**Sample Sets:**

* **Small:** 200 samples, 55,000 probes (Target)
* **Medium:** 500 samples, 100,000 probes (Rembrant)
* **Large:** 500 samples, 500,000 probes (TCGA-GBM)

**Measured Workflows:**

* **Query by annotation**
* **Query by genes (1)**
* **Query by genes (20)**
* **Query by genes (all)**
* **KM Plot by genes (1)**
* **KM Plot by genes (20)**
* **IGV Viewer Generation**
* **Gene Expression Plot by gene (1)**
* **Gene Expression Plot by gene (20)**
* **Copy Number by gene (1)**
* **Copy Number by gene (20)**
* **Copy Number by gene (all)**
* **Copy Number 1 MBase**
* **Copy Number 20 MBase**
* **Copy Number All**
* **Gene Pattern Principal component analysis**
* **Gene Pattern Comparative marker selection**

**Measurements will include the average run time and memory usage over 100 runs.**

**First measure for a single user and then for concurrent users (10, 25, 50)**