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| --- | --- |
| A screenshot of a cell phone  Description automatically generated | CTR Bioinformatics Core FacilityCentre for Trophoblast Research, Physiology, Development and Neuroscience, University of Cambridge,Downing Site, Cambridge, CB2 3DY<http://www.trophoblast.cam.ac.uk>Email: ctr-bioinformatics@pdn.cam.ac.uk  |

# CTR Bioinformatics Project Costing

|  |  |
| --- | --- |
| Date | **/01/2023** |
| CTR Project Code |  **to be completed by CTR-BFX** |
| Group Leader  | **@cam.ac.uk** |
| Additional Contact  | **@cam.ac.uk** |
| Project Title  |  |

*Project Type (tick all that apply)*

Raw data processing (and storage): [ ]

Analysis (and storage): [ ]

Storage only: [ ]

Bespoke 1:1 Mentoring: [ ]

Teaching: [ ]

*Experimental design*

 I have discussed with Bioinformatics team prior to data collection: Yes [ ]  / No [ ]

 I have read the guidance for sample numbers and sex (see p5): Yes [ ]  / No [ ]

### Payment Details (*to be completed by PI*)

|  |  |
| --- | --- |
| Department |  |
| Payment Details (cost centre/grant code) |  |

### Costing Estimate (*to be completed by CTR-BFX*)

**Current rates:**

|  |  |  |  |
| --- | --- | --- | --- |
| Analysis | **£95 per hr** | Storage | RDS: **£5.40** per 100GB per year (during analysis) |
| 1:1 Mentoring / Teaching | **£40 per hr** |  | RCS: **£3.10** per 100Gb per year (required for raw data backup, and archiving)  |

**1:1 Mentoring / Teaching**

|  |  |
| --- | --- |
| **£0** | X hours 1:1 mentoring / teaching |

**Analysis**

|  |  |
| --- | --- |
| **£0** | X hours bioinformatics analysis |

**Storage Costs**

|  |  |
| --- | --- |
| **£0** | RCS X00Gb for X years |
| **£0** | RDS X00Gb for X months |

**Total = £0**

### Work to be undertaken (*to be completed by PI*):

*Please briefly describe the analysis required and context of the project. Please also include the data type (e.g. RNA-Seq) and where the data is to be generated (e.g. CGS or publicly available with GEO code). If there are known issues with the data e.g. low RIN, please include details.*

E.g.

We want to investigate the effect of whale song on trophoblast stem (TS) cell maintenance.

Experimental plan

We will culture trophoblast stem cells under stem cell conditions in the presence/absence of 75dB whale song for 5 days and generate mRNA libraries.

We will generate 6 biological replicates for each condition (2 conditions x 6 replicates = 12 samples). Libraries will be sequenced by the department of marine arts on one lane of a NovaSeq 6000 in a paired-end 100bp run.

We want to identify genes which are significantly differentially expressed between TS cells cultured in the presence/absence of whale song.

Enter text here

### Expected Outputs (*to be completed by PI*):

1. E.g. CSV file with gene counts
2. E.g. differential expression results including adj p-value and fold change
3. E.g. heatmap of differentially expressed genes, and gene ontology analysis with publication standard plots
4. E.g. methods section for publication
5. E.g. data submission in repository

Enter text here

### Check Points (*to be completed by CTR-BFX*)

e.g., costings assume the datasets are of good quality or the data is provided as a suitably processed expression matrix (e.g., Seurat compatible) with metadata.

If data not in correct format or requires additional processing

* Charge **X hours** and do **NOT** proceed

If data is in correct format and already processed

* Charge **X hours** to complete project

### Additional Work to be undertaken (*To be completed by PI*)

*If further analysis is required after the initial costed project is completed, please add details here.*

Enter text here

**Further analysis requested**

### Additional Costing Estimate (*to be completed by CTR-BFX*)

**1:1 Mentoring / Teaching**

|  |  |
| --- | --- |
| **£0** | 0 hours 1:1 mentoring / teaching |

**Analysis**

|  |  |
| --- | --- |
| **£0** | 0 hours bioinformatics analysis |

**Storage Costs**

|  |  |
| --- | --- |
| **£0** | RCS 0Gb for 0 years |
| **£0** | RDS 0Gb for 0 months |

**Total = £0**

### Comments and additional details (to be completed by CTR-BFX):

**Feasibility / Potential Issues / Comments**

**Data sources (e.g., sequencing facility, GEO or EMTAB accessions)**

### Comments and additional details (to be completed by Bioinformatics Committee):

*Any additional comments from the Bioinformatics Committee to be added here:*

### Authorship Expectations

Bioinformatics work is undertaken under the understanding that contributions meeting the conditions below will warrant authorship.

“Substantial contributions to the conception or design of the work; or the acquisition, analysis, or interpretation of data; or the creation of new software used in the work; or have drafted the work or substantively revised it; AND to have approved the submitted version (and any substantially modified version that involves the author’s contribution to the study); AND to have agreed both to be personally accountable for the author’s own contributions and to ensure that questions related to the accuracy or integrity of any part of the work, even ones in which the author was not personally involved, are appropriately investigated, resolved, and the resolution documented in the literature” (McNutt et al, 2018, PNAS).

*Further information for authorship guidelines:*

1. University of Cambridge Research Integrity: Guidelines for authorship [[Link](https://www.research-integrity.admin.cam.ac.uk/research-integrity/guidance/guidelines-authorship)]
2. International Committee of Medical Journal Editors: Defining the Role of Authors and Contributors [[ICMJE Link](http://www.icmje.org/recommendations/browse/roles-and-responsibilities/defining-the-role-of-authors-and-contributors.html)]
3. Transparency in authors' contributions and responsibilities to promote integrity in scientific publication. (McNutt et al, 2018, PNAS, [[DOI Link](https://doi.org/10.1073/pnas.1715374115)])

### Sample, Replicate and Sample Sex Guidance

For RNA-seq experiments, if two or more sample groups are to be compared the minimum recommendation is **6** biological replicates per group, and ideally **12**. Samples failing QC should also be accounted for. **NB**: these guidelines are based on RNA-seq using yeast as a model organism, however more complex or variable samples and sequencing approaches may require more replicates.

1. Gierliński *et al*, 2015, Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment, Bioinformatics, 31(22):3625-30 [[DOI Link](https://doi.org/10.1093/bioinformatics/btv425)]
2. Schurch *et al*, 2016, How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?, RNA, 22(6):839-51 [[DOI Link](https://doi.org/10.1261/rna.053959.115)]

Referees commonly question experimental design where sample sex is not accounted for. The sample sex should either be equally balanced, or for a single sex.

### Costings Approval Procedure

We will aim to approve project scope and costs within 14 working days of submitting completed form. The following diagram illustrates the project approval procedure.

