details).

[Should we have these commands with listing captions? JG]

It is worth noting that {rix} can generate Nix expressions even without Nix installed on your system—you can write a `default.nix` file without Nix, but you cannot build or enter the resulting environment unless Nix is installed (Rodrigues & Baumann, 2025).

Step II: Specifying the Computational Environment

The initial step in establishing a reproducible environment is to create a script that will generate the environment specification. We recommend creating a file named `generate_env.R` (or similar) in the project directory. This script will use the `rix()` function from the {rix}

package to produce a `default.nix` file—a declarative specification that precisely defines all software dependencies required for the project.

In the case where we use literate programming for generating the manuscript, we implement the following environment specification, which can be found on the GitHub repository as a file named `generate_env.R` (Listing 1):

Note that we have more than just the R packages specified for the simulation scripts. This happens because we also included what is needed for the manuscript generation, not solely for the simulation code. In Appendix B, we mention more specifically the reasons for adding each package in `r_pkgs()` and `tex_pkgs()`. For now, we focus more on clarifying the different arguments for the `rix()` function.

The Environment Generation Script

The `rix()` function⁴ constructs this specification through a series of parameters that collectively describe the computational environment. Each parameter serves a distinct purpose in defining the environment’s characteristics.

Specifying the R version (line 1).

[Maybe use line numbers from the code chunk? Alternatively maybe just list the argument? I wonder if we highlight the relevant line of code? JG].. Researchers must first determine which version of R to use. This can be accomplished in two ways: The `r_ver` argument accepts an exact version string (e.g., “4.3.3”) or special designations such as “latest-upstream” for the most recent stable release. Alternatively, the `date` argument specifies a particular date (e.g., “2024-11-15”), which ensures that R and all packages correspond to the versions available on that date. The date-based approach is generally preferable for reproducibility, as it captures a complete snapshot of the R ecosystem at a single point in time. For this tutorial, as shown on top, we use the `date` parameter to ensure temporal consistency across all software components (Rodrigues & Baumann, 2025) (see `{rix}` documentation for more: <https://docs.ropensci.org/rix/articles/>

⁴ For an overarching information on the function `rix()`, we suggest the following `{rix}` documentation: <https://docs.ropensci.org/rix/articles/c-using-rix-to-build-project-specific-environments.html>

[d2-installing-system-tools-and-texlive-packages-in-a-nix-environment.html](#)).

Declaring R package dependencies (line 2). The `r_pkgs` argument accepts a character vector listing all required R packages by their CRAN names. These packages will be installed from the version repository corresponding to the specified date or R version. It is important to list all packages that the analysis will load directly; dependencies of these packages are automatically resolved by Nix. For packages requiring specific versions not corresponding to the chosen date, researchers can specify exact versions using the syntax "`packagename@version`" (e.g., "`ggplot2@2.2.1`"). For packages available only on GitHub or other Git repositories, the `git_pkgs` argument accepts a list structure containing repository URLs and specific commit hashes. For example:

This ensures that exact development versions are obtained ([Rodrigues & Baumann, 2025](#)). For our simulation study, all packages were used with their CRAN versions (see `{rix}` documentation for more details: <https://docs.ropensci.org/rix/articles/d2-installing-system-tools-and-texlive-packages-in-a-nix-environment.html>).

Including system-level dependencies (line 3). Many R-based workflows require tools beyond R packages. The `system_pkgs` parameter specifies system-level software such as Quarto for document generation, Git for version control, or Pandoc for document conversion. Critically, we include Quarto as a system package because this tutorial demonstrates full computational reproducibility—not merely of the simulation code, but of the complete manuscript itself. Our manuscript uses the `apaquarto` extension for APA formatting, stored in the project's `_extensions/` directory ([Rodrigues & Baumann, 2025](#)) (see `{rix}` documentation for more: <https://docs.ropensci.org/rix/articles/d2-installing-system-tools-and-texlive-packages-in-a-nix-environment.html>).

Specifying LaTeX packages (line 4). The `tex_pkgs` parameter specifies LaTeX packages needed for PDF compilation. When any packages are listed, Nix automatically includes a minimal TeXLive distribution (`scheme-small`) as a base, to which the specified packages are added. Determining the required LaTeX packages typically involves some trial and

error—Quarto’s error messages during, for example, the PDF rendering indicate which packages are missing, and these can then be added to `tex_pkgs` (see `{rix}` documentation for more:

<https://docs.ropensci.org/rix/articles/>

<d2-installing-system-tools-and-texlive-packages-in-a-nix-environment.html>).

Configuring the development environment (line 5). The `ide` parameter determines whether an integrated development environment should be included in the Nix environment. Setting `ide = "rstudio"` installs a project-specific version of RStudio within the Nix environment. This is required for RStudio because, unlike other editors, RStudio cannot interact with Nix shells unless it is itself installed via Nix. Note that on macOS, RStudio is only available through Nix for R versions 4.4.3 or later (or dates after 2025-02-28); for earlier versions, alternative editors must be used. Other supported IDEs include Positron (`ide = "positron"`), Visual Studio Code (`ide = "code"`), and command-line tools such as Radian (`ide = "radian"`). These editors can either be installed within the Nix environment using the `ide` parameter, or researchers can use an already-installed version by setting `ide = "none"` (or `ide = "other"`) and configuring `direnv` to automatically load the Nix environment when opening the project folder. Each IDE installed via Nix is project-specific and will not interfere with system-wide installations. See the `{rix}` documentation for detailed configuration instructions:

<https://docs.ropensci.org/rix/articles/e-configuring-ide.html>.

Setting file output parameters (line 6 and 7). The `project_path` parameter indicates where the `default.nix` file should be written (“`.`” denotes the current directory), while `overwrite` controls whether an existing file should be replaced. Adding to this, setting `print = TRUE`, which is another argument, displays the generated specification in the console for immediate verification (Rodrigues & Baumann, 2025).

Multi-language environment support. While this tutorial focuses on R, researchers working across multiple programming languages can include Python or Julia in their environments. The `py_conf` parameter accepts a list specifying a Python version and required packages (e.g., `py_conf = list(py_version = "3.12", py_pkgs =`

`c("polars", "pandas"))`. Similarly, `jl_conf` enables Julia package installation. This capability is particularly useful, for example, for projects requiring statistical computing in R alongside machine learning pipelines in Python or numerical optimization in Julia (Rodrigues & Baumann, 2025) (see `{rix}` documentation for more:

<https://docs.ropensci.org/rix/articles/d1-installing-r-packages-in-a-nix-environment.html>.

[We should include a code chunk like the github one above showing how to add python packages?JG]

Generating the Environment Specification

To execute the script for Example 1 [1 not 2?(JG)], either run from the terminal `Rscript generate_env.R`, source it from within R using `source("generate_env.R")`, or run the `rix::rix()` function above. This will generate the `default.nix` file in the project directory. This file serves as the formal, machine-readable specification of the computational environment. Importantly, `rix()` automatically invokes `rix_init()`, which creates a project-specific `.Rprofile` file that prevents package library conflicts and disables `install.packages()` to maintain environment integrity. There may be exemptions to this, which we comment briefly in the next section.

Step III: Building and Using the Reproducible Environment

Once the `default.nix` file has been generated, the next step is to build the environment and use it to reproduce either the simulation analyses or the complete manuscript. This section demonstrates both workflows.

Building the Environment

From the terminal, navigate to the study directory containing the `default.nix` file and execute (Listing 4):

This command builds the environment according to the specification. The first execution will download and install all required packages, which may take a few minutes depending on network speed and system resources. Subsequent builds use cached packages and complete in seconds. Upon successful completion, a symbolic link named `result` appears in the project

directory, pointing to the constructed environment in the Nix store.

[Footnote: make sure you configure cache?JG]

To activate the environment, run (Listing 5):

This command drops the user into a shell where all specified packages and tools are available. The shell prompt typically changes to indicate that a Nix environment is active (e.g., [nix-shell:~/project]\$).

[you can drop into a specific ide (here RStudio) by typing in `rstudio` this will open up the project in RStudio. Does this work? JG]

As mentioned, it is worth noting that Nix shells do not fully isolate you from your existing system by default. For R users, this has a practical implication: packages installed in your regular R library (outside of Nix) could potentially be loaded when running R from within the Nix environment. The {rix} package addresses this automatically—when you call `rix()`, it also executes `rix_init()`, which creates a project-specific `.Rprofile`. This file configures R to ignore external package libraries and also disables `install.packages()` within the environment. The rationale is straightforward: any new packages should be added to `default.nix` and the environment rebuilt, preserving full reproducibility (Rodrigues & Baumann, 2025). However, for stricter isolation⁵ that also prevents access to other system programs not specified in `default.nix`, use the `--pure` flag (Listing 6):

Reproducing the Complete Manuscript⁶

Beyond reproducing computational results, the Nix environment enables full manuscript reproducibility. The manuscript source file (`article.qmd`) combines narrative text, executable

⁵ For example, when preparing this manuscript without the `--pure` flag, `quarto render` worked successfully. However, when using the `--pure` flag, the build failed. Running `quarto check` from within the Nix shell (i.e., `nix-shell --run "quarto check"`) revealed that Quarto was still accessing the system's LaTeX installation (`/Library/TeX/texbin`) rather than being restricted to only what was specified in `default.nix`.

⁶ See the {rix} documentation for more:

<https://docs.ropensci.org/rix/articles/z-advanced-topic-building-an-environment-for-literate-programming.html>

code chunks, and references to simulation outputs. In our specific case, we integrate the simulation run itself in the manuscript as well as the reporting (i.e., performance metrics calculation and visualization). In other words, the code in the separate .R files are included as code chunks (see `article.qmd` in the GitHub repository).

This is not needed and most researchers would in fact probably not include the simulation run itself in the manuscript as many simulations take days to be completed. Thus, in this case, one could just proceed with the `Rscript 03_run_simulation.R` inside the nix shell. Then, in the `article.qmd` load the obtained results and integrate the code chunks that produce the performance metrics and visualization (see Figure 1).

To render the manuscript (Listing 7):

This command executes all code chunks in the manuscript, incorporates results and figures, and generates a formatted PDF following APA style guidelines via the `apaquarto` extension ([Schneider, 2024](#)). This extension is saved in the project repo already.

To download this extension for your own work you can install the extension by using the terminal (Listing 8):

or in the console (Listing 9):

The final document (docx, .pdf, or .html) is saved directly in the project folder. Because Quarto is installed as a system-level package in our Nix specification, the rendering occurs entirely within a fully reproducible environment, ensuring consistent output across machines regardless of local software configurations. If desired, the manuscript can also be reproduced interactively by opening the project folder in the user's preferred IDE and running the code chunks directly.

[Maybe footnote? Although we use `apaquarto` in this example, many alternative manuscript templates are available, and Nix is agnostic to the specific template employed, provided the necessary extensions are installed. (JG)]

Reproducing the Simulation

As described before, our Example 1 contains multiple scripts. For streamlined execution, we provide a master script (`06_run_all.R`) that runs the complete simulation and calculates the

results as well as visualizations. The script begins by loading the required packages, then proceeds through three steps: first, it sources `03_run_simulation.R`, which in turn loads the data generation function (`01_data_generation.R`) and the model estimation functions (`02_models.R`) to run the Monte Carlo simulation; second, it sources `04_performance_metrics.R` to calculate the performance criteria from the saved simulation results; and third, it sources `05_plots.R` to generate the figures (see Figure 1). The script has the following content (Listing 10):

Thus, to reproduce the simulation from within the Nix shell, meaning after running `nix-build` and `nix-shell` (Listing 11):

Alternatively, individual scripts can be executed separately (i.e., `Rscript 03_run_simulation.R`). Therefore, the key advantage of executing within `nix-shell` is that all dependencies—R version, packages, and system tools—match exactly those specified in `default.nix`.

Additional Considerations for Advanced Workflows

Workflow Orchestration: {targets} and {riexpress}

Complex simulation studies often benefit from workflow management systems that track dependencies between computational steps, cache intermediate results, and enable selective re-execution when inputs change. Two complementary approaches exist within the Nix ecosystem: using `{targets}` inside a Nix environment, or using `{riexpress}` to leverage Nix itself as the build automation tool.

Using {targets} Within Nix. As mentioned, the `{targets}` package (Landau, 2021) provides workflow orchestration for R-based projects. This combination ensures both computational reproducibility (via Nix controlling the environment) and computational efficiency (via targets' intelligent caching). To integrate `{targets}` with Nix, simply include “targets” in the `r_pkgs` parameter of `rix()`, [code listing? (JG)]and execute the pipeline within `nix-shell` using `Rscript -e 'targets::tar_make()'`. The `{targets}` metadata directory (`_targets/`) should be excluded from version control while the `_targets.R` configuration file should be

committed alongside `default.nix` (Rodrigues & Baumann, 2025). This approach is ideal for projects that remain within the R ecosystem and do not require different computational environments for different pipeline steps (see `{rix}` documentation: <https://docs.ropensci.org/rix/articles/z-advanced-topic-reproducible-analytical-pipelines-with-nix.html>).

Using `{rixpress}` for Polyglot Pipelines. The `{rixpress}` package (Rodrigues, 2025), a sister package to `{rix}`, uses Nix itself as the build automation tool rather than operating within a Nix environment. Each pipeline step becomes a Nix derivation, providing hermetic builds with sandboxed execution and content-addressable caching. The key advantage of `{rixpress}` emerges in multi-language workflows: different steps can execute in different Nix-defined environments (e.g., one step using R 4.2.0 with specific packages, another using Python 3.12 with machine learning libraries, another using Julia for numerical optimization). The package interface, inspired by `{targets}`, uses functions like `rxp_r()`, `rxp_py()`, and `rxp_jl()` to define pipeline steps, with automatic serialization handling data transfer between languages. Objects are stored in the Nix store and can be inspected interactively using helper functions like `rxp_read()` and `rxp_load()` (see `{rixpress}` documentation: <https://docs.ropensci.org/rixpress/articles/intro-concepts.html>).

Converting Existing `{renv}` Projects

Many researchers have existing projects using `{renv}` for package management. The `renv2nix()` function facilitates migration by reading an `renv.lock` file and generating an equivalent Nix specification. This conversion is particularly valuable for projects where `{renv}` encountered system dependency issues or where stricter reproducibility guarantees are desired. However, researchers should note that while `{renv}` snapshots R package versions, Nix additionally pins system libraries and compilers, potentially exposing previously hidden dependencies on system configuration (Rodrigues & Baumann, 2025) (see `{rix}` documentation: <https://docs.ropensci.org/rix/articles/f-renv2nix.html>).

Containerization with Docker

Institutions with existing Docker-based infrastructure may wish to combine Nix with containers. While this might seem redundant—both technologies provide isolation—the

combination offers complementary benefits: Nix ensures bit-reproducible builds across systems, while Docker provides a familiar deployment mechanism for non-Nix-aware computing environments. The approach is to use Nix as the base layer within a Docker container (Rodrigues & Baumann, 2025). This strategy is particularly relevant, for example, for projects requiring deployment to cloud computing platforms or high-performance computing clusters where Docker is the standard containerization technology (see {rix} documentation: <https://docs.ropensci.org/rix/articles/z-advanced-topic-using-nix-inside-docker.html>).

Discussion

Reproducibility in computational research is often treated as a matter of transparency—making data and code available. This tutorial has argued that transparency alone is insufficient without the ability to reliably reconstruct the computational environments in which analyses are executed. For simulation studies in particular, where results depend critically on software versions, system libraries, and random number generation, environment-level reproducibility is not optional but essential.

By introducing Nix and the {rix} package, we demonstrated a practical and accessible approach to fully specifying and rebuilding computational environments for simulation-based research. This approach enables analyses and manuscripts to be rerun identically across machines and over time, transforming reproducibility from an aspirational goal into a verifiable property of the research workflow.

Importantly, adopting environment reproducibility does not require abandoning existing analytic practices. Nix is agnostic to programming language, editor, workflow structure, and manuscript template, allowing researchers to retain familiar tools while strengthening the reliability of their work. In this sense, reproducible environments serve as enabling infrastructure—supporting, rather than replacing, other best practices such as version control, workflow orchestration, and transparent reporting.

If reproducibility is to function as a cornerstone of cumulative science, then the ability to reconstruct computational environments must become a routine part of methodological practice.

Tools such as Nix and {rix} lower the barrier to achieving this goal, making fully reproducible simulation research feasible without requiring deep systems expertise. We hope this tutorial helps normalize environment-level reproducibility as a standard component of rigorous computational research in psychology and beyond.

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Listing 1 Environment specification for the manuscript using rix()

```
library(rix)

rix(
  date = "2025-08-25", # line 1
  r_pkgs = c( # line 2
    "rix", "quarto", "knitr", "marginaleffects", "simhelpers",
    "ggplot2", "doParallel", "doRNG", "cowplot", "dplyr", "svglite",
    "rvinecopulib"
  ),
  system_pkgs = c("quarto"), # line 3
  tex_pkgs = c( # line 4
    "amsmath", "ninecolors", "apa7", "scalerel", "threeparttable",
    "threeparttablex", "endfloat", "environ", "multirow", "tcolorbox",
    "pdfcol", "tikzfill", "fontawesome5", "framed", "newtx",
    "fontaxes", "xstring", "wrapfig", "tabulararray", "siunitx",
    "fvextra", "geometry", "setspace", "fancyvrb", "anyfontsize"
  ),
  ide = "rstudio", # line 5
  project_path = ".", # line 6
  overwrite = TRUE # line 7
)
```

Listing 2 Example for the git_pkgs argument

```
git_pkgs = list(
    package_name = "marginaleffects",
    repo_url = "https://github.com/vincentarelbundock/marginaleffects",
    commit = "304bff91dc31ae28b227a8485bfa4f7bdc86d625"
)
```

Listing 3 Including Python packages

```
py_conf = list(py_version = "3.12",
               py_pkgs = c("polars","pandas"))
```

Listing 4 Building the Nix environment

```
nix-build
```

Listing 5 Activating the Nix environment

```
nix-shell
```

Listing 6 Activating the Nix environment with strict isolation

```
nix-shell --pure
```

Listing 7 Rendering the manuscript with Quarto

```
quarto render article.qmd
```

Listing 8 Installing the apaquarto extension

```
quarto use template wjschne/apaquarto
```

Listing 9 Installing the apaquarto extension from R

```
quarto::quarto_use_template("wjschne/apaquarto")
```

Listing 10 Master script for running the complete simulation workflow

```
library(marginaleffects); library(simhelpers); library(rvinecopulib)

library(doParallel); library(doRNG); library(ggplot2); library(cowplot);

library(dplyr)

source("03_run_simulation.R")
source("04_performance_metrics.R")
source("05_plots.R")
```

Listing 11 Running the complete simulation workflow

```
Rscript 06_run_all.R
```

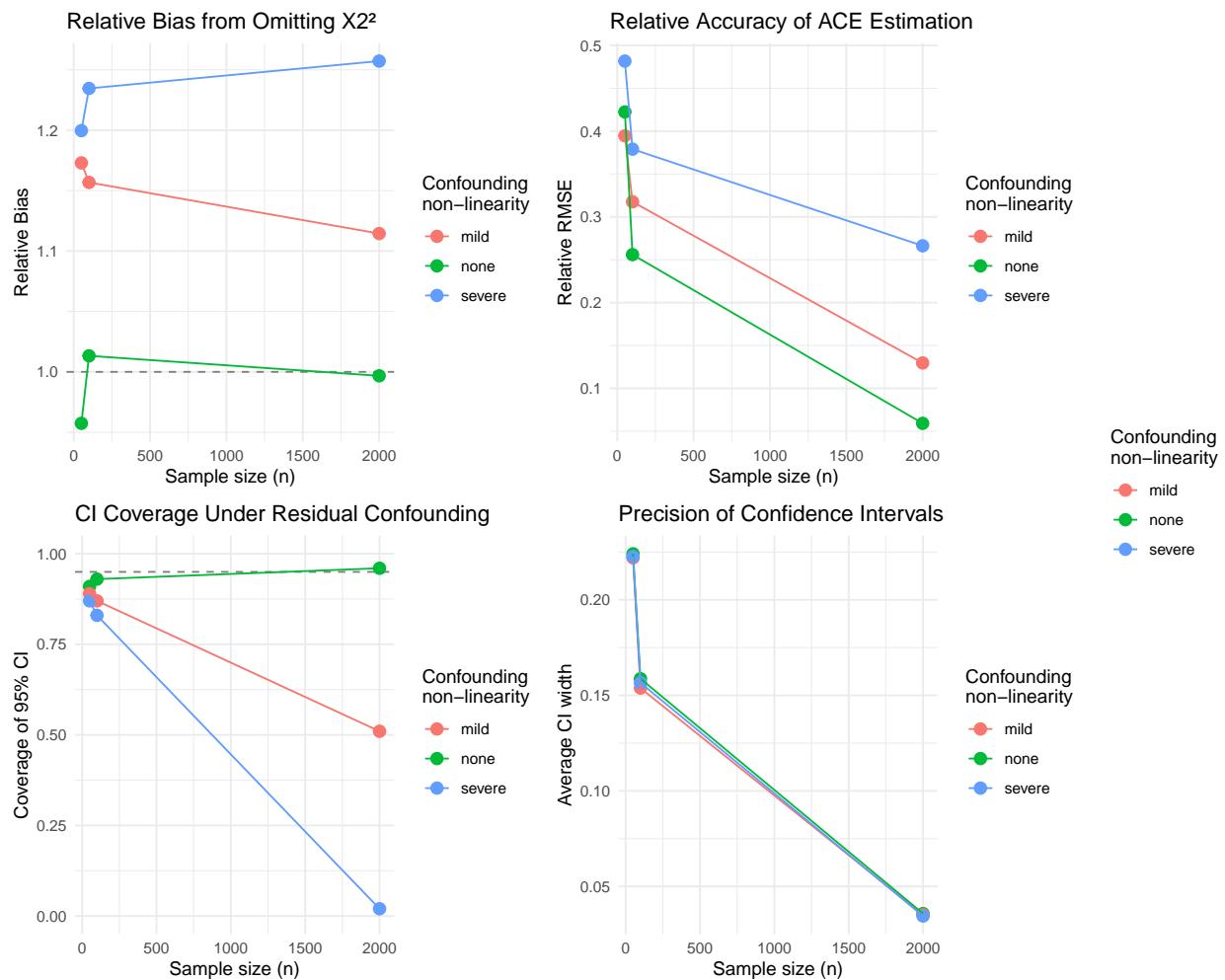
Table 1

Performance metrics for ACE estimator across simulation conditions

Sample Size	Confounding	Relative Bias	Relative RMSE	Coverage	CI Width
50	none	0.957	0.422	0.910	0.224
100	none	1.013	0.256	0.930	0.159
2000	none	0.997	0.059	0.960	0.036
50	mild	1.173	0.395	0.890	0.222
100	mild	1.157	0.318	0.870	0.154
2000	mild	1.114	0.130	0.510	0.035
50	severe	1.200	0.482	0.870	0.223
100	severe	1.235	0.379	0.830	0.157
2000	severe	1.257	0.266	0.020	0.035

Figure 1

Performance of ACE estimator across sample sizes and confounding severity. Panel A shows relative bias, Panel B shows relative RMSE, Panel C shows coverage probability of 95% confidence intervals (dashed line at nominal 0.95 level), and Panel D shows average confidence interval width. Results demonstrate that model misspecification induces systematic bias that persists across sample sizes, while increasing sample size improves precision but not accuracy under misspecification.



Appendix A

Simulation Study Design

Here we present a rather short description following recommendations from previous research, but ideally even more may be reported (Morris et al., 2019; Pawel et al., 2025; Siepe et al., 2024; White et al., 2024). This mimics a methods or similar section in articles.

Factorial Design. The simulation employs a full factorial design with two factors: sample size ($n \in \{50, 100, 2000\}$) and degree of confounding non-linearity ($\gamma_2 \in \{0, 0.3, 0.8\}$, labeled as none, mild, and severe). The parameter γ_2 controls the strength of the quadratic confounder effect on the outcome (see Data Generation). This yields nine conditions, each replicated $K = 1000$ times.

Data Generation. For each replication, data are generated following a causal structure where a confounder X_2 affects both treatment assignment and the outcome. The confounder and treatment error term are generated using the `{rvinecopulib}` package: pairs (U_1, U_2) are drawn from an independence copula via `rbi_cop()`, then transformed to standard normals via $X_2 = \Phi^{-1}(U_1)$ and $\epsilon = \Phi^{-1}(U_2)$. The independence copula is simply $C(u, v) = uv$, meaning the resulting uniforms are independent—mathematically equivalent to calling `rnorm()` directly. We use `{rvinecopulib}` intentionally because it depends on C++ libraries.

Treatment assignment follows $X_1 = \alpha_0 + \alpha_1 X_2 + \alpha_2 X_2^2 + \epsilon$ where $\alpha_0 = 0$, $\alpha_1 = 0.5$, and $\alpha_2 = 0.2$. This creates confounding because X_2 influences treatment assignment through both linear and quadratic terms. The binary outcome is generated from the true logistic regression model:

$$\text{logit}(P(Y = 1 | X_1, X_2)) = \beta_0 + \beta_1 X_1 + \gamma_1 X_2 + \gamma_2 X_2^2$$

with parameters $\beta_0 = -0.5$, $\beta_1 = 0.7$ (the causal effect of interest), $\gamma_1 = -0.4$, and γ_2 varying by condition. The analyst misspecifies the outcome model by omitting the quadratic confounder term, fitting instead:

$$\text{logit}(P(Y = 1 | X_1, X_2)) = \beta_0 + \beta_1 X_1 + \gamma_1 X_2$$

This misspecification creates residual confounding because the omitted term $\gamma_2 X_2^2$ is

correlated with X_1 (since X_1 depends on both X_2 and X_2^2), violating the conditional exchangeability assumption given linear adjustment alone.

Estimand. The target estimand is the average causal effect (ACE) of X_1 on Y , properly adjusted for confounding:

$$\text{ACE}(X_1) = \mathbb{E} \left[\frac{\partial P(Y = 1 | X_1, X_2)}{\partial X_1} \right] = \mathbb{E} \left[\beta_1 \cdot \frac{\exp(\eta)}{(1 + \exp(\eta))^2} \right]$$

where $\eta = \beta_0 + \beta_1 X_1 + \gamma_1 X_2 + \gamma_2 X_2^2$ is the correctly specified linear predictor, and the expectation is taken over the joint distribution of (X_1, X_2) . For each γ_2 condition, the “true” ACE (denoted θ) is approximated once using a very large sample ($N = 200,000$) with the correctly specified model including X_2^2 .

Estimator. The causal effect is estimated from the misspecified model (omitting X_2^2) as:

$$\widehat{\text{ACE}}(X_1) = \frac{1}{n} \sum_{i=1}^n \tilde{\beta}_1 \cdot \frac{\exp(\tilde{\eta}_i)}{(1 + \exp(\tilde{\eta}_i))^2}$$

where $\tilde{\eta}_i = \tilde{\beta}_0 + \tilde{\beta}_1 X_{i1} + \tilde{\gamma}_1 X_{i2}$ and $\tilde{\beta} = (\tilde{\beta}_0, \tilde{\beta}_1, \tilde{\gamma}_1)$ are maximum likelihood estimates from the misspecified logistic regression.

Performance Criteria. Table 1 presents the performance criteria used to evaluate the ACE estimator across simulation conditions.

Computational Details. The simulation was conducted on a MacBook Pro (...), running macOS Sequoia 15.6.1 All analyses were performed in R [@] (version X). Parallel processing was implemented through the {doParalell} package (version X) ([Corporation & Weston, 2022](#)), with {doRNG} (version X) ([Gaujoux, 2025](#)) to ensure independent and reproducible random number streams. For data generation we used the {rvinecopulib} package (version X) ([Nagler & Vatter, 2025](#)). The estimator was implemented using the {marginaleffects} package (version X) ([Arel-Bundock et al., 2024](#)). Data wrangling was performed with {dplyr} (version X) ([Wickham et al., 2023](#)). Method performance was assessed through multiple metrics following the formulas from the {simhelpers} package (version X) ([Joshi & Pustejovsky, 2025](#)). Figures were produced with {ggplot2} (version X) ([Wickham, 2016](#)) and {cowplot} (version X) ([Wilke, 2025](#)). Finally,

this paper was written with apaquarto [@] (see GitHub repository for more information on reproducing the manuscript and analyses).

Appendix B
Clarifying the packages used

Table B1

Performance criteria for evaluating the ACE estimator. $\hat{\theta}_k$ denotes the ACE estimate from replication k (for $k = 1, \dots, K$), where $K = 1000$ is the number of replications, and θ denotes the true ACE for a given condition. For coverage and width criteria, A_k and B_k denote the lower and upper endpoints of the 95% confidence interval from replication k , $W_k = B_k - A_k$ is the interval width, c_β is the estimated coverage probability, and $I(\cdot)$ is an indicator function equaling 1 if the condition is true and 0 otherwise. The Monte Carlo standard error (MCSE) quantifies the simulation uncertainty in each performance measure estimate

Criterion	Estimate	MCSE
Bias	$\frac{1}{K} \sum_{k=1}^K \hat{\theta}_k - \theta$	$\sqrt{\frac{1}{K(K-1)} \sum_{k=1}^K (\hat{\theta}_k - \bar{\hat{\theta}})^2}$
Variance	$\frac{1}{K-1} \sum_{k=1}^K (\hat{\theta}_k - \bar{\hat{\theta}})^2$	$\sqrt{\frac{K-1}{K} \cdot \frac{1}{K-1} \sum_{k=1}^K (\hat{\theta}_k - \bar{\hat{\theta}})^2}$
RMSE	$\sqrt{\frac{1}{K} \sum_{k=1}^K (\hat{\theta}_k - \theta)^2}$	$\sqrt{\frac{K-1}{K} \sum_{j=1}^K \left(\sqrt{(\hat{\theta}_j - \theta)^2} - \overline{RMSE} \right)^2}$
Relative Bias	$\frac{1}{\theta K} \sum_{k=1}^K \hat{\theta}_k$	$\frac{1}{\theta} \sqrt{\frac{1}{K(K-1)} \sum_{k=1}^K (\hat{\theta}_k - \bar{\hat{\theta}})^2}$
Relative RMSE	$\frac{1}{\theta} \sqrt{\frac{1}{K} \sum_{k=1}^K (\hat{\theta}_k - \theta)^2}$	$\frac{1}{\theta} \sqrt{\frac{K-1}{K} \sum_{j=1}^K \left(\sqrt{(\hat{\theta}_j - \theta)^2} - \overline{RMSE} \right)^2}$
Coverage	$\frac{1}{K} \sum_{k=1}^K I(A_k \leq \theta \leq B_k)$	$\sqrt{\frac{c_\beta(1-c_\beta)}{K}}$
Width	$\frac{1}{K} \sum_{k=1}^K (B_k - A_k)$	$\sqrt{\frac{1}{K(K-1)} \sum_{k=1}^K (W_k - \bar{W})^2}$