

**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

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

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 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, reproducibility may be interpreted as sharing only a manuscript. Further along the spectrum, it may involve providing partial code, complete analysis scripts, or publicly accessible datasets. At the highest level, reproducibility entails documenting a fully specified computational environment that allows others to recreate identical results—from raw data to final manuscript output—with minimal friction. As a result, researchers may implicitly target different points on this continuum and efforts to improve reproducibility can diverge substantially in both goals and implementation.

Open science initiatives have made considerable progress in encouraging movement along this continuum. For example, journals have begun offering open-science badges (Kidwell et al., 2016) and platforms like the Open Science Framework (OSF) have created “challenges” to make data and code sharing increasingly routine (Levenstein & Lyle, 2018). However, these efforts largely occupy the lower and middle portions of the continuum, emphasizing what is shared rather than how shared materials can be executed in practice.

Data and code are never fully self-sufficient to reproduce a set of findings. Assuming the data and code are error-free, reproducibility depends on a hierarchy of software components—collectively referred to as *dependencies*—including the programming language version, the packages used in the analysis, and the system libraries on which those packages rely. When these dependencies differ from those used in the original analysis, code may fail, behave

inconsistently 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 set of software dependencies 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 (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 software ecosystem 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}

Imagine you have just been awarded an extraordinarily prestigious (and generously funded) grant to conduct a large-scale simulation study. The study is designed to evaluate the performance of several statistical models under varying data-generating conditions (see Appendix A for full technical details).

This tutorial is organized around this scenario. We use a stylized simulation study to ground the discussion in a concrete and familiar example, mirroring the structure of a typical methods manuscript. The scenario describes both the statistical design and the computational workflow one might reasonably encounter in practice. Although the example is illustrative rather than substantive—readers can follow the tutorial without engaging deeply with the simulation details—it provides a tangible reference point for discussing reproducibility challenges.

In a conventional workflow, simulation studies are typically implemented across multiple component files, each corresponding to a distinct analytical stage. In our case, the simulation is organized into five sequential scripts: data generation (01_data_generation.R), model specification (02_models.R), simulation execution (03_run_simulation.R), performance metric calculation (04_performance_metrics.R), and results visualization (05_plots.R). This modular structure reflects common practice and facilitates development and debugging.

However, because our focus is on the reproducibility of the *entire manuscript*, we embed all simulation code directly within this document as executable code chunks in a single .qmd file. When the document is rendered, the simulation runs from start to finish, producing the reported results and figures automatically. This approach is not required—and would be impractical for many real-world simulation studies, which are often too computationally intensive to execute during manuscript compilation. We return to this trade-off later in the tutorial.

Now suppose a researcher attempts to reproduce the simulation results reported in the article. What might prevent them from obtaining identical outcomes? The natural first concern is package versioning. Installing R packages at a later time may lead to errors if functions have been renamed or deprecated, or to subtly different results due to changes in default settings or

numerical implementations. Beyond R packages themselves, many packages rely on system-level libraries that must be installed separately from R. Our simulation illustrates this dependency structure directly: the `{rvinecopulib}` package interfaces with a C++ backend and links against external libraries such as Boost, Eigen, and RcppThread [`@rvinecopulib`].

The R language version introduces another layer of dependency. Code written for R 4.3 may rely on syntax or functionality that is unavailable in earlier versions (e.g., R 4.0). More subtly, changes to R’s random number generation across major versions mean that identical code executed with the same seed can nevertheless produce different random sequences. For simulation studies—where specific random draws often underpin reported results—this version sensitivity is consequential.

Finally, when analyses are embedded in a literate programming workflow—that is, documents that combine narrative text and executable code—additional layers of software dependencies arise. For example, rendering R Markdown (`.rmd`) or Quarto documents (`.qmd`) requires both a document conversion tool (e.g., Pandoc, which converts `.rmd` or `.qmd` files into formats such as PDF or HTML) and a typesetting system such as a LaTeX distribution or Typst. Each of these components introduces its own versioning constraints and platform-specific installation requirements. Taken together, these layers highlight that reproducibility depends not only on code and data, but also on the broader computational environment in which analyses are executed.

Nix and {rix}: A Comprehensive Solution

A potential solution to the above issue is Nix ([Dolstra et al., 2004](#)). Nix is a software ecosystem centered on a purely functional package manager and build system designed to make software environments reproducible, declarative, and isolated across platforms (think Apple’s or Android’s application store). In practical terms, this means that Nix allows researchers to specify *exactly* which versions of programming languages, packages, and system libraries an analysis requires, and to recreate that same environment reliably on another machine.

Unlike familiar tools such as `install.packages()` in R, `apt-get` on Linux, or `uv` in

Python—which typically manage only a single layer of the software stack—Nix handles language versions, package versions, and system-level dependencies within a single framework (Rodrigues & Baumann, 2025). Rather than installing software into shared system directories, Nix builds each environment as an explicit, self-contained specification. As a result, multiple environments can coexist without conflict, and analyses can be rerun months or years later under identical computational conditions.

This unified approach directly addresses the fragmented landscape described above. Where researchers would otherwise need to coordinate separate tools for package management, interpreter versions, and system dependencies, Nix brings all three together within a single declarative model, lowering the barrier to fully reproducible computational workflows.

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:](https://)

[//docs.ropensci.org/rix/articles/b1-setting-up-and-using-rix-on-linux-and-windows.html](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 or r from GitHub for the latest version(Listing 1) ¹

Listing 1 Installing {rix} from CRAN or developmental version

```
install.packages("rix") # CRAN

# developmental
install.packages(
  "rix",
  repos = c(
    "https://ropensci.r-universe.dev"
  )
)
```

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 2):

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

¹ 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).

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()` function² 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. 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/d2-installing-system-tools-and-texlive-packages-in-a-nix-environment.html>).

Declaring R package dependencies. 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:

² 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>

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. 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. 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. The `ide` parameter controls whether an integrated development environment (IDE) is included in the Nix environment, allowing users to interactively develop and run code within their editor of choice. When `ide` is specified, the project can be opened directly in the corresponding IDE, with all dependencies provided by the Nix environment. For example, setting `ide = "rstudio"` installs a project-specific version of RStudio inside the Nix environment. This is required for RStudio because, unlike most other editors, it cannot attach to an external Nix shell unless it is itself installed via Nix. On macOS,

RStudio is only available through Nix for R versions 4.4.3 or later (or environments dated 2025-02-28 or later); for earlier R versions, alternative editors must be used. Other supported IDEs include Positron (`ide = "positron"`), Visual Studio Code (`ide = "code"`), and command-line interfaces such as Radian (`ide = "radian"`). These tools may either be installed directly within the Nix environment using the `ide` parameter, or users may rely on an existing system installation by setting `ide = "none"` (or `ide = "other"`) and configuring `direnv` to automatically load the Nix environment when the project directory is opened. All IDEs installed via Nix are project-specific and do not interfere with system-wide installations. Detailed configuration instructions are provided in the `{rix}` documentation:

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

Setting file output parameters. 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 (Listing 4) 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, `j1_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>).

Generating the Environment Specification

After defining the computational environment by running `rix()` (Listing 2) in your R console, a file named `default.nix` is generated. This file serves as the complete environment

specification and contains all information required to recreate the project in a fully reproducible manner.

Step III: Building and Using the Reproducible Environment

Once this step is complete, build the reproducible environment by navigating to the study directory in a terminal. You may use either the integrated Terminal in RStudio (Tools → Terminal → New Terminal) or an external system terminal from which you are running the Nix project. From the study directory, run the following command (Listing @lst-nix-build):

The expected output should look similar to (Listing 6):

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 path to the constructed environment in the Nix store is printed (here, `/nix/store/qa7fq20m2f94szsnqzciwv8h4n81w43v-nix-shell`), and a symbolic link named `result` appears in the project directory pointing to this location.

Note that the warnings indicate that you are not configured as a trusted user, so Nix cannot use the `rstats-on-nix` binary cache and will instead compile packages from source, which is slower. To enable binary caching, install the `cachix` client and configure the `rstats-on-nix` cache. See https://docs.ropensci.org/rix/articles/z-binary_cache.html for instructions.

To activate the environment, run (Listing 7):

The expected output (if you have configured yourself as a trusted user, otherwise the same warnings will appear) should look similar to (Listing 8):

This command drops the user into a shell where all specified packages and tools are available. The shell prompt changes to indicate that a Nix environment is active (here, `[nix-shell:~/Desktop/AMPPS/Why-risk-it-when-you-can-rix-it]$`). To verify that R is being provided by Nix rather than a system installation, run `which R`. This should return a path within `/nix/store/`. Moreover, from within the Nix shell, users can launch their IDE by typing its name (e.g., `rstudio` or `positron`), which opens the IDE with the Nix environment active

(Listing 9)

Reproducing the Complete Manuscript³

The manuscript source file in the project repository (`article.qmd`) combines narrative text, executable 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.

To render the manuscript enter the below code in the terminal (Listing 10):

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 11):

or in the console (Listing 12):

The final document (`.docx`, `.pdf`, or `.html`) is saved directly in the project folder⁴. 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.

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

³ See the `{rix}` documentation for more:

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

⁴ 6

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 13):

Reproducing the Simulation and Results

As previously mentioned, and although we recommend it, researchers may not want or know how to use dynamic document generation. In this case, one could still follow the same steps shown thus far focusing only on the `.R` files while still benefiting from a reproducible computational environment.

To illustrate it, after following Steps I-III, without needing to define packages for the document rendering in Step I, the simulation study may be reproduced (Listing 14) as follows:

In this same way one may also execute the `.R` file associated with the performance criteria calculation and visualization. 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`.

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`.

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`.

Additional Considerations for Advanced Workflows

Workflow Orchestration: {targets} and {rixpress}

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 {rixpress} 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()`, 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 2 Environment specification for the manuscript using rix()

```
library(rix)

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

Listing 3 Example for the `git_pkgs` argument

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

Listing 4 Including Python packages

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

Listing 5 Building the Nix environment

```
felipelfv@Felipes-MacBook-Pro Why-risk-it-when-you-can-rix-it % nix-build
```

Listing 6 Expected output from `nix-build`

```
unpacking 'https://github.com/rstats-on-nix/nixpkgs/archive/2025-08-25.tar.gz'  
into the Git cache...  
warning: ignoring untrusted substituter...  
warning: ignoring the client-specified setting...  
/nix/store/qa7fq20m2f94szsnqzciwv8h4n81w43v-nix-shell
```

Listing 7 Activating the Nix environment

```
felipelfv@Felipes-MacBook-Pro Why-risk-it-when-you-can-rix-it % nix-shell
```

Listing 8 Expected output from `nix-shell`

```
unpacking 'https://flakehub.com/f/DeterminateSystems/nixpkgs-weekly/...'  
into the Git cache...  
[nix-shell:~/Desktop/AMPPS/Why-risk-it-when-you-can-rix-it]$
```

Listing 9 Activating RStudio

```
felipelfv@Felipes-MacBook-Pro Why-risk-it-when-you-can-rix-it % rstudio
```

Listing 10 Rendering the manuscript with Quarto

```
[nix-shell:~/Desktop/AMPPS/Why-risk-it-when-you-can-rix-it]$  
quarto render Manuscript/article.qmd
```

Listing 11 Installing the apaquarto extension

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

Listing 12 Installing the apaquarto extension from R

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

Listing 13 Activating the Nix environment with strict isolation

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

Listing 14 Running the complete simulation workflow

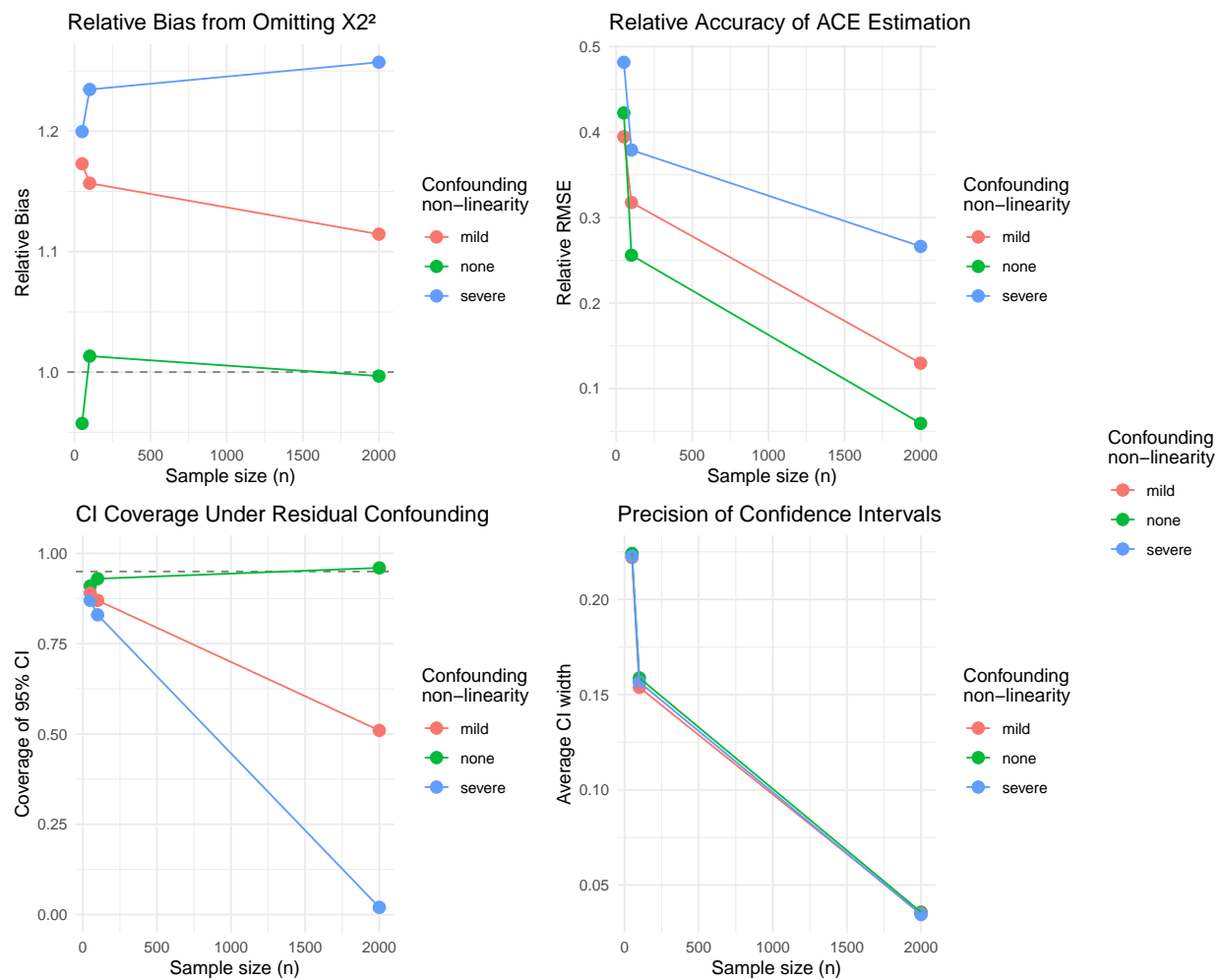
```
[nix-shell:~/Desktop/AMPPS/Why-risk-it-when-you-can-rix-it]$  
Rscript Simulation_Scripts/03_run_simulation.R
```

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 `rbicop()`, 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:

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

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:

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

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:

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

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 4.5.2). Parallel processing was implemented through the `{doParallel}` package (version 1.0.17), with `{doRNG}` (version 1.8.6.2) to ensure independent and reproducible random number streams. For data generation we used the `{rvinecopulib}` package (version 0.7.3.1.0). The estimator was implemented using the `{marginaleffects}` package (version 0.31.0). Data wrangling was performed with `{dplyr}` (version 1.1.4). Method performance was assessed through multiple metrics following the formulas from the `{simhelpers}` package (version 0.3.1). Figures were produced with `{ggplot2}` (version 4.0.1).

and `{cowplot}` (version 1.2.0).

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	$\frac{1}{K} \sum_{k=1}^K (B_k - A_k)$	$\sqrt{\frac{1}{K(K-1)} \sum_{k=1}^K (W_k - \bar{W})^2}$