**Reviewer Report**

**Title: GigaSOM.jl: High-performance clustering and visualization of huge cytometry datasets**

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**Reviewer name: Chris Armit**

**Reviewer Comments to Author:**

This technical note describes GigaSOM.jl, a Julia toolkit for clustering and visualisation of large cytometry data. The core objective achieved by GigaSOM.jl is the ability to quickly cluster and visualise large flow cytometry datasets through use of Self-Organising-Maps (SOM), which enable efficient and accurate clustering of millions of cells.  Validation of GigaSOM.jl clustering was established by comparison with FlowSOM, which is an established toolkit that has been described previously (Gassen et al., FlowSOM: Using selforganizing maps for visualization and interpretation of cytometry data. Cytometry Part A 2015;87(7):636-645.). From a 'Big Data' perspective, the utility of the GigaSOM.jl toolkit is showcased in the context of a large flow cytometry dataset that was generated by the International Mouse Phenotyping Consortium (IMPC) and that consisted of 1,167,129,317 splenocytes from 2,905 samples, including genetically modified single-gene knockout mice and control samples. Asinh transformations (i.e. inverse hyperbolic sine transformations) of fluorescent marker expression values from the splenocyte dataset were used to train a 32Ã—32 SOM, and this was subsequently rasterized to produce the visualisation shown in Figure 5. The manuscript is well written and I see great reuse potential in the GigaSOM.jl toolkit for clustering and dimension reduction of massive flow cytometry datasets. The source code of GigaSOM.jl is available from GitHub (https://github.com/LCSB-BioCore/GigaSOM.jl) under the OSI-approved Apache-2.0 License.

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