***Bioinformatics Analysis Checklist***

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| Background |
| ***Project name \**** | *Used for quoting and record keeping* |
| ***Contact \**** | *Name* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*Staff #* \_\_\_\_\_\_\_\_\_\_\_ *Used for publication tracking**Email* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*Phone* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |
| ***Supervisor \**** | *Name* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*Staff #* \_\_\_\_\_\_\_\_\_\_\_ *Used for publication tracking* |
| ***Biological question*** |  |
| ***Experiment type \**** | [ ] Genomic[ ] RNA/Transcriptomic[ ] ChIPseq[ ] Pipeline/Software Development[ ] Other \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |
| ***Experiment design*** |  |
| ***Genus/Species*** |  |
|  |
| ***Finance*** *Note: no charges will be raised until* authorisation provided |
| ***Cost Centre \**** |  |
| ***WBS # \**** |  |
| ***WBS Authority \**** | *Person authorised to charge to CC/WBS #* |
| ***School \**** | [ ] Life Sciences[ ] Molecular Sciences[ ] Other \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ School Manager \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ |
| *Depending on the type of analysis you wish to perform please complete the relevant sections below* |
| Post sequencing additions |
| **[ ] *FastQC*** | *Run FastQC on each of your sample files* |
| **[ ] *Mapping*** | *Reference version* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*Location/URL of reference* \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*Mapping software* [ ] Bowtie2 [ ] Tophat [ ] BWA [ ] Other: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_*Parameters*  |
| **[ ] *Denovo assembly*** |  |
|  |
| [ ] RNAseq/Transcriptomics  |
| ***Differential Expression*** | You will be provided a CSV/Excel file of counts for each sample*What count values do you want?*[ ] Raw counts[ ] RPKM / FPKM (recommended)[ ] Log2 CPM[ ] Other \_\_\_\_\_\_\_\_\_\_\_ |
| **[ ] *Gene set testing*** | *What Genes you are interested in?**If the list is large please attach text file (one gene per line)* |
| **[ ] *Pathway / GO term analysis*** | *What Pathway or GO terms are you interested in?**If the list is large please attach text file (one pathway/GO-term per line)* |
| ***Other RNAseq/Transcriptomics Analysis*** |
|  |
| [ ] ChIP-Seq  |
|  | [ ] Peak calling |
|  | [ ] Data visualisation |
|  | [ ] Motif analysis |
|  | [ ] Gene assignment |
|  |
| [ ] Other Analysis |
| *We can perform other research and development style analysis for you on a weekly rate. For this we would provide an estimate of time needed. At given intervals progress updates will be given and you can decide to continue, cancel or extend the arrangement.* |
|  | *Do you have an analysis protocol that you would like us to follow?* [ ] Yes [ ] No*How many weeks of our time do you anticipate it taking?* \_\_\_\_\_ weeks*Do you require exclusive access to a Bioinformatician?* [ ] Yes [ ] No If yes, *how many days per week?* \_\_\_\_\_ |
| ***Description of Analysis*** |
| *Please provide details of the analysis you require. Attach a separate document if it is long or requires figures to explain.* |

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| [ ] Software / Pipeline development |
| ***Algorithm detail*** | *Have you performed all steps of Pipeline by hand? I.e. run all commands*[ ] Yes, can provide details[ ] Yes, but some details are patchy[ ] No, but can provide a detailed paper describing protocol[ ] No, it’s new analysis |
| ***Robustness*** | *How long do you plan to use software / pipeline?*[ ] This project only (quick and dirty)[ ] Other projects like it[ ] Many projects*Where will it be installed?*[ ] La Trobe HPC (i.e. LIMS-HPC)[ ] Collaborators HPCs[ ] Anywhere (i.e. published software) |
| ***Userbase*** | *Who will be using the software / pipeline once finished?*[ ] Just you[ ] Your Lab / Collaborators[ ] Anyone on the web |
| ***Description of processing required*** |
|  |
|  |
| Further information |
| *Please provide any further relevant information not provided above* |