FURTHER PARTICULARS – REF: LS0222

DATA ANALYSIS GROUP
COLLEGE OF LIFE SCIENCES

LIFE SCIENCES RESEARCH DATA ANALYST/BIOINFORMATICIAN

Job Description

Modern biological research is increasingly dependent on the access to and manipulation of large datasets. These include the analysis of data from high-throughput DNA sequencing, microarray techniques, multi-wavelength time-resolved microscopy and mass-spectrometry as well as the effective exploitation of large public databases and tools. Frequently, a research project will, in addition to extensive laboratory-based experiments, require the development of novel analytic methods in order to make best use of the available data. As experimental data acquisition has scaled, the requirement for new computational software resources has also grown, but is often not met.

At Dundee we have strong research groups in both laboratory-based "wet" biological research and computational "dry" research and we are dedicated to driving the fusion of these two disciplines. This appointment will join existing staff in the Data Analysis Group (DAG www.compbio.dundee.ac.uk/dag) in the College of Life Sciences, headed by Professor of Bioinformatics, Geoff Barton. The DAG was established in 2009, has a successful track record of research at the interface between computing, statistics, mathematics and biology and has contributed to several high-profile publications[1-12]. Projects normally involve deep analysis of data in close collaboration with experimentalists and have spanned a wide range of biological areas and computational/mathematical techniques. The new appointment will be in daily contact with colleagues in computational biology, but will also join the pool of expertise and advice on computational analysis for data-intensive "wet" biological research across the College. Accordingly, the new appointment will join a team that acts responsively to requests from laboratory-based researchers for assistance and input into research projects as well as being pro-active in identifying opportunities for collaboration within the College by attending group meetings to gain close familiarity with the goals of the 7 Research Divisions (http://www.lifesci.dundee.ac.uk/research). In addition to solving computational problems in collaboration with laboratory scientists, the new appointment will also contribute to the development of new computational methods and tools to solve the specific collaborative problems, but which may be of wide applicability.

The DAG enjoys access to the excellent, managed computing facilities in the College of Life Sciences, including 400+ core CPU cluster, 250Tb Storage Area Network and multi-petabyte backup. The new appointment will not be expected to perform systems admin. tasks, but as with all members of the DAG, will interact with the skilled computing support team to help tune facilities to their needs.

The DAG is currently housed in excellent office space which is centrally located in the College of Life Sciences research complex. At the end of 2013 the DAG will relocate to the purpose-built second floor of the new CTIR building (see www.lifesci.dundee.ac.uk/ctir for more details) which will put existing research groups in Bioinformatics, Mathematical Biology, Biophysics and Imaging together. The new CTIR will be linked at every floor to the laboratories in the College of Life Sciences and so maintain and enhance the excellent

physical links between computational and experimental biology groups that we currently enjoy.

Requirements for the job

- A Ph.D. that included a substantial computational data analysis and programming component, followed by a minimum of 3-years' postdoctoral experience of computational methods applied in a scientific research environment.
- Strong demonstrated programming skills at least one scripting language (e.g. Perl/Python) in a Unix/Linux environment.
- Strong ability to adapt to new ideas and learn new techniques as required for the job.
- Knowledge of biological concepts, database methods, and standard bioinformatics tools, libraries and techniques and familiarity with one or more data analysis packages (e.g. R) would be advantageous.
- We welcome applications by individuals from research fields outside biology (e.g. Physics, Mathematics, Chemistry) who would enjoy the challenge of applying their skills to biological problems.
- For appointment on the lower grade we require a Ph.D. which included a substantial data analysis and programming component.
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Candidate Profile

We are looking for mathematicians/bioinformaticians/physicists/chemists or researchers in other scientific disciplines with strong programming and data analysis skills and the ability and enthusiasm to apply these to a range of biological problems. You might have gained these skills in biological research environment, perhaps by carrying out Ph.D. research in bioinformatics, alternatively, you might be a scientist with a strong research background in a non-biological discipline, but with excellent computational skills who is seeking to apply their expertise in a different and challenging field. You will wish to contribute to the cutting-edge research of a number of different groups while extending your range of skills and experience in programming and data analysis.

Strong interpersonal and communication skills are essential as is the ability to work as part of a team. You will have the ability to discuss research projects from a wide range of biological research fields and gain sufficient understanding of the topic to be able to apply your computational and data analysis skills to the problem, or to advise on the best way forward.

Informal enquiries may be made to Prof. Geoff. Barton - g.j.barton@dundee.ac.uk.

Recent publications that include members of the Data Analysis Group as co-authors (DAG members shown in bold)

1. Tibarewal, P., Zilidis, G., Spinelli, L., Schurch, N., Maccario, H., Gray, A., Perera, N. M., Davidson, L., Barton, G. J., and Leslie, N. R., *PTEN protein phosphatase activity correlates with control of invasion, gene expression and tumour suppression, but not AKT.* **Sci Signal**, 2012. **in press**.
2. Klotz-Noack, K., McIntosh, D., Schurch, N., Pratt, N., and Blow, J. J., *Re-replication induced by geminin depletion occurs from G2 and is enhanced by checkpoint activation.* **Journal of Cell Science**, 2012. **in press**.
3. Bioisvert, F.-M., Ahmad, Y., Gierlinski, M., Charriere, F., Lamont, D., Scott, M., Barton, G. J., and Lamond, A. I., *A Quantitative Spatial Proteomics Analysis of Proteome Turnover in Human Cells.* **Molecular and Cellular Proteomics**, 2012(in press).
4. Gkikopoulos, T., Singh, V., Tsui, K., Awad, S., Renshaw, M. J., Scholfield, P., Barton, G. J., Nislow, C., Tanaka, T. U., and Owen-Hughes, T., *The SWI/SNF complex acts to constrain distribution of the centromeric histone variant Cse4.* **EMBO J**, 2011. **30**(10): p. 1919-27.
5. Gkikopoulos, T., Schofield, P., Singh, V., Pinskaya, M., Mellor, J., Smolle, M., Workman, J. L., Barton, G. J., and Owen-Hughes, T., *A role for Snf2-related nucleosome-spacing enzymes in genome-wide nucleosome organization.* **Science**, 2011. **333**(6050): p. 1758-60.
6. Gandhi, S. R., Gierlinski, M., Mino, A., Tanaka, K., Kitamura, E., Clayton, L., and Tanaka, T. U., *Kinetochore-dependent microtubule rescue ensures their efficient and sustained interactions in early mitosis.* **Dev Cell**, 2011. **21**(5): p. 920-33.
7. Boisvert, F. M., Ahmad, Y., Gierlinski, M., Charriere, F., Lamont, D., Scott, M., Barton, G., and Lamond, A. I., *A quantitative spatial proteomics analysis of proteome turnover in human cells.* **Mol Cell Proteomics**, 2011.
8. van Koningsbruggen, S., Gierlinski, M., Schofield, P., Martin, D., Barton, G. J., Ariyurek, Y., den Dunnen, J. T., and Lamond, A. I., *High-resolution whole-genome sequencing reveals that specific chromatin domains from most human chromosomes associate with nucleoli.* **Mol Biol Cell**, 2010. **21**(21): p. 3735-48.
9. Remenyi, J., Hunter, C. J., Cole, C., Ando, H., Impey, S., Monk, C. E., Martin, K. J., Barton, G. J., Hutvagner, G., and Arthur, J. S., *Regulation of the miR-212/132 locus by MSK1 and CREB in response to neurotrophins.* **Biochem J**, 2010. **428**(2): p. 281-91.
10. Golebiowski, F., Matic, I., Tatham, M. H., Cole, C., Yin, Y., Nakamura, A., Cox, J., Barton, G. J., Mann, M., and Hay, R. T., *System-wide changes to SUMO modifications in response to heat shock.* **Sci Signal**, 2009. **2**(72): p. ra24.
11. Cole, C., Sobala, A., Lu, C., Thatcher, S. R., Bowman, A., Brown, J. W., Green, P. J., Barton, G. J., and Hutvagner, G., *Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs.* **RNA**, 2009. **15**(12): p. 2147-60.
12. Muramoto, T., Cannon, D., Gierlinski, M., Corrigan, A., Barton, G. J., and Chubb, J. R., *Live imaging of nascent RNA dynamics reveals distinct types of transcriptional pulse regulation.* **Proc Natl Acad Sci U S A**, 2012. **109**(19): p. 7350-5.