TP Conversion de fichiers

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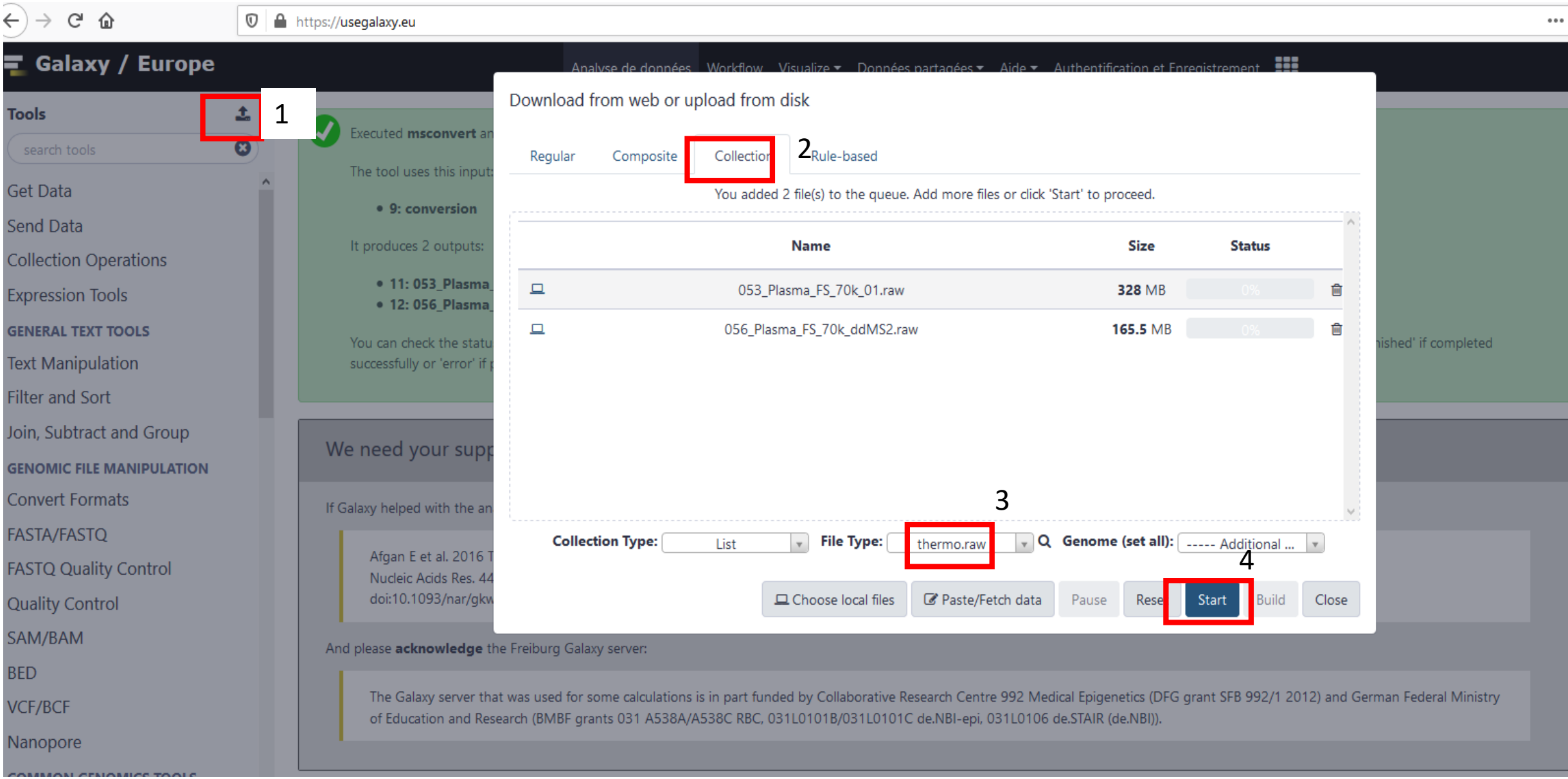
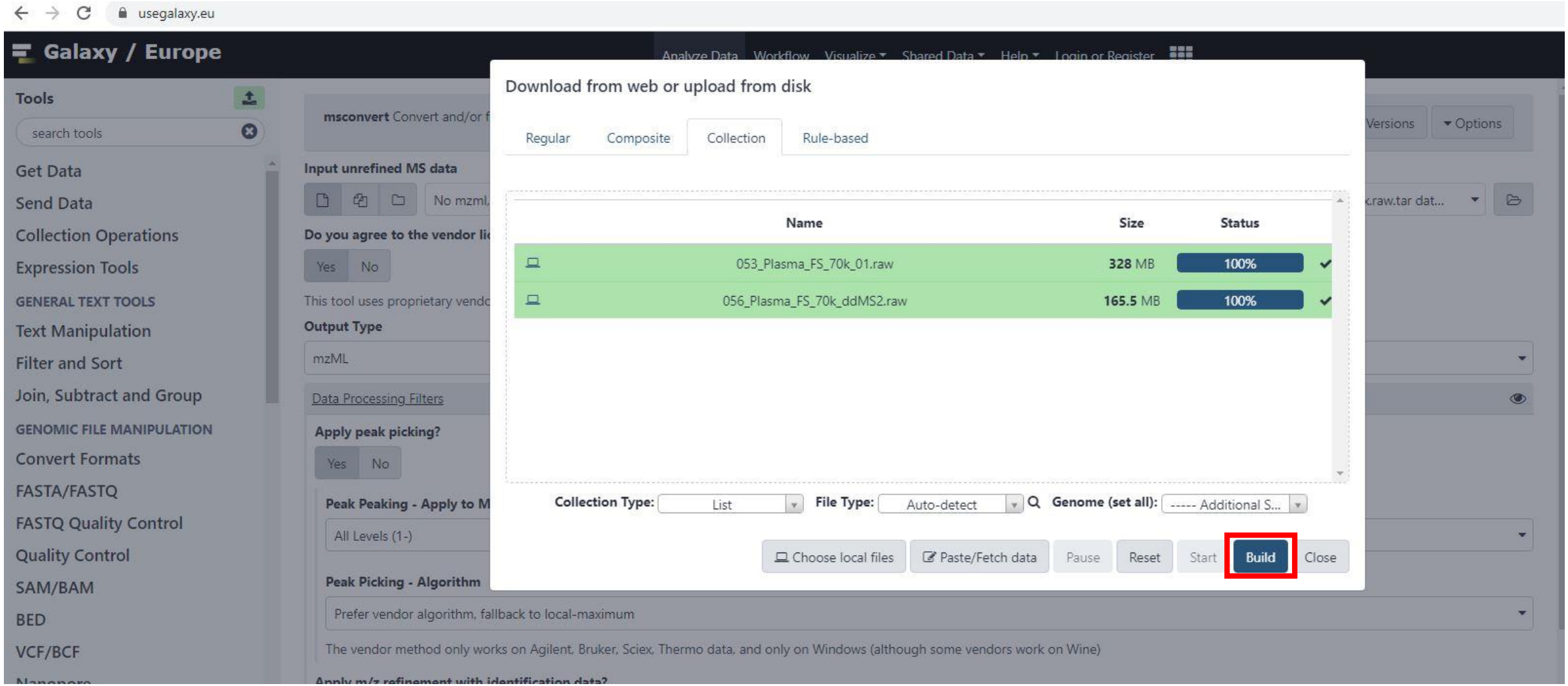

https://usegalaxy.eu
Galaxy / Europe
Analyse de données
Workflow
Visualize
Données partagées
Aide
Authentification et Enregistrement
Tools
1
search tools
Get Data
Send Data
Collection Operations
Expression Tools
GENERAL TEXT TOOLS
Text Manipulation
Filter and Sort
Join, Subtract and Group
GENOMIC FILE MANIPULATION
Convert Formats
FASTA/FASTQ
FASTQ Quality Control
Quality Control
SAM/BAM
BED
VCF/BCF
Nanopore
Executed msconvert
The tool uses this input:
• 9: conversion
It produces 2 outputs:
• 11: 053_Plasma_
• 12: 056_Plasma_
We need your supp
If Galaxy helped with the an
Afgan E et al. 2016
Nucleic Acids Res. 44
doi:10.1093/nar/gkw
And please acknowledge the Freiburg Galaxy server:
The Galaxy server that was used for some calculations is in part funded by Collaborative Research Centre 992 Medical Epigenetics (DFG grant SFB 992/1 2012) and German Federal Ministry of Education and Research (BMBF grants 031 A538A/A538C RBC, 031L0101B/031L0101C de.NBI-epi, 031L0106 de.STAIR (de.NBI)).
Download from web or upload from disk
Regular
Composite
Collection
2
Rule-based
You added 2 file(s) to the queue. Add more files or click 'Start' to proceed.
Name
Size
Status
053_Plasma_FS_70k_01.raw
328 MB
056_Plasma_FS_70k_ddMS2.raw
165.5 MB
3
Collection Type:
List
File Type:
thermo.raw
Genome (set all):
----- Additional ...
4
Choose local files
Paste/Fetch data
Pause
Rese
Start
Build
Close



Cliquez sur **Build** et nommer votre dossier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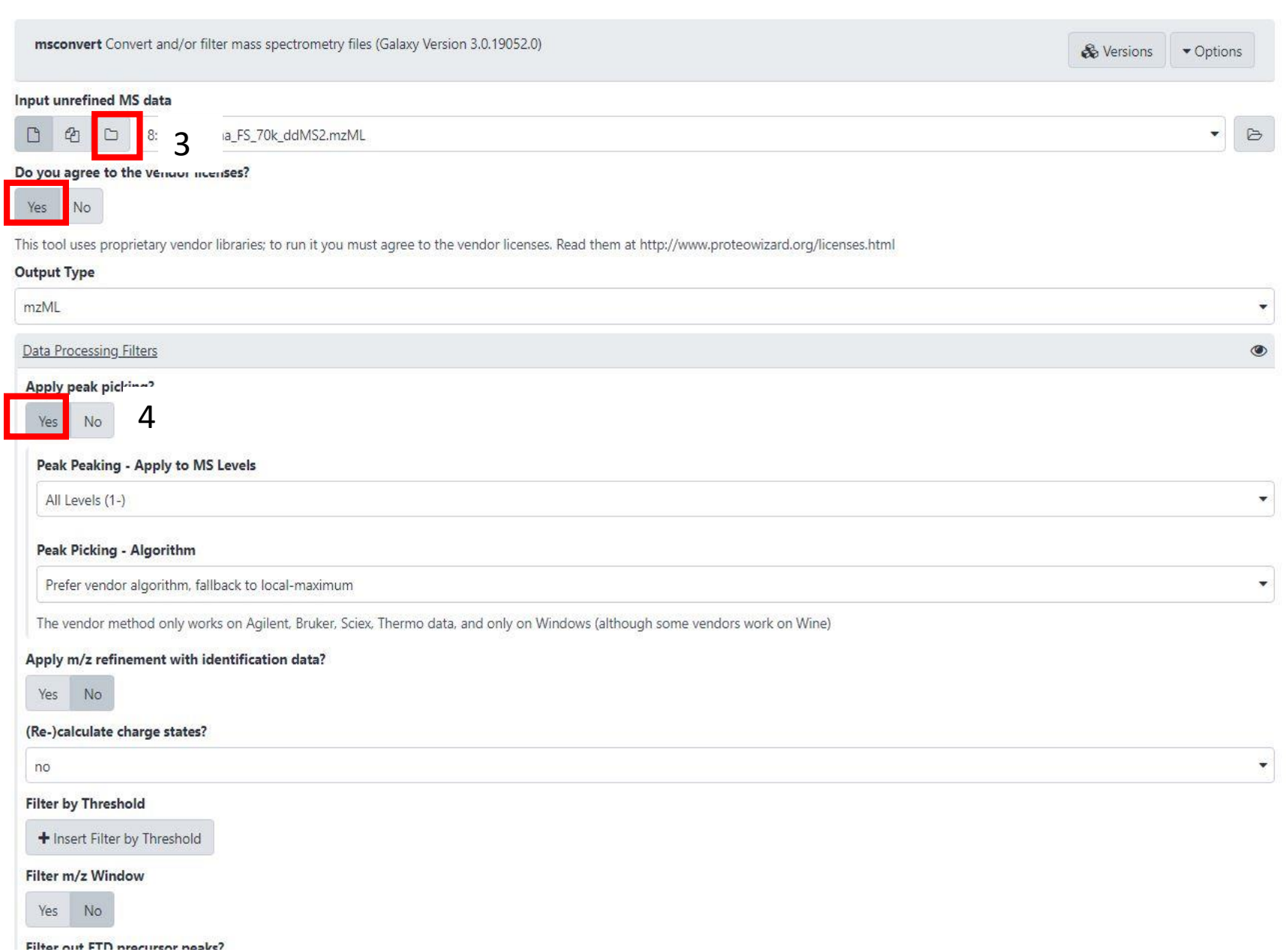
Tools
msconvert
1
Convert Formats
msms_extractor Extract MS/MS scans from the mzML file(s) based on PSM report
2
idconvert Convert mass spectrometry identification files
msconvert Convert and/or filter mass spectrometry files
msconvert Subset Peak List against list of scan numbers or indices.
Proteomics
DIA_Umpire_SE DIA signal extraction
Metabolomics
Process Scans (and SIM-Stitch) - Read, filter and average MS scans
Workflows
All workflows


msconvert Convert and/or filter mass spectrometry files (Galaxy Version 3.0.19052.0)
Versions
Options
Input unrefined MS data
3
a_FS_70k_ddMS2.mzML
Do you agree to the vendor licenses?
Yes
No
This tool uses proprietary vendor libraries; to run it you must agree to the vendor licenses. Read them at http://www.proteowizard.org/licenses.html
Output Type
mzML
Data Processing Filters
Apply peak picking?
Yes
No
4
Peak Peaking - Apply to MS Levels
All Levels (1-)
Peak Picking - Algorithm
Prefer vendor algorithm, fallback to local-maximum
The vendor method only works on Agilent, Bruker, Sciex, Thermo data, and only on Windows (although some vendors work on Wine)
Apply m/z refinement with identification data?
Yes
No
(Re-)calculate charge states?
no
Filter by Threshold
+ Insert Filter by Threshold
Filter m/z Window
Yes
No