



Project Title

12th March 2019

Redmine issue: #9999
NBIS staff: Supp Ortstaff (supp.ortstaff@nbis.se)
Request by: Re Quester (re.quester@ki.se)
Principal investigator: Prin Cipal (prin.cipal@ki.se)
Organisation: Karolinska Institutet





Table of Contents

Support request	3	
Project history	3	
Practical information Data responsibilities	4 4	
Materials and methods M&M 1	5	
Results Results 1	6	
Closing procedures	7	
R session info	7	





Support request

(As copy and pasted from Redmine issue.)

Project history

A brief summary of the project's key points.

2018-12-19 Meeting with the group to plan data analyes





Practical information

Data responsibilities

Unfortunately, NBIS does not have resources to keep any files associated with the support request; we kindly suggest that you safely store the results delivered by us. In addition, we kindly ask that you remove the files from UPPMAX/UPPNEX. The main storage at UPPNEX is optimized for high-speed and parallel access, which makes it expensive and not the right place for long-term archiving. Please be considerate of your fellow researchers by not taking up this expensive space.

The responsibility for data archiving lies with universities and we recommend asking your local IT for support with long-term data storage. The Data Center at SciLifeLab may also be of help with discussing other options.

Please note that special considerations may apply to human-derived, sensitive personal data. This should be handled according to specific laws and regulations as outlined at the NBIS website.

Acknowledgments

If you are presenting the results in a paper, at a workshop or at aconference, we kindly remind you to acknowledge us according to the signed NBIS User Agreement:

NBIS staff should be included as co-authors if the support work leads to a publication and when this is merited in accordance to the ethical recommendations for authorship, i.e. the ICMJE recommendations. If applicable, please include Supp Ortstaff, National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Stockholm University as co-author. If the above is not applicable, please acknowledge NBIS like so: Support by NBIS (National Bioinformatics Infrastructure Sweden) is gratefully acknowledged.

In addition, Uppmax kindly asks you to acknowledge UPPMAX and SNIC. If applicable, please add: The computations were performed on resources provided by SNIC through Uppsala Multidisciplinary Center for Advanced Computational Science (UPPMAX) under Project /b2000000.

In any and all publications based on data from NGI Sweden, the authors must acknowledge SciLifeLab, NGI and Uppmax, like so: The authors would like to acknowledge support from Science for Life Laboratory, the National Genomics Infrastructure, NGI, and Uppmax for providing assistance in massive parallel sequencing and computational infrastructure.





Materials and methods

M&M 1





Results

Results 1





Closing procedures

You should soon be contacted by one of our managers, Jessica Lindvall (jessica.lindvall@nbis.se) or Henrik Lantz (henrik.lantz@nbis.se), with a request to close down the project in our internal system and for invoicing matters. If we do not hear from you within **30 days** the project will be automatically closed and invoice sent. Again, we would like to remind you about data responsibility and acknowledgements, see Data responsibilities and Acknowledgements.

You are naturally more than welcome to come back to us with further data analysis request at any time via http://nbis.se/support/support.html. Thank you for using NBIS, we wish you the best of luck with your future research!

R session info

- R Under development (unstable) (2019-01-10 r75962), x86_64-apple-darwin15.6.0
- Running under: macOS Mojave 10.14.2
- Matrix products: default
- BLAS: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
- LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: knitr 1.21, nvimcom 0.9-75
- Loaded via a namespace (and not attached): compiler 3.6.0, digest 0.6.18, evaluate 0.12, magrittr 1.5, stringi 1.2.4, stringr 1.3.1, tools 3.6.0, xfun 0.4