Provide credentials as:
{"user": "<username>", "password": "<password>"}

These are replaced within parameters of function calls, e.g. loaded from a library.

List of tasks to be executed. They can be specified in place, loaded from a library or from an external file.

Runs an external script, e.g. here to just wait for n seconds to give the import time to complete.

```json
{
    "credentials": "credentials.json",
    "server":  "https://test.genexplain.com",
    "reconnect": true,
    "verbose": true,
    "replaceStrings": [
            ["$BASE_FOLDER$", "data/Projects/Automatic_testing/Data/example_folder"],
            ["$STUDY$", "GSE2639_HUVEC_TNF"],
            ["$LIMMA_FILE$","TNF vs. Control"]
    ],
    "tasks": [
        {
            "do": "createFolder",
            "path": "data/Projects/Automatic_testing/Data",
            "name": "example_folder"
        },

        {
            "do": "imPort",
            "file": "cola/automat/GSE2639_HUVEC/GSE2639_HUVEC_TNF_CEL_files.zip",
            "path": "$BASE_FOLDER$",
            "importer": "ZIP-archive (*.zip)",
            "wait": true,
            "progress": true,
            "parameters": [{"name": "cleanupFolder",      "value":false},
                           {"name": "preserveExtension", "value":false},
                           {"name": "preserveArchiveStructure", "value":true },
                           {"name": "importFormat", "value": "Affymetrix CEL file (*.cel)"}]
        },

        {
            "do": "external",
            "showOutput": true,
            "bin": "sh",
            "params": ["gxp_wait.sh", "10"]
        },

        {
            "do": "createFolder",
            "path": "$BASE_FOLDER$",
            "name": "$STUDY$"
        },
        {
            "do": "analyze",
            "method": "Affymetrix normalization",
            "wait": true,
            "progress": true,
            "parameters": [
                {
                    "name":"celFiles",
                    "value":
                        [
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50777.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50778.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50779.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50780.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50781.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50782.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50783.CEL",
                            "$BASE_FOLDER$/GSE2639_HUVEC_TNF_CEL_files/GSM50784.CEL"
                        ]
                },
                {"name":"method","value":"RMA"},
                {"name":"bgCorrection","value":"RMA"},
                {"name":"normMethod","value":"quantiles"},
                {"name":"pmCorrection","value":"pmonly"},
                {"name":"summarization","value":"medianpolish"},
                {"name":"cdf","value":""},
                {"name":"outputLogarithmBase","value":"log2"},
                {"name":"outputPath","value":"$BASE_FOLDER$/$STUDY$/Normalized (RMA)"}
            ]
        },

        {
            "do": "analyze",
            "method": "Normalization quality plots",
            "wait": true,
            "progress": true,
            "parameters": [
                {
                    "name":"inputTablePath",
                    "value": "$BASE_FOLDER$/$STUDY$/Normalized (RMA)"
                },
                {"name":"inputLogarithmBase","value":"log2"},
                {"name":"outputFolderPath","value":"$BASE_FOLDER$/$STUDY$/Normalization_QC_plots"}
            ]
        },

        {
            "do": "analyze",
            "method": "PCA",
            "wait": true,
            "progress": true,
            "parameters": [
                {
                    "name":"inputTablePath",
                    "value": "$BASE_FOLDER$/$STUDY$/Normalized (RMA)"
                },
                {
                    "name": "firstName",
                    "value": "Control"
                },
                {
                    "name": "firstColumns",
                    "value": ["GSM50777.CEL", "GSM50778.CEL", "GSM50779.CEL", "GSM50780.CEL"]
                },
                {
                    "name": "secondName",
                    "value": "TNF"
                },
                {
                    "name": "secondColumns",
                    "value": ["GSM50781.CEL", "GSM50782.CEL", "GSM50783.CEL", "GSM50784.CEL"]
                },
                {"name":"outputFolderPath","value":"$BASE_FOLDER$/$STUDY$/PCA"}
            ]
        },
        {
            "do": "analyze",
            "method": "Limma",
            "wait": true,
            "progress": true,
            "parameters": [
                {
                    "name":"inputTablePath",
                    "value": "$BASE_FOLDER$/$STUDY$/Normalized (RMA)"
                },
                {
                    "name":"inputLogarithmBase",
                    "value": "log2"
                },
                {
                    "name": "firstName",
                    "value": "TNF"
                },
                {
                    "name": "firstColumns",
                    "value": ["GSM50781.CEL", "GSM50782.CEL", "GSM50783.CEL", "GSM50784.CEL"]
                },
                {
                    "name": "secondName",
                    "value": "Control"
                },
                {
                    "name": "secondColumns",
                    "value": ["GSM50777.CEL", "GSM50778.CEL", "GSM50779.CEL", "GSM50780.CEL"]
                },
                {
                    "name": "outputFolderPath",
                    "value":"$BASE_FOLDER$/$STUDY$/Limma"
                }
            ]
        },

        {
            "do": "analyze",
            "method": "Convert table",
            "wait": true,
            "progress": true,
            "parameters": [
                {
                    "name":"sourceTable",
                    "value": "$BASE_FOLDER$/$STUDY$/Limma/$LIMMA_FILE$"
                },
                {
                    "name": "species",
                    "value": "$SPECIES$"
                },
                {
                    "name": "sourceType",
                    "value": "Probes: Affymetrix"
                },
                {
                    "name": "targetType",
                    "value": "Genes: Ensembl"
                },
                {
                    "name": "outputTable",
                    "value": "$BASE_FOLDER$/$STUDY$/Limma/$LIMMA_FILE$ Genes Ensembl"
                }
            ]
        },

        {
            "do": "analyze",
            "method": "Convert table",
            "wait": true,
            "progress": true,
            "parameters": [
                {
                    "name":"sourceTable",
                    "value": "$BASE_FOLDER$/$STUDY$/Limma/$LIMMA_FILE$"
                },
                {
                    "name": "species",
                    "value": "$SPECIES$"
                },
                {
                    "name": "sourceType",
                    "value": "Probes: Affymetrix"
                },
                {
                    "name": "targetType",
                    "value": "Proteins: Transpath"
                },
                {
                    "name": "outputTable",
                    "value": "$BASE_FOLDER$/$STUDY$/Limma/$LIMMA_FILE$ Proteins Transpath"
                }
            ]
        }
    ]
}
```