Meet the toolkit

Eleutherodactylus Research Studio · Fall 2026

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Today's goal

By the end of class, you will:

1. Log into the EDU Pod
2. Render a Quarto document — first to a web page, then to PDF
3. Submit that PDF to Canvas

That's the whole pipeline this course runs on. Everything you produce this semester — worksheets, figures, manuscript drafts — comes out of it.

The tools, one job each

Tool	What it is	What we use it for
R	A programming language for data analysis	Measuring calls, statistics, figures
RStudio	The workbench where you write and run R	Your home screen all semester
Quarto	Turns text + code into documents	Worksheets, reports, manuscripts
GitHub	Shared home for code, with full history	Team projects (starting week 2)

None of these are “computer science” — they’re how modern biology gets done. Every figure in the papers we’ll write starts as R code in a Quarto document.

Why documents made of code?

- A Quarto document mixes **prose and live R code** — the figures and numbers in it are *computed when you render*, not pasted in
- Change the data, re-render, everything updates: no stale figures, no copy-paste errors
- This is how the manuscripts your teams produce will be built
- Today's document is a toy; the machinery is the real thing

The EDU Pod: your computer for this course

- A **Linux server** run by UT's Biomedical Research Computing Facility — not your laptop
- You use it through your **web browser**: RStudio runs on the server, you see it in a tab
- Everything is **already installed** and identical for everyone — no setup, no "works on my machine"
- Your laptop only needs a browser and campus internet

Log in at https://edupod.cns.utexas.edu

- UT EID in **all lowercase** — uppercase fails
- Off campus? Connect to the UT VPN first

Where your files live

- Your files live **on the server**, not on your laptop
- **Your home directory** (`~`) — private, yours, persists all semester
- **The shared course directory** (`/stor/work/FRI_Bio206_TD_Spring2026`) — where I post worksheets, starter files, and data; everyone in the class can read it
- To get a file **onto your laptop** (e.g., to submit to Canvas): Files pane → check the box next to the file → **More** → **Export** → it downloads in your browser

Anatomy of a Quarto document

Three ingredients in one `.qmd` file:

1. **YAML header** — settings between `---` fences at the top (title, author, output format)
2. **Markdown text** — prose with simple formatting (`**bold**`, `# headings`)
3. **Code chunks** — R code between ```` ```{r} ```` fences that runs when you render

Hit **Render** and Quarto executes the code, weaves in the results, and produces the output document.

Hands-on: Hello, Quarto

We're following the official tutorial (linked on the Resources page), with a shortcut — the starter file is already on the pod:

1. Log in: https://edupod.cns.utexas.edu (lowercase EID)
2. In the R **Console**, copy the starter file to your home directory:

```
file.copy("/stor/work/FRI_Bio206_TD_Spring2026/hello.qmd", "~/")
```

3. Files pane → click `hello.qmd` to open it
4. Click **Render** → a web page appears. Look at how the code chunks became figures.

Hands-on: now make it a PDF

5. In the YAML header, change the format line to:

```
format: typst
```

6. **Render** again → now you get a PDF *(one document, many output formats — that's the point)*
7. Files pane → check the box next to `hello.pdf` → **More** → **Export** → downloads to your laptop
8. Upload the PDF to the Canvas assignment

Heads-up: on the pod, always use `format: typst` for PDFs — `format: pdf` fails here (missing fonts). This is on the Resources page so you don't have to remember it.

When you stop working: quit your session

RStudio on the pod keeps your session alive after you close the tab. Don't just walk away — end it:

1. **Save your files** (the `.qmd` is what matters; it lives in your home directory and persists)
2. Click the **orange power icon** (top right) → **Quit Session**

Why:

- Lingering sessions eat memory on a server the whole class shares
- Old resumed sessions eventually go stale and produce bizarre errors ("can't find" functions that plainly exist). If that ever happens to you: save, Quit Session, log back in. **Session → Restart R is not enough**
- You lose the Environment pane's objects — and that's fine. Your document recreates them when you render. The script is the record, not the session

What about GitHub?

- GitHub stores code the way a museum stores specimens: **everything cataloged, nothing lost**, every change recorded and reversible
- Your team's analysis code will live there — you'll each contribute to a shared repository
- **Today:** just make sure you have a free account at github.com and know your username
- We'll set up access and learn the workflow **week 2**, when teams are announced

Before Monday

- **Team preferences due Mon Aug 31** — form/instructions on the site
- Have your **GitHub username** ready
- If anything today didn't work — login, render, export — email me *now*, not week 3

https://ut-fri-biodiversity.github.io/eleuth-calls/

Monday: data organization & tidy data — the foundation for everything your team measures.