

# Cloud-R: toward a community-backed R in the cloud

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<http://epigenomics.ncu.edu.tw/Cloud-R>

Cloud-*R* is a web-based platform for R embodying the latest cloud computing concept [1]. As the volume of genomic data continues to explode, a computation environment with larger memory and more CPUs for R than a personal computer is in need. Cloud computing, aided by wider Internet penetration and faster Web communications, represents a paradigm shift in computation toward deployment of applications to remote server computers. We propose to let users run their R programs through web browsers. Cloud-*R* is such a Web server that provides R utilities over the Internet. A basic requirement of Cloud-*R* design is that user experience of Cloud-*R* be identical to that of regular R. Users, after free registration, enjoy the following conveniences: (1) Cache of client environment settings; (2) Space for uploading and downloading data; (3) Graphs in PNG/PDF format for downloading. Cloud-*R* adheres to the idea of open software. More importantly, to the goal of virtually limitless computational resources for R, users' computational resources (i.e. computers) can be connected to Cloud-*R* [2]. The contributions of users' hardware can be made and withdrawn at anytime by themselves. Such an 'open resource' model increases the utilization of otherwise idling computers, benefiting the R community at large. Examples of running R at Cloud-*R* are demonstrated in the Cloud-*R* homepage, so are step-by-step instructions of connecting and dis-connecting user's computers to Cloud-*R*.

## References

- [1] K. H. Lin, H. Y. Hsieh and S. C. Wang, "Cloud-*R*: an R biostatistical computation and graphics environment in the cloud" is submitted to NAR.
- [2] REvolution Computing with support, contributions from Pfizer and Inc. nws: R functions for NetWorkSpaces and Sleigh. R package version 1.7.0.0. <http://nws-r.sourceforge.net/>.