Problem Statement and Objectives:
With ageing population requiring increasing treatment of chronic and fatal diseases, providing personalised healthcare is proving particularly challenging due to time and resource constraints. To tackle this challenge, a promising solution is computational full genome sequencing, which facilitates in-depth understanding of the microbial ecology and genetic basis of many complex human diseases and their traits. Traditionally genome sequencing is carried out using computing servers, which are characterised by high computational costs, incurring excessive energy consumption and low throughput. Hence, to enable personalised healthcare using this technology, there are two key research questions and challenges as follows:

1. Can the computational cost be scaled down drastically using partial sequencing, precision scaling or input resizing?
2. Can the energy consumption be reduced significantly through adaptive resource allocation and system-level (hardware/software) controls?

To keep Newcastle at the forefront of this innovative technology, this project will address the above research questions and set up the design, and implementation of the first electronic genomic lab system prototype, called gLab. The specific objectives are the following:

1. To study the genome sequencing tasks (alignment, searching, filtering and post-processing) and to analyse the trade-off between output precision, performance and energy consumption.
2. Underpinning such analyses, to develop the design- and run-time optimisation and adaptation requirements through application-level knobs (input resizing, data-width scaling, and mode switching) and system-level controls (resource allocations, voltage/frequency scaling, etc.).
3. To implement gLab on high-performance, high-density field-programmable gate arrays (FPGAs).

The overall aim will be to enable low-cost, personalised diagnostic services, and potentially to facilitate further research. The project will benefit from complementary and cross-disciplinary collaboration between the Microsystems Research Group and Institute of Genetic Medicine in Newcastle University. The related academics in both groups have strong track records in scientific and technical aspects of the project. The project will benefit from industrial collaboration (e.g. internship) with Altera (currently being discussed).

Background and Motivation:
Research works over the last 30 years have resulted in considerable progress in the searches for the genetic mutations causing Mendelian (inheritance-based) and non-Mendelian (non-inheritance-based) diseases. In particular, the past two decades have seen remarkable advances towards automated, computational methods to derive evolutionary knowledge of these diseases through full genome sequencing. Using these methods, significant research efforts are ongoing to quantify the extent to which genetic variants contribute to both single gene disorders and complex diseases, such as type II diabetes and cancer. For example, Genomics England’s 100,000 genomes project, of which the Newcastle upon Tyne Hospital Foundation NHS Trust is a designated Genomic Medicine Centre, is attempting to bring a genomic revolution to healthcare through such quantification. However, there are considerable scientific, technical and computational challenges to steer such revolution towards personalised, cost-effective and energy-efficient diagnostics services. This project aims to address these challenges through...
design, optimisation and implementation of \textit{gLab}: a low-cost genome sequencing system.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{gLab_design_methodology.png}
\caption{\textit{gLab} design and implementation methodology}
\end{figure}

**Methodology**

In line with the objectives, Fig. 1 shows the design and implementation methodology of the proposed \textit{gLab} system, organised in the following three major tasks:

**Task A: Application-level Investigation:** To achieve significant reduction in the computational complexity, the application-level opportunities will be investigated, such as computational scaling (i.e. reducing the number of steps), data precision scaling (i.e. varying data-width) and input resizing (i.e. using the shortest sequence for the required diagnostics task). Synthesizing the above knobs will require in-depth understanding of the different genome sequencing tasks, such as alignment, search, filtering and post-processing using a Matlab/C application model.

**Task B: Design- and Run-time Optimisation and Adaptation:** Based on the application-level investigation, a set of design-time optimisations will be applied to ensure energy-efficiency by design. This will include adopting a target platform and technology node, and the design of parallel accelerators with suitable resource mapping. This will then be followed by run-time optimisations and adaptations to ensure dynamic energy efficiency using adaptive input resizing, computation and precision (bit-width) scaling, optimal voltage/frequency allocations, etc. To facilitate adaptation and dynamic programming on FPGA, OpenCL will be used.

**Task C: Implementation and Validation:** The \textit{gLab} implementation will be achieved through the following two steps. First, the target logic of the design will be bitmapped onto the target FPGA platform. Second, implementation will be tested for functional correctness with different sequencing tasks. Appropriate algorithmic adjustments or even logic remapping will be carried out to ensure the functional correctness using samples from the Institute of Genetic Medicine at Newcastle, and from freely available databases from various other sources.

The \textit{gLab} implementation will aim to achieve significant energy and cost savings to enable genomic revolution for personalised healthcare. Fig. 1 shows demonstrative comparisons between a modern high-end genome sequencing server (using 4 Intel Xeon Phi nodes, 300 Watts max. each) and three Altera Stratix 10 systems.

**Timeline**

<table>
<thead>
<tr>
<th>Task</th>
<th>Time</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>1-12m</td>
<td>Understand the full genome algorithm using MATLAB (sequencing, pruning, filtering and post-processing)</td>
</tr>
<tr>
<td>A2</td>
<td>7-24m</td>
<td>Study the computational trade-offs of the sequencing tasks and their input needs (using C implementation)</td>
</tr>
<tr>
<td>B1</td>
<td>19-24m</td>
<td>Formulate the input resizing relationships: how can these tasks be scaled to requirements (using C)</td>
</tr>
<tr>
<td>B2</td>
<td>19-36m</td>
<td>Parallelisation of tasks and designing optimal accelerators for these tasks (using C and OpenCL)</td>
</tr>
<tr>
<td>C1</td>
<td>31-42m</td>
<td>Mapping tasks to FPGA fabric (using OpenCL)</td>
</tr>
<tr>
<td>C2</td>
<td>36-45m</td>
<td>Validation and case studies (from IGM)</td>
</tr>
<tr>
<td>D</td>
<td>13-45m</td>
<td>Publications (high-impact journals, dissertations, etc.)</td>
</tr>
</tbody>
</table>

**References & Further Reading**

**Electronic System Design and Optimisation:**


**Genomics:**


**Further Information**

For further details regarding this project, contact Dr Rishad Shafik: Merz Court E4.14, Newcastle University, Newcastle, NE1 7RU, E-mail: Rishad.Shafik@newcastle.ac.uk.