**PGRR Search Repository Java Methods**

**(DataSelection class)**

1. getFilters()

Parameters: no

Return: JSONObject in the format:

{results:[{key:Disease,value:[“acc”,"blca","brca"]},

{key:"Sample Type",value:["Primary solid Tumor","Metastatic"]}]}

Filter PHP functions have no parameters and return JSON string.

1.1 Display Filters

|  |  |  |
| --- | --- | --- |
| **Filter Display Name** | **From getFilters() Method** | **Filter Tooltip** |
| Disease | *y* | Filter by disease |
| Tissue Source Site | *y* | Filter by tissue source |
| Sample Type | *y* | Filter by sample type |
| Analyte Type | *y* | Filter by molecular analyte |
| Center | *y* | Filter by processing center |
| Data Type: Analysis Type | *y* | Filter by data type and corresponding analysis type |
| Platform | *y* | Filter by analysis platform |
| Data Level | *y* | Filter by data level |
| Genome Reference | *y* | Filter by genome reference name |
| Snapshot By Date | **No.** Calendar values in “YYYY-MM-DD” format | Snapshot by creation date |

2. Search Results Functions

***getSearchRepositoryResultTotal***(String json)

Parameters:

@param json – String in the same format as getFilters() output

Return: int – number of records for selected filter values

***getSearchRepositoryResults***(String json, String startRecord, String endRecord)

Parameters:

@param json – String in the same format as getFilters() output

@param startRecord – String not “0” - inclusive first returned record

@param endRecord – String - inclusive last returned record

Return: JSONObject of paged filtered results

***getFilePathsAllMeta***(String json, String returnFormat)

Parameters:

@param json – String in the same format as getFilters() output

@param returnFormat: currently supports “csv”, “tsv”

Return javax.ws.rs.core.Response of TSV text with a all metadata parameters (filePath, disease, tissue\_source, patientBarcode, patientUUID, sampleBarcode, sampleUUID, sampleType, analyteType, aliquotBarcode, aliquotUUID, dataType, center, platform, level, refGenomeName, refGenomeURL, is\_data\_public, version, dateCreated, dateArchived, file\_size\_in\_bytes, md5Checksum, pgrrUUID.

***getFilePathsMinMeta***(String json, String returnFormat)

Parameters:

@param json – String in the same format as getFilters() output

@param returnFormat: currently supports “csv”, “tsv”

Return javax.ws.rs.core.Response of TSV text with a minimal number of parameters (filePath, disease, patientBarcode, patientUUID, sampleBarcode, sampleUUID, sampleType, aliquotBarcode, aliquotUUID, dataType, center, platform, level, dateCreated, pgrrUUID.