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Pioneering Minds

POSITRON

Slave Trajanoski

January 2026



Introduction to Positron



- ▶ **The "Next-Gen" IDE:** Built by Posit (formerly RStudio), it is a fork of Code OSS (the open-source foundation of VS Code).
- ▶ **The Mission:** To provide a purpose-built IDE for Data Science that feels like RStudio but has the power and extensibility of VS Code.
- ▶ **Core Philosophy:** * Polyglot First: Native, top-tier support for both R and Python.
 - ▶ **Architecture:** The IDE is separate from the R/Python engine. If your R session crashes while processing a large VCF file, the IDE stays open.
 - ▶ **Familiarity:** Retains the "4-pane" layout (Console, Editor, Environment, Plots) that R users love.

Key Features for Bioinformaticians



- ▶ **Headline:** Why move beyond RStudio?
 - ▶ **Language Agnostic:** Seamlessly switch between R (for Tidyverse/Bioconductor) and Python (for Deep Learning/Snakemake) in the same workspace.
 - ▶ **Modern Data Explorer:** Lightning-fast for large data frames. Built-in filtering, sorting, and summary statistics (histograms in column headers) without writing a line of code.
 - ▶ **Multi-Session Support:** Run multiple R sessions simultaneously. You can run a long-running alignment in one console while testing visualization code in another.
 - ▶ **Remote Development:** Built-in support for SSH and Dev Containers, making it much easier to work on high-performance computing (HPC) clusters compared to RStudio Desktop.

Positron vs. RStudio Desktop



Feature	RStudio Desktop	Positron
Foundation	Custom Qt-based	VS Code (Code OSS)
Stability	R crash often = IDE crash	R crash \neq IDE crash (Kernel based)
Python Support	Via reticulate (secondary)	Native / First-class citizen
Extensions	RStudio Add-ins (Limited)	Full VS Code Extension Marketplace
Performance	Can lag with large scripts/data	Built for speed and high-concurrency
Project Management	.Rproj files	Folder-based (Workspaces)
AI Integration	Limited	Native "Positron Assistant" & Copilot

Transitioning (The "Bioinfo" Workflow)



- ▶ **Headline:** Making the Switch
- ▶ **What stays the same:** Your R code, your packages (BiocManager works perfectly), and the general layout.
- ▶ **What is different:** * Workspaces: You open a folder instead of a .Rproj file.
 - ▶ **Command Palette:** Cmd/Ctrl + Shift + P is the heart of the IDE (just like VS Code).
 - ▶ **Quarto/Rmd:** Positron is heavily optimized for Quarto. Note: Inline output for .Rmd is currently handled via the Plot/Console panes rather than inside the editor.
- ▶ **Bioinformatics Tip:** Use the Testing Pane in Positron to manage unit tests for your custom R packages or pipelines—it is much more robust than the RStudio "Build" tab.

Conclusion & Future



- ▶ **Headline:** Is it ready for production?
- ▶ **Current Status:** Positron is in Beta. It is stable for daily work, but RStudio remains the "conservative" choice for validated pipelines.
- ▶ **The Verdict:** If your bioinformatics work is increasingly "R + Python" or if you find RStudio lagging with large datasets, Positron is the clear upgrade.
- ▶ **Next Step:** Download it alongside RStudio—they can coexist on your machine without conflict!

Being an HPC "Good Citizen"



- ▶ **Headline: Scaling Positron to the Cluster Without Crashing Login Nodes**
 - ▶ **The Problem:** Default VS Code/Positron behavior indexes every file and runs "Extension Hosts" that can consume 2GB+ of RAM and 100% of a CPU core on the login node.
 - ▶ **The Solution: The "Interactive Compute" Workflow**
 - ▶ **Step 1:** Use `srun` (Slurm) to reserve a compute node for your IDE.
 - ▶ **Step 2:** Use an SSH Tunnel or ProxyJump to connect Positron directly to that compute node.
 - ▶ **Step 3:** Use File Watcher Exclusions. Tell Positron to ignore your `/projects/` directories so it doesn't try to index 50,000 FASTQ files.



Thank You!

Contact

CF Computational Bioanalytics, Center for medical research

Neue Stiftingtalstraße 6 West, Turm/Stiege:P, 4.Stock

8010 Graz

+43 316 385 73024

slave.trajanoski@medunigraz.at