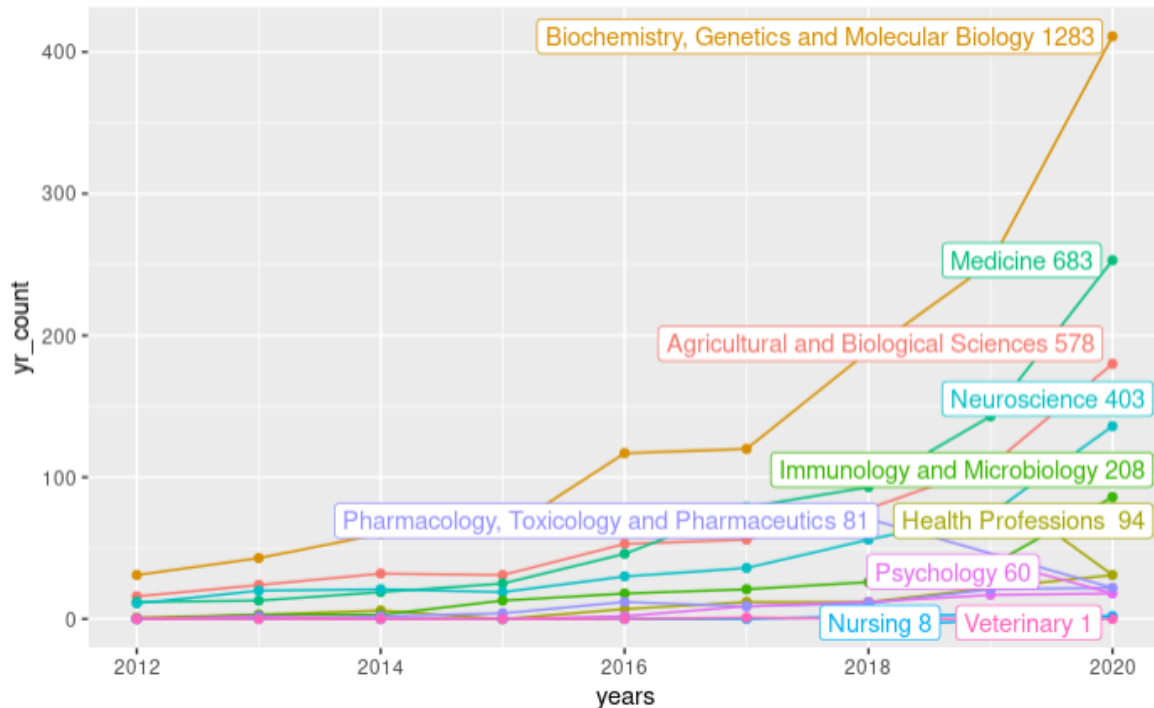


The following plot tracks the number of citations, according to [Scopus](#), involving “scipy” or “scipy.org” in each of several categories as functions of time. SciPy’s effect on research in medicine and related fields is strong and its growth rate is accelerating.



Many thanks to Breck Baldwin for collecting the data and preparing the figure.

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SciPy for Biomedicine #16191

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This is a meta-issue recording action items from a review of biomedical articles that cite SciPy and the results of a survey sent to authors of over 50 of these papers. In some cases, we can offer to resolve the issue (e.g. fix a bug); in other cases, we can offer to perform a feasibility study, solicit feedback from the broader SciPy community, and open a separate enhancement issue for further discussion.

- ☐ [Vaccine optimization for COVID-19: Who to vaccinate first?](#) used `optimize.minimize` to study how COVID vaccination priority should be assigned. The researchers reported having to “repair” solutions returned by SciPy’s Nelder-Mead solver, but had the researchers used a solver capable of enforcing problem constraints, this might have been avoided. To resolve this, we will improve the documentation of the optimizers to ensure that researchers find the appropriate solver for their problem (e.g. a flowchart or decision tree).
- ☐ [Modeling and forecasting the early evolution of the Covid-19 pandemic in Brazil](#) used the `solve_ivp` method to numerically integrate a system of ordinary differential equations. We will investigate the feasibility of adding faster integrators to `solve_ivp` to improve `solve_ivp`’s performance, potentially leveraging Boost, the C++ library added to SciPy as part of EOSS-0000000432. We will document our findings in an enhancement issue.
- ☐ [Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19](#) used the `hierarchy.fcluster` function to perform T cell receptor (TCR) clustering analysis. We will resolve the [two open bug reports](#) about `fcluster` to facilitate future use.
- ☐ An author of [The impact of reducing signal acquisition specifications on neuronal spike sorting](#) suggested "having helper functions within `scipy.signal.fft` that 1) converts the fft coefficients to power (V^2/Hz) and 2) converts power and phase to fft coefficients would be nice. I always forget how to do the conversion and a function that does this would be nice to have". We will add features to perform these conversions.
- ☐ The same author suggested improving the speed of `scipy.signal.resample` and "having an option to resample via a non-Fourier method in the case the signal is not periodic". We will investigate options for improving the performance of `resample` and for adding resampling of non-periodic signals and document our findings in an enhancement issue.
- ☐ An author of [COVID-19 pandemic-related lockdown: response time is more important than its strictness](#) reported about `scipy.stats.curve_fit`: "Non-linear optimizations is not trivial, as you have to tweak parameters (tolerances, jacobians parameters, methods of optimization). If you could

of [A General Model to Calculate the Spin–Lattice Relaxation Rate \(R1\) of Blood](#) also reported using `curve_fit`, noting that "It was super easy to use". In response, we will add a feature for performing curve fitting using SciPy's global optimizers.

- ☐ An author of [pymia: A Python package for data handling and evaluation in deep learning-based medical image analysis](#) suggested "I would love to have some of the `ndimage` functions working on `pytorch` or `tensorflow` tensors. Often, I need to cast to `np.ndarray` just to use the SciPy functions." This is not currently in scope, but there are other efforts in progress to offer GPU and distributed memory support throughout SciPy.
- ☐ An author of [Quantitative imaging of apoptosis following oncolytic virotherapy by magnetic resonance fingerprinting aided by deep learning](#) mentioned "Generally, I think that enriching the documentation with additional practical examples and perhaps links to relevant examples or papers that used the functions could be helpful". Documentation improvements are ongoing, but the message of this and other comments below is clear: we will dedicate time to documentation improvements rather than viewing it as a background task.
- ☐ An author of [Empirical mode decomposition for automatic artifact elimination in electrogastrogram](#) noted "For example there are excellent methods in SciPy as `resample`, which I need very often, but I'm not aware of them and have never used them. If I may add, it might be helpful to have more tutorials online, not just for research, but for education as well." This echoes a comment above about documentation improvements.
- ☐ An author of [Covasim: An agent-based model of COVID-19 dynamics and interventions](#) said "We noticed that `scipy.stats` is a bit slow to import -- about 0.3 s. For this reason we import it only within the function rather than globally, to reduce Covasim load time. If there were a way to reduce the import time, that would be appreciated." This will be addressed in our overhaul of the univariate distribution infrastructure so that distributions are not instantiated at load time ([🔗 ENH: stats: univariate distribution meta-issue #15928](#)).
- ☐ An author of [Empirical mode decomposition for automatic artifact elimination in electrogastrogram](#) noted "it would be great to add asymmetrical windows. I don't mean about `sym` parameter in `signal.windows.blackman` as it generates either symmetric window or periodic window, but to the design of a window." We will research options for adding support for asymmetric windows and document our findings in an enhancement issue.
- ☐ An author of [TorchIO: A Python library for efficient loading, preprocessing, augmentation and patch-based sampling of medical images in deep learning](#) suggested "From my point of view, the obvious enhancement that would facilitate biomedical research is adding support to perform operations in physical space, i.e., assuming that images have a certain origin, orientation and spacing." We will assess whether this is in scope of SciPy and, if so, we will report our findings in an enhancement issue.
- ☐ An author of [Modeling COVID-19 Dynamics in Illinois under Nonpharmaceutical Interventions](#) wrote that "...stochastic differential equation solvers might be a valuable addition..." but noted that "it might require a level of effort and domain expertise beyond the justifiable scope of SciPy itself." Stochastic differential equation solvers would indeed be useful and probably in scope, so we will investigate the feasibility of including one (likely vendored) in SciPy and report our findings in an enhancement issue.