Fred Hutch
Cancer Center

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3/26/24

Dear R Consortium Reviewers,

I am excited to support this proposal to improve the Biostrings package by Aidan Lakshman. I first met Aidan at the BioC 2022 conference, and have since worked with him on his submitted improvements to Biostrings. His proposed project would be of extreme importance to both the biological sciences community and the R ecosystem as a whole.

Aidan has repeatedly engaged with Biostrings and has shown excellent development ability in his submissions. One such example is enforcing the amino acid character set on AAStringSet objects, a large improvement to the package that had been requested for years by many users. In light of my observation of his ability and the motivation he has shown to improve Biostrings, I have no doubt that he will be successful in this grant.

Regarding the proposal itself, Biostrings is a foundational aspect of modern bioinformatics. Thousands of analyses are only possible due to Biostrings providing the ability to work with sequencing data in R. Ensuring Biostrings is robust and well maintained into the future is therefore a critical contribution to the scientific community and will do volumes to ensure R continues to be regarded as the top software language for biological analysis.

This project doubles as a valuable opportunity to invest in a young developer in the R development community. I know that investing my time to mentor Aidan will lead to further contributions to the R ecosystem, both for Bioconductor and for the broader community. An investment from ISC to further his proposed project would be similarly impactful.

Thank you for consideration of this proposal. Please feel free to reach out to me as needed.

Sincerely,

Hervé Pagès
Bioconductor Core Developer
Fred Hutchinson Cancer Research Center