

“Pandemic Pass?” replication code

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To maximize replicability, we wrote our manuscript using [Quarto](#), which allowed us to mix computational figures, text, and tables with the actual prose of the manuscript. This means that there’s no need to rely on comments within code to identify the location of each appropriate result in the manuscript—all results are programmatically included when rendering the document.

We use the [{renv}](#) package to create a stable version-specific library of R packages, and we use the [{targets}](#) package to manage all the file dependencies and run the analysis. {targets} is especially helpful with long-running objects like the main models, which take ≈ 40 minutes to run—as long as upstream dependencies don’t change, the models only need to run once, and can be loaded from {targets}’s data store thereafter.

Because it can sometimes be difficult to set up and configure version-specific libraries of R packages and install specific versions of Stan, we provide four methods for replicating our analysis:

1. **Running a pre-built Docker container with Docker Compose.** This uses a [pre-built Docker container](#) that has all the packages already installed. This is the recommended approach, since the complete computational environment will be replicated, including non-R software like [Quarto](#), [pandoc](#), [LaTeX](#), [dvisvgm](#), fonts, and other auxiliary elements.
2. **Running a Docker container built and orchestrated with Docker Compose.** This is the same as method 1, but uses a more barebones initial Docker image and then installs all R-related things.
3. **Restoring a project-specific library of all required R packages on your computer with {renv}.** This is the next recommended approach, since {renv} will install package versions as of July 2024 when we ran this code prior to publication. However, you’re responsible for installing all the non-R elements, like [Quarto](#) and [LaTeX](#) (detailed instructions are included below).
4. **Installing the most current versions of all required R packages on your computer systemwide.** This is the least recommended approach, since the included script will grab the latest version of all R packages from CRAN and install them in your system library. As with method 2, you’re still responsible for installing all the non-R elements on your own.

The original pre-cleaned data for the analysis is accessible in [mountainous-mackerel/data/raw_data](#). The {targets} pipeline cleans this data and creates objects named [weekly_panel](#) and [quarterly_panel](#)—load them into an R session with `targets::tar_load(weekly_panel)` or `targets::tar_load(quarterly_panel)`.

The complete {targets} pipeline generates two output artifacts:

- **Manuscript:** HTML and PDF versions of the manuscript and appendix, located at [mountainous-mackerel/manuscript/output/](#) (or at <http://localhost:8888/analysis/paper.html> if you run the pipeline with Docker Compose).
- **Analysis notebook:** A static website containing more complete details about the data, hypotheses, statistical methods, model diagnostics, and other information, located at [mountainous-mackerel/_site](#) (or at <http://localhost:8888> if you run the pipeline with Docker Compose).

Getting started

The repository for the paper itself is accessible at <https://github.com/andrewheiss/mountainous-mackerel> and should be cloned into this repository into a folder named `mountainous-mackerel`. You can either download the repository from GitHub or run this command in the terminal:

```
git clone https://github.com/andrewheiss/mountainous-mackerel.git
```

Make sure the folder structure looks like this:

```
.
├── README.md
├── README.pdf
├── docker-compose.yml
├── Dockerfile
├── ...
├── img/
├── ...
└── mountainous-mackerel
    ├── README.md
    ├── mountainous-mackerel.Rproj
    └── ...
```

Method 1: Pre-built Docker Compose (recommended)

The entire analysis can be run in a Docker container based on R 4.4.0, with all packages locked at specific versions defined in [mountainous-mackere1/renv.lock](#).

Here's how to do this:

1. Install Docker Desktop on your computer (instructions for [macOS](#) or [Windows](#)).
2. Make sure Docker is running.
3. In the Docker Desktop settings, make sure you allocate at least 8 CPUs and 16 GB of RAM.

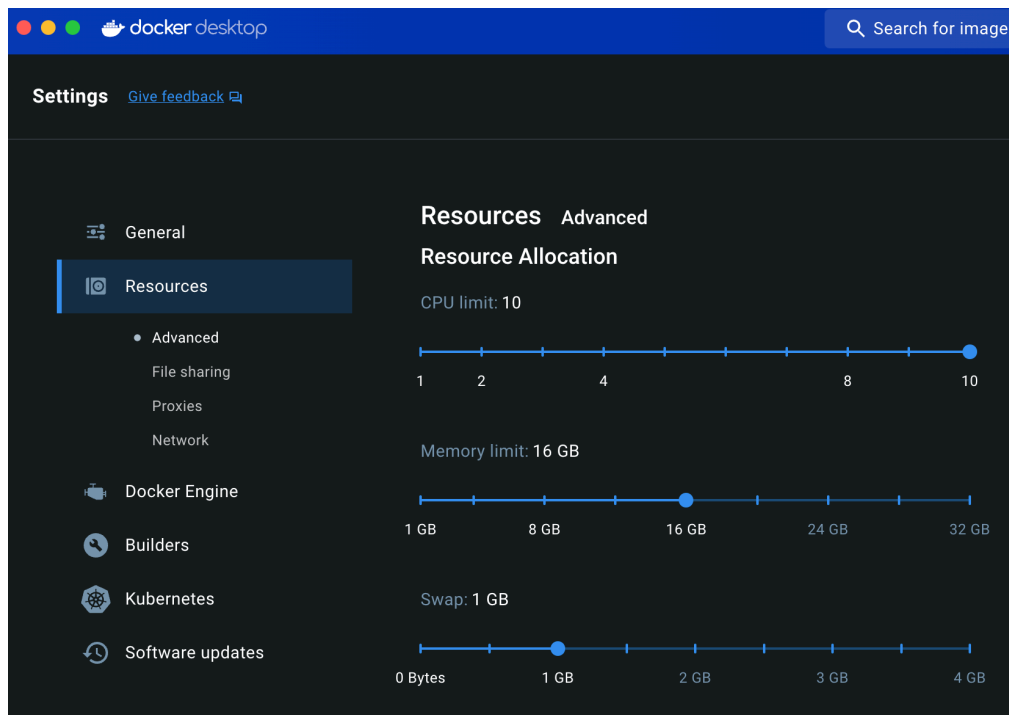


Figure 1: Docker Desktop resource settings

4. Build the analysis with Docker Compose. There are two general approaches:
 - **Using Visual Studio Code or Positron (recommended):** If you [download Visual Studio Code](#) or [Positron](#) and [its Docker extension](#), you can right click on the [docker-compose-prebuilt.yml](#) file in the File Explorer sidebar and select “Compose Up”.

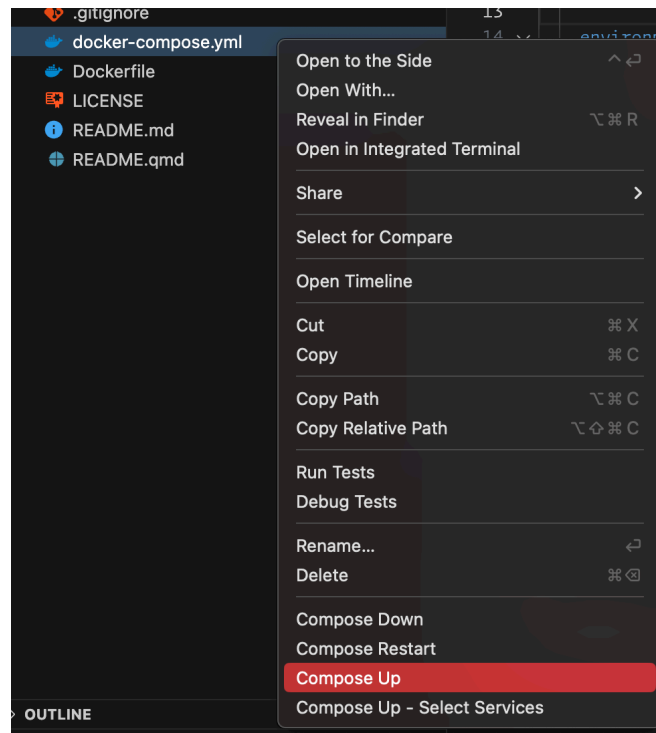


Figure 2: Docker Compose contextual menu in the Visual Studio Code sidebar

- **Using the terminal:** Using a terminal, navigate to this replication code directory and run this:

```
docker compose -f docker-compose-prebuilt.yml up -d
```

5. Wait for the **pre-built container** to get pulled from Docker Hub.
6. Visit <http://localhost:8787> and open an RStudio session inside the newly-built container in your browser. Any edits you make here will also be reflected on your local computer.
7. Run the {targets} pipeline by running `targets::tar_make()` in the R console. Wait; it takes ≈20 minutes to run the models, build the statistical notebook website, and render the manuscript in multiple formats. Subsequent runs of the pipeline should be fairly instant, though.

i Expected errors

For whatever reason, when the pipeline runs in Docker, it will show errors like **Error: object 'who_region' not found** and **Error: cannot open file '/home/rstudio/mountainous-mackerel/renv/staging/1/R6/R/R6.rdb': No such file or directory**.

These can be disregarded—everything builds fine and nothing stops with the errors—it's not clear why those are appearing ::shrug::

8. When the pipeline is all the way done, visit <http://localhost:8888> to see the analysis notebook and finished manuscript (at <http://localhost:8888/analysis/paper.html>).

You can also see these outputs on your computer: the analysis notebook is at [mountainous-mackerel/_site](#) and the manuscript and appendix files are at [mountainous-mackerel/manuscript/output/](#).

Method 2: Docker Compose

The entire analysis can be run in a Docker container based on R 4.4.0, with all packages locked at specific versions defined in [mountainous-mackere1/renv.lock](#).

Here's how to do this:

1. Install Docker Desktop on your computer (instructions for [macOS](#) or [Windows](#)).
2. Make sure Docker is running.
3. In the Docker Desktop settings, make sure you allocate at least 8 CPUs and 16 GB of RAM.

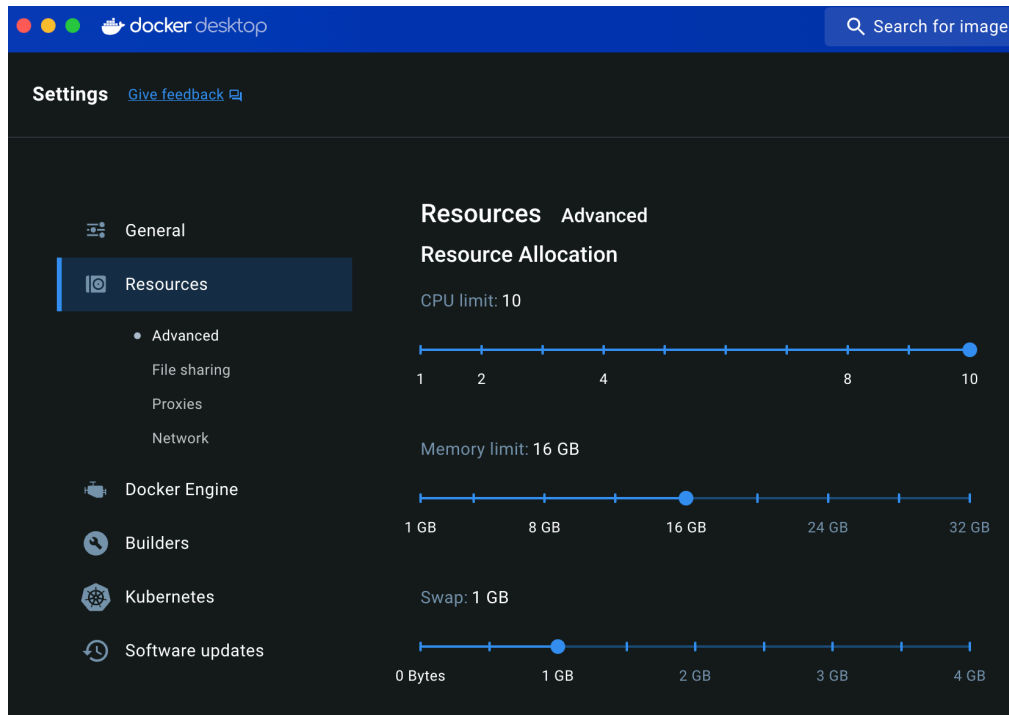


Figure 3: Docker Desktop resource settings

4. Build the analysis with Docker Compose. There are two general approaches:
 - **Using Visual Studio Code or Positron (recommended):** If you [download Visual Studio Code](#) or [Positron](#) and [its Docker extension](#), you can right click on the [docker-compose-prebuilt.yml](#) file in the File Explorer sidebar and select “Compose Up”.

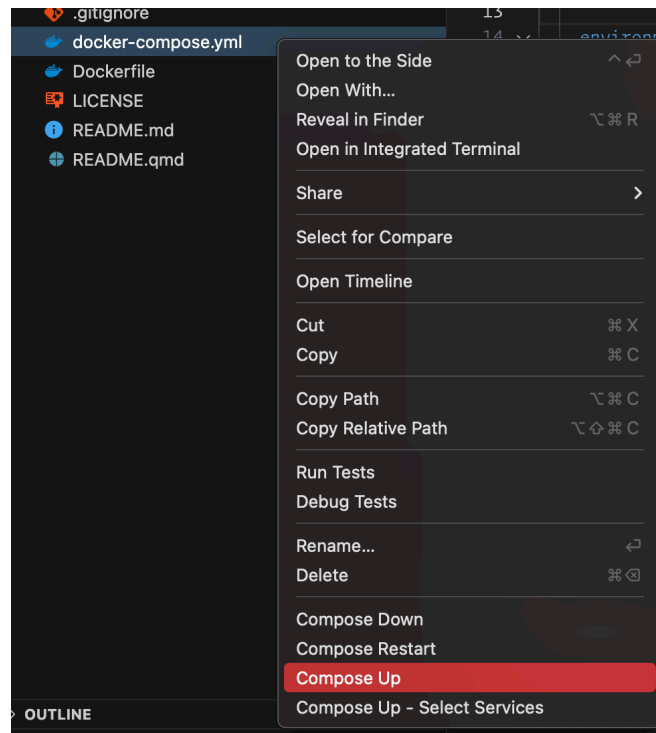


Figure 4: Docker Compose contextual menu in the Visual Studio Code sidebar

- **Using the terminal:** Using a terminal, navigate to this replication code directory and run this:

```
docker compose -f docker-compose-prebuilt.yml up -d
```

5. Wait for the container to build. It takes ≈ 20 minutes to build the {renv} library (but only the first time you run this; subsequent runs of `docker compose` should be instant), and it takes about ≈ 20 minutes to run the analysis (but only the first time; subsequent runs of `targets::tar_make()` should be instant).
6. Visit <http://localhost:8787> and open an RStudio session inside the newly-built container in your browser. Any edits you make here will also be reflected on your local computer.
7. Run the {targets} pipeline by running `targets::tar_make()` in the R console. Wait again; it takes ≈ 20 minutes to run the models, build the statistical notebook website, and render the manuscript in multiple formats. Subsequent runs of the pipeline should be fairly instant, though.

Expected errors

For whatever reason, when the pipeline runs in Docker, it will show errors like `Error: object 'who_region' not found` and `Error: cannot open file '/home/rstudio/mountainous-mackerel/renv/staging/1/R6/R/R6.rdb': No such file or directory`.

These can be disregarded—everything builds fine and nothing stops with the errors—it's not clear why those are appearing ::shrug::

8. When the pipeline is all the way done, visit <http://localhost:8888> to see the analysis notebook and finished manuscript (at <http://localhost:8888/analysis/paper.html>).

You can also see these outputs on your computer: the analysis notebook is at `mountainous-mackerel/_site` and the manuscript and appendix files are at `mountainous-mackerel/manuscript/output/`.

Method 3: Run locally with {renv} and project-specific packages

It's also possible to not use Docker and instead run everything locally in a special R package library that is separate from your system library.

0. Install these preliminary things:

- **R 4.4.0** (or later) and **RStudio**.
- **Quarto 1.6.1** (or later). As of this writing, the current stable version of Quarto is 1.5; [download 1.6.x from GitHub](#).
- **A C++ compiler and GNU Make**. Complete instructions for macOS, Windows, and Linux are available at [CmdStan's documentation](#). In short, do this:

- **macOS**: Run this terminal command and follow the dialog that pops up after to install macOS's Command Line Tools:

```
xcode-select --install
```

- **Windows**: [Download and install Rtools from CRAN](#)
- **Linux**: Run this terminal command (depending on your distribution; this assumes Ubuntu/Debian):

```
sudo apt install g++ make
```

- (macOS only): [Download and install XQuartz](#)
- **Ghostscript**: The multilevel model diagrams in the appendix are drawn with [TikZ](#), and Quarto uses [dvisvgm](#) to convert these into SVGs instead of PDFs when rendering to non-PDF outputs.
- **macOS**: The easiest way to install Ghostscript on macOS is through Homebrew. Run this terminal command after installing Homebrew:

```
brew install ghostscript
```

The resulting system libraries for using it live at `/opt/homebrew/opt/ghostscript/lib/libgs.dylib`. This is already set as the `LIBGS` environment variable in `manuscript/appendix.qmd`.

- **Windows**: [Download Ghostscript](#) and install it.
- **Linux**: Run this terminal command (depending on your distribution; this assumes Ubuntu/Debian):

```
sudo apt install ghostscript
```

- **Fonts:** Download and install these fonts (or install them from [misc/fonts](#) in this repository). On Windows, install these as an administrator so that R and Quarto have access to them.

- [Noto Sans](#)
- [Linux Libertine](#)
- [Libertinus Math](#)

1. Open [mountainous-mackerel/mountainous-mackerel.Rproj](#) to open a new RStudio project.
2. Run this to install `{cmdstanr}`. This is supposed to happen automatically as part of `renv::restore()` below, since `{cmdstanr}` is in the lockfile, but [due to an issue with {renv}](#) (fixed in the development version as of 2024-08-06), it doesn't install correctly because it is hosted at <https://stan-dev.r-universe.dev> instead of CRAN. So for now, until the next stable release of `{renv}`, it's easiest to install `{cmdstanr}` in a separate step.

```
install.packages("cmdstanr", repos = c("https://stan-dev.r-universe.dev",
"https://packagemanager.posit.co/cran/latest"))
```

3. Run `renv::restore()` to install all the packages.
4. Run `cmdstanr::install_cmdstan()` to install [CmdStan](#).
5. Run `tinytex::install_tinytex()` to install a minimal LaTeX installation if you don't have one installed already.

TinyTex should install any additional LaTeX packages that it needs when it comes across anything that's missing. You can help it along by installing those non-core packages first with this R command:

```
tinytex::tlmgr_install(
  # tikz things
  c("dvisvgm", "adjustbox", "collectbox", "currfile", "filemod", "gincitex",
    "standalone", "fp", "pgf", "grfext", "libertine", "libertinustlmath",
  # template things
  "nowidow", "tocloft", "orcidlink", "abstract", "titling", "tabularray",
  "ninecolors", "enumitem", "textcase", "titlesec", "footmisc", "caption",
  "pdflscape", "ulem", "multirow", "wrapfig", "colortbl", "tabu",
  "threeparttable", "threeparttablex", "environ", "makecell", "sidenotes",
  "marginnote", "changepage", "siunitx", "mathtools", "setspace",
  "ragged2e", "fancyhdr", "pdftex", "preprint")
)
```

6. (Finally!) Run `targets::tar_make()` to run the full analysis pipeline. This will take ≈ 20 minutes the first time.

Expected errors

For whatever reason, when the pipeline runs it will show errors like `Error: object 'who_region' not found`.

These can be disregarded—everything builds fine and nothing stops with the errors—it's not clear why those are appearing ::shrug::

7. When the pipeline is all the way done, find the analysis notebook at [mountainous-mackerel/_site](#) and the manuscript and appendix files at [mountainous-mackerel/manuscript/output/](#).

Method 4: Run locally with packages installed systemwide

Finally, it's also possible to not use Docker *and* not use {renv} and instead run everything using R packages that you install systemwide.

0. Install these preliminary things:

- **R 4.4.0** (or later) and **RStudio**.
- **Quarto 1.6.1** (or later). As of this writing, the current stable version of Quarto is 1.5; [download 1.6.x from GitHub](#).
- **A C++ compiler and GNU Make**. Complete instructions for macOS, Windows, and Linux are available at [CmdStan's documentation](#). In short, do this:

- **macOS**: Run this terminal command and follow the dialog that pops up after to install macOS's Command Line Tools:

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- **Windows**: [Download and install Rtools from CRAN](#)
- **Linux**: Run this terminal command (depending on your distribution; this assumes Ubuntu/Debian):

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sudo apt install g++ make
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The resulting system libraries for using it live at `/opt/homebrew/opt/ghostscript/lib/libgs.dylib`. This is already set as the `LIBGS` environment variable in `manuscript/appendix.qmd`.

- **Windows**: [Download Ghostscript](#) and install it.
- **Linux**: Run this terminal command (depending on your distribution; this assumes Ubuntu/Debian):

```
sudo apt install ghostscript
```

- **Fonts:** Download and install these fonts (or install them from [misc/fonts](#) in this repository). On Windows, install these as an administrator so that R and Quarto have access to them.

- [Noto Sans](#)
- [Linux Libertine](#)
- [Libertinus Math](#)

1. **Before** opening [mountainous-mackerel/mountainous-mackerel.Rproj](#), open [mountainous-mackerel/.Rprofile](#) and remove or comment out the line that says `source("renv/activate.R")`:

```
# source("renv/activate.R")
```

This will disable {renv} and will make it so R doesn't try to automatically install all the packages specified in [mountainous-mackerel/renv.lock](#).

2. **Also before** opening [mountainous-mackerel/mountainous-mackerel.Rproj](#), run [misc/install_packages.R](#). This uses {pacman} to install all required R packages. It downloads the latest versions of each package from CRAN and installs them systemwide. It will also install {cmdstanr} and LaTeX through {tinytex}.
3. Open [mountainous-mackerel/mountainous-mackerel.Rproj](#) to open a new RStudio project.
4. Run `targets::tar_make()` to run the full analysis pipeline. This will take ≈ 20 minutes the first time.

Expected errors

For whatever reason, when the pipeline runs it will show errors like `Error: object 'who_region' not found`.

These can be disregarded—everything builds fine and nothing stops with the errors—it's not clear why those are appearing ::shrug::

5. When the pipeline is all the way done, find the analysis notebook at [mountainous-mackerel/_site](#) and the manuscript and appendix files at [mountainous-mackerel/manuscript/output/](#).