# Introduction to STRaM Analysis Workflow in Galaxy (STRaM Loci Ver. 18)

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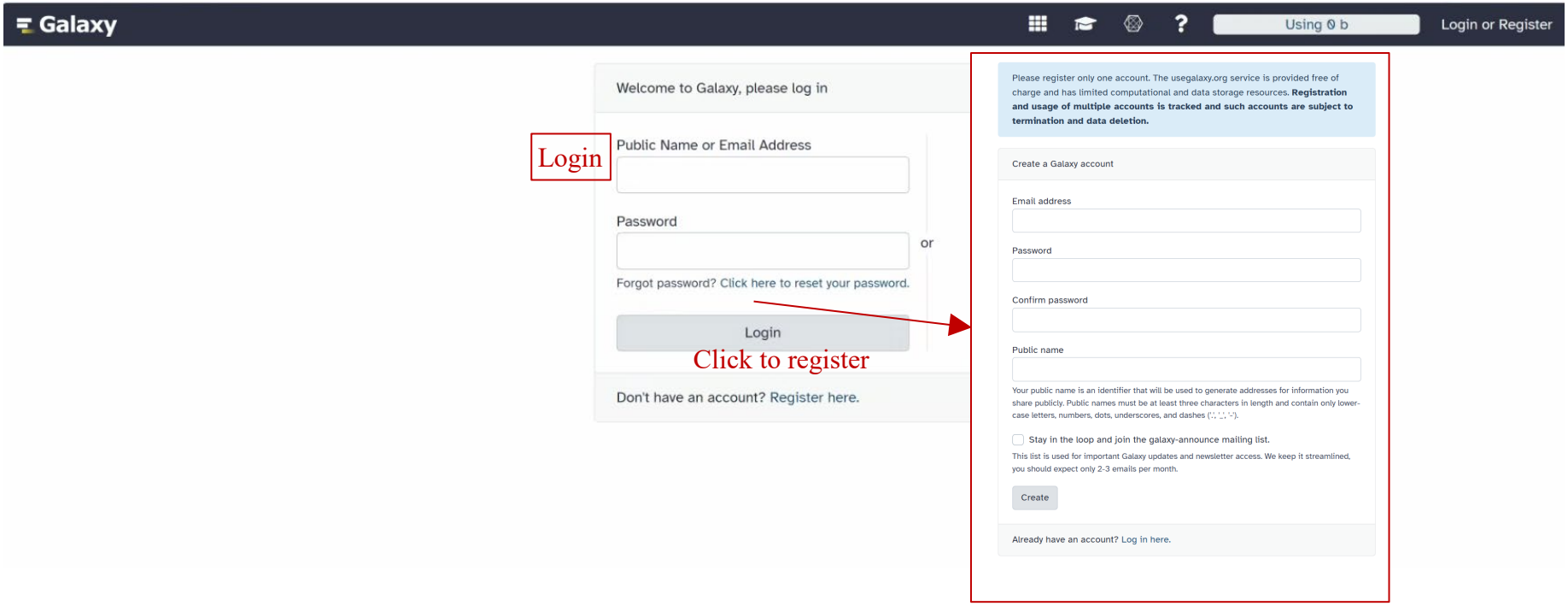
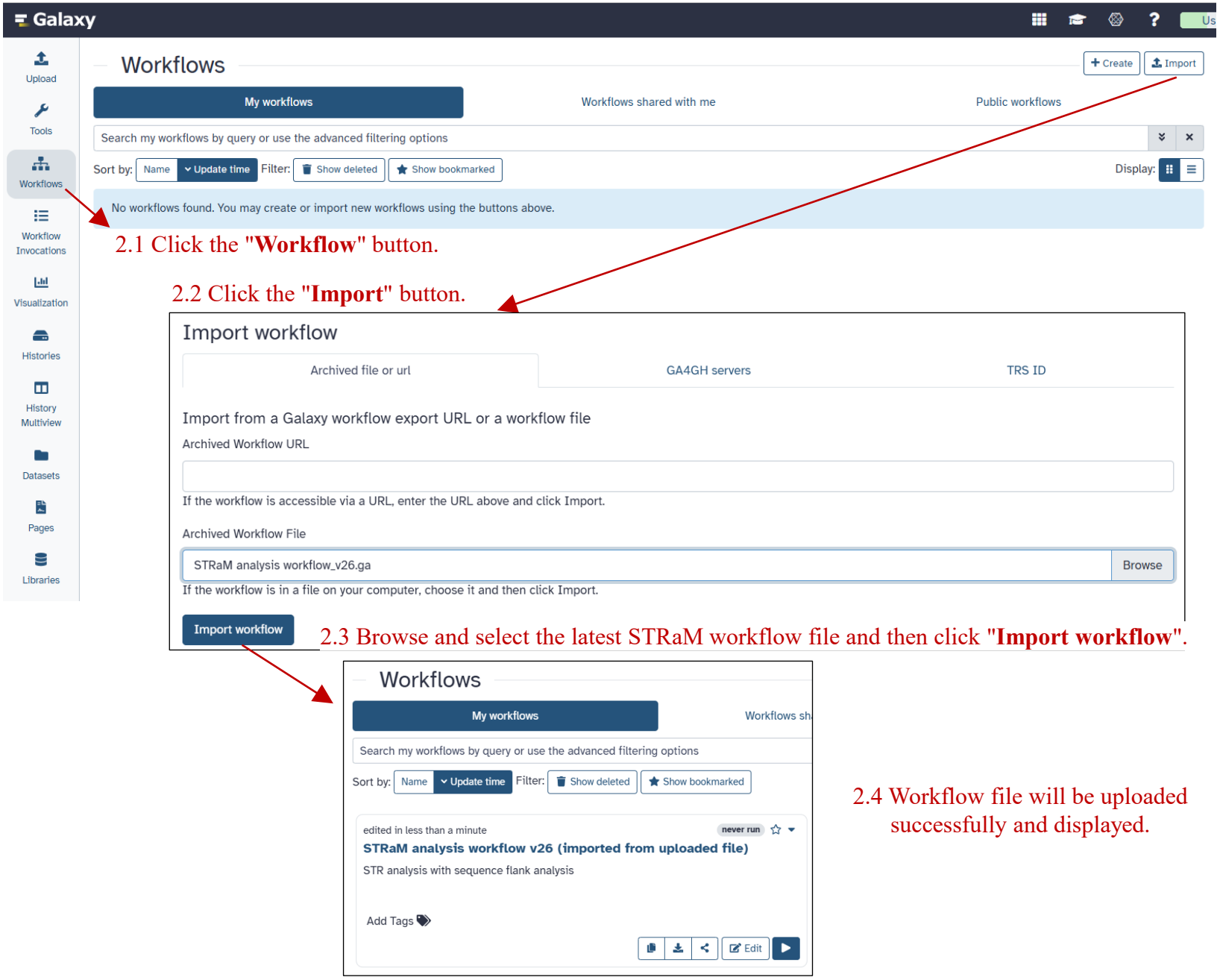
2025.05

# 1. Apply for a web or lab Galaxy platform account

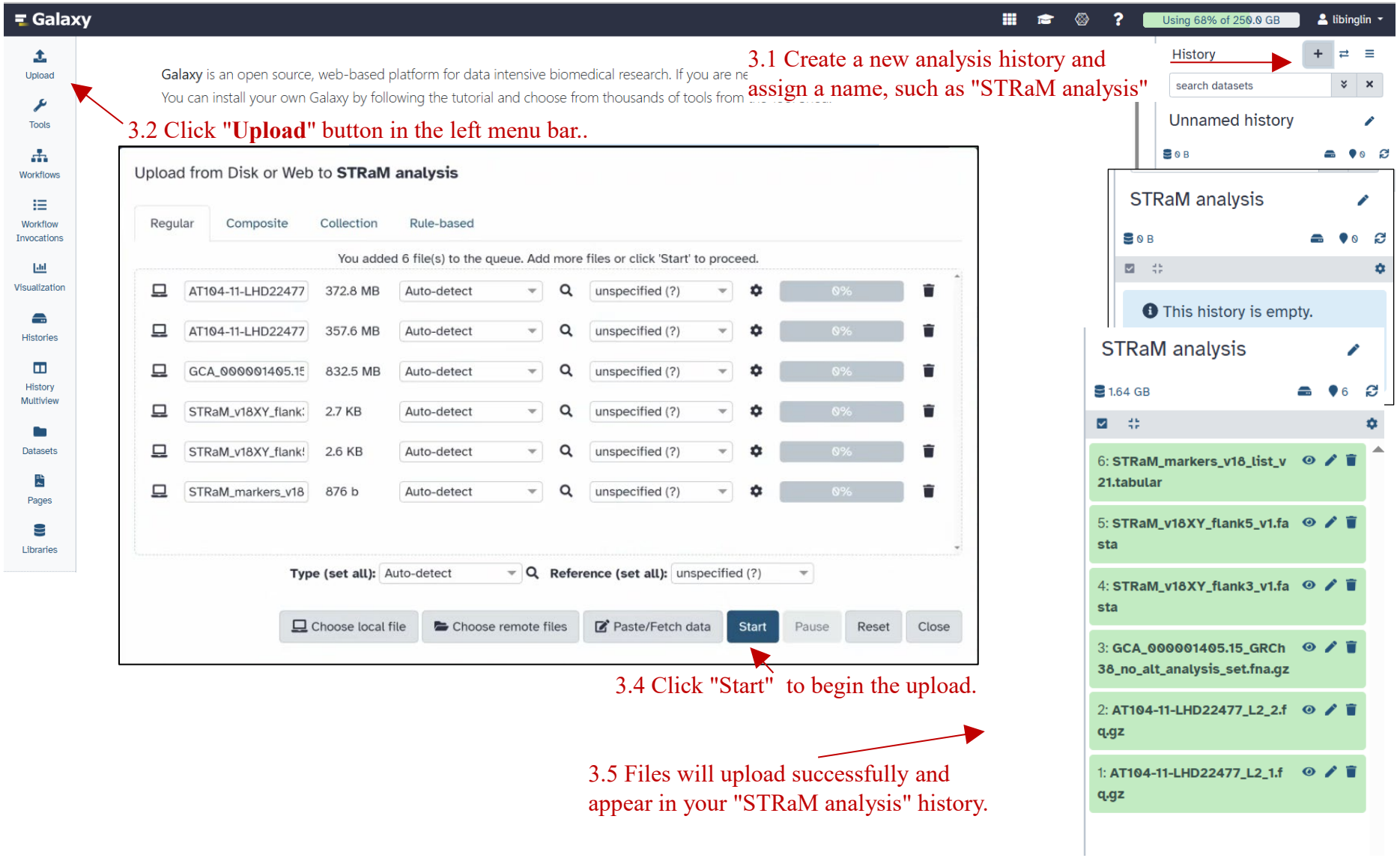



Galaxy of Web Platform (https://usegalaxy.org/)

# 2. Import STRaM analysis workflow

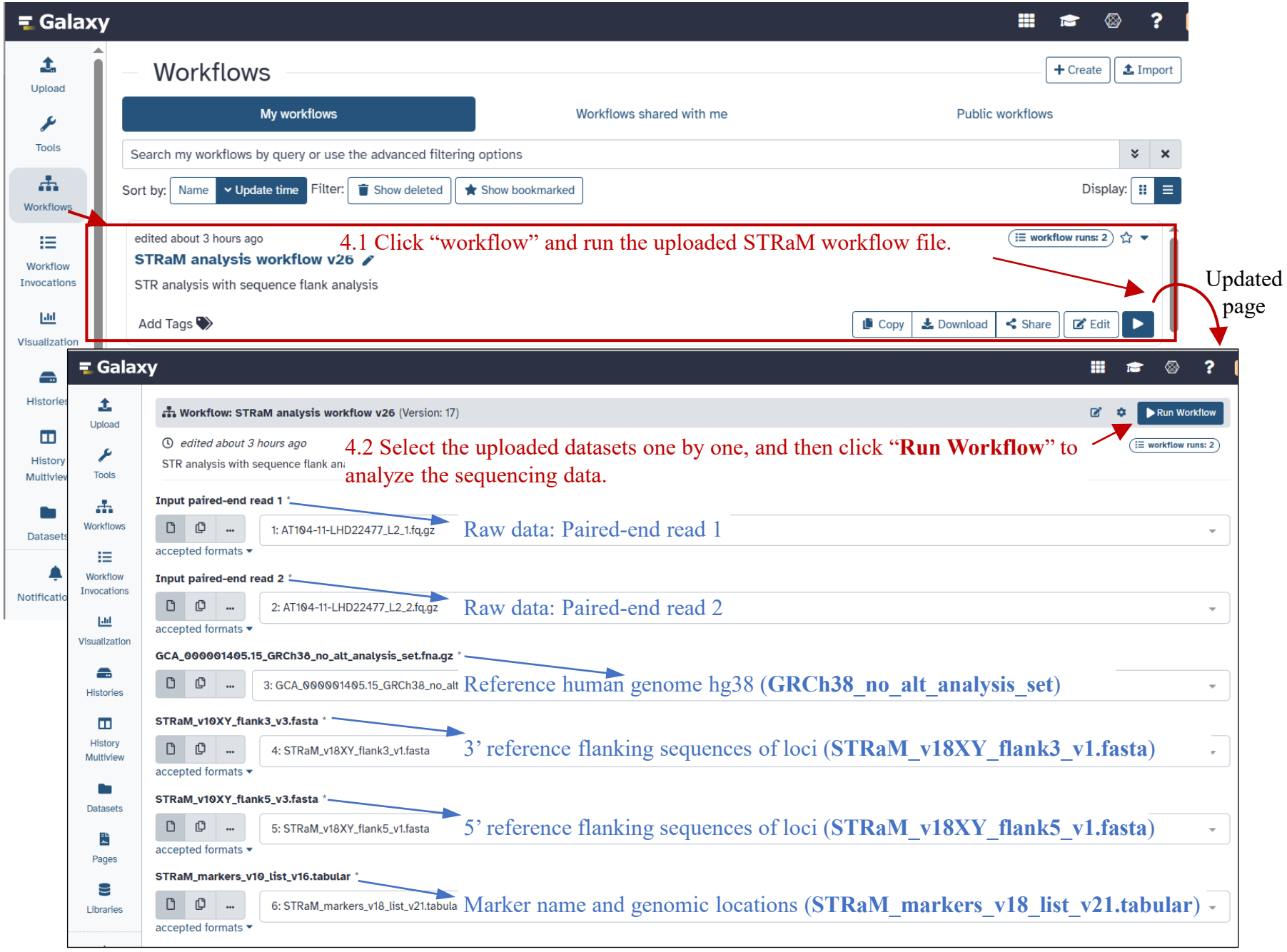


# 3. Upload all datasets into a new history in Galaxy Server

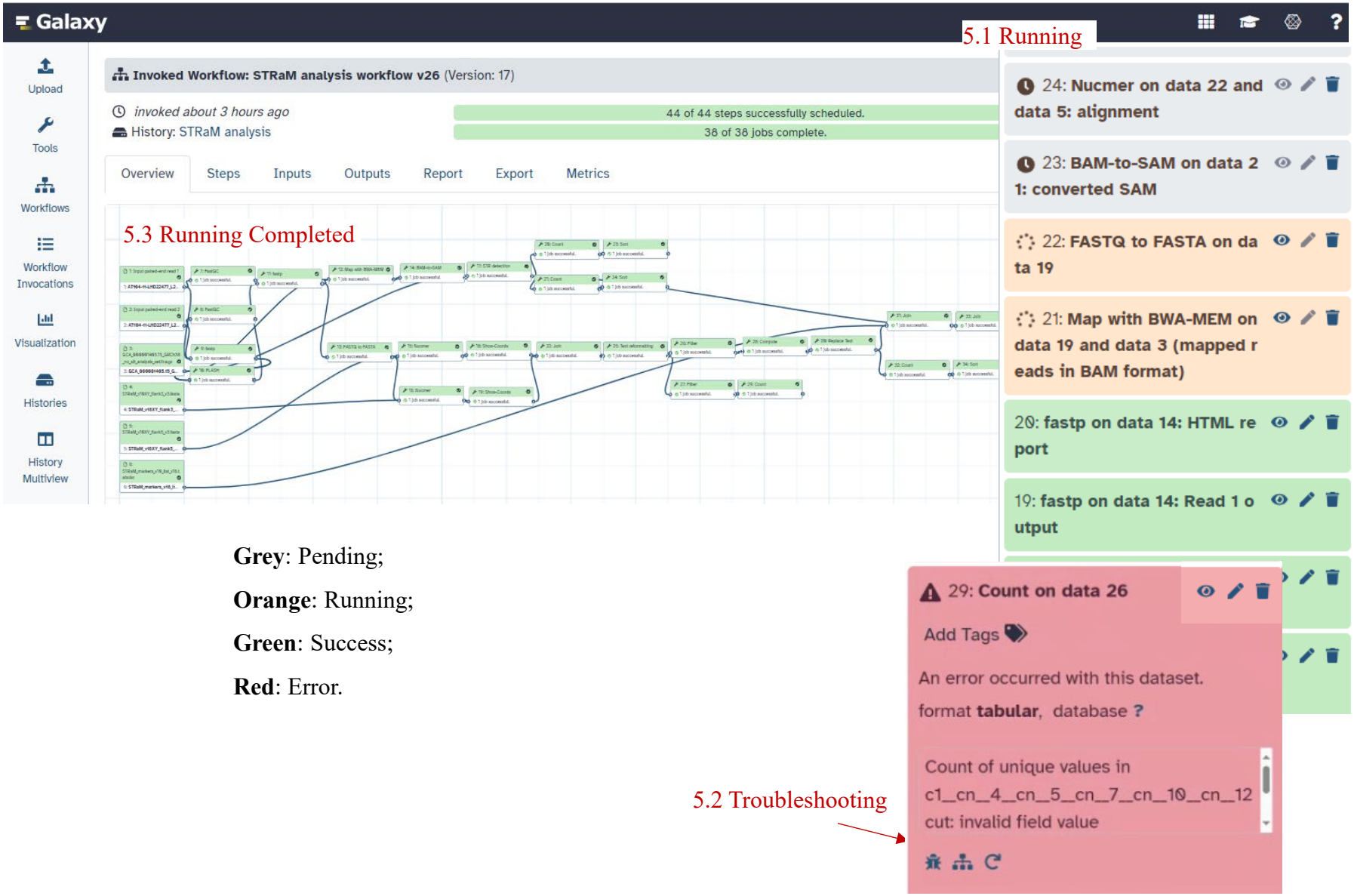



Note: The Raw data file shoule be uploaded before the reference genome file.

# 4. Run STRaM analysis workflow



# 5. Running




**Grey**: Pending;

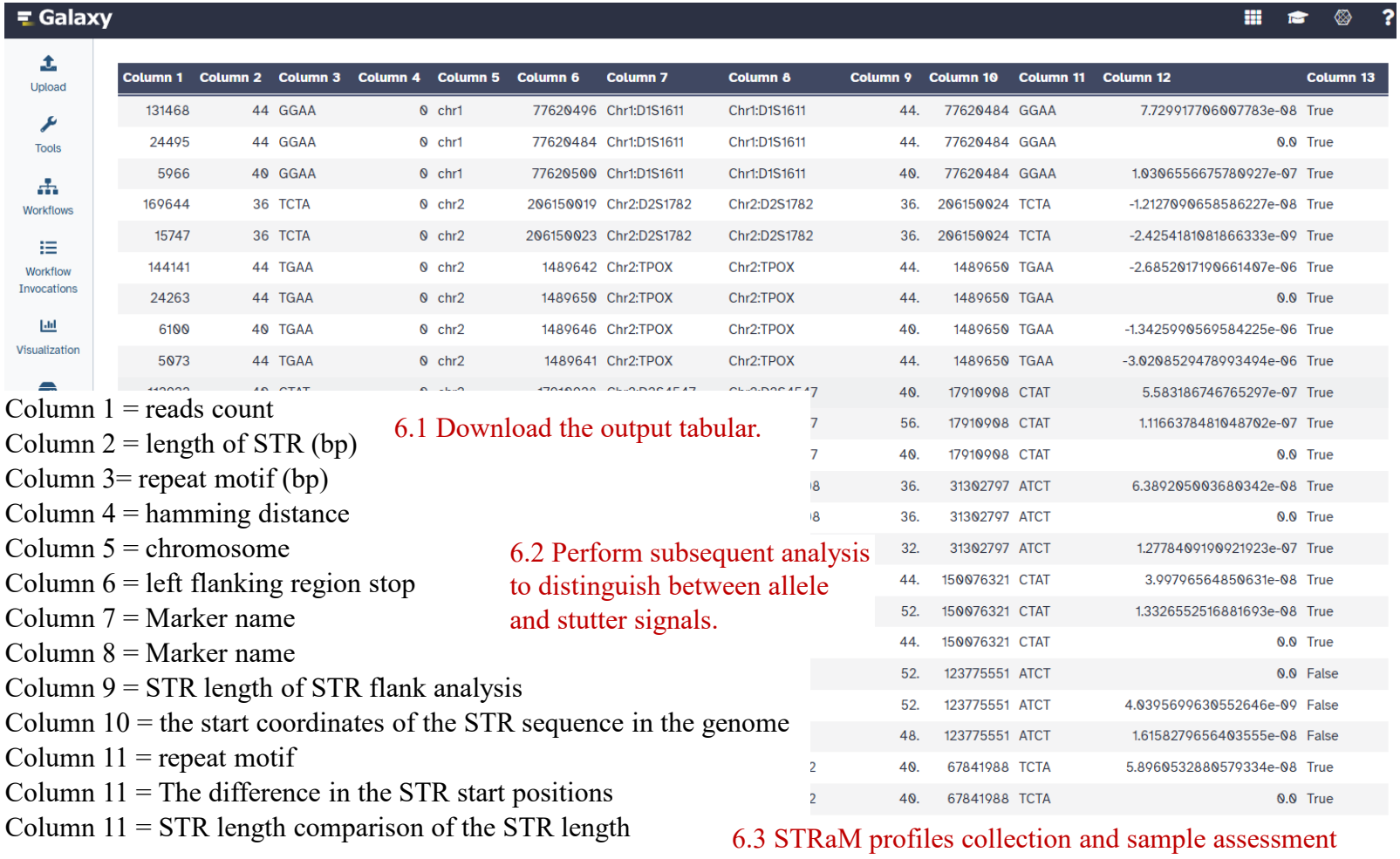
**Orange**: Running;

**Green**: Success;

**Red**: Error.

Note: Since the web platform is updated regularly, some tools may encounter errors. Troubleshooting is required for these tools according to error reports.

# 6. Result output




| Column 1 | Column 2 | Column 3 | Column 4 | Column 5 | Column 6 | Column 7 | Column 8 | Column 9 | Column 10 | Column 11 | Column 12 | Column 13 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 131468 | 44 | GGAA | 0 | chr1 | 77620496 | Chr1:D1S1611 | Chr1:D1S1611 | 44. | 77620484 | GGAA | 7.729917706007783e-08 | True |
| 24495 | 44 | GGAA | 0 | chr1 | 77620484 | Chr1:D1S1611 | Chr1:D1S1611 | 44. | 77620484 | GGAA | 0.0 | True |
| 5966 | 40 | GGAA | 0 | chr1 | 77620500 | Chr1:D1S1611 | Chr1:D1S1611 | 40. | 77620484 | GGAA | 1.0306556675780927e-07 | True |
| 169644 | 36 | TCTA | 0 | chr2 | 206150019 | Chr2:D2S1782 | Chr2:D2S1782 | 36. | 206150024 | TCTA | -1.2127099658586227e-08 | True |
| 15747 | 36 | TCTA | 0 | chr2 | 206150023 | Chr2:D2S1782 | Chr2:D2S1782 | 36. | 206150024 | TCTA | -2.4254181081866333e-09 | True |
| 144141 | 44 | TGAA | 0 | chr2 | 1489642 | Chr2:TPOX | Chr2:TPOX | 44. | 1489650 | TGAA | -2.6852017190661407e-06 | True |
| 24263 | 44 | TGAA | 0 | chr2 | 1489650 | Chr2:TPOX | Chr2:TPOX | 44. | 1489650 | TGAA | 0.0 | True |
| 6100 | 40 | TGAA | 0 | chr2 | 1489646 | Chr2:TPOX | Chr2:TPOX | 40. | 1489650 | TGAA | -1.3425990569584225e-06 | True |
| 5073 | 44 | TGAA | 0 | chr2 | 1489641 | Chr2:TPOX | Chr2:TPOX | 44. | 1489650 | TGAA | -3.0208529478993494e-06 | True |
| | | | | | | | | 40. | 17910908 | CTAT | 5.583186746765297e-07 | True |
| | | | | | | | | 56. | 17910908 | CTAT | 1.1166378481048702e-07 | True |
| | | | | | | | | 40. | 17910908 | CTAT | 0.0 | True |
| | | | | | | | | 36. | 31302797 | ATCT | 6.389205003680342e-08 | True |
| | | | | | | | | 36. | 31302797 | ATCT | 0.0 | True |
| | | | | | | | | 32. | 31302797 | ATCT | 1.2778409190921923e-07 | True |
| | | | | | | | | 44. | 150076321 | CTAT | 3.99796564850631e-08 | True |
| | | | | | | | | 52. | 150076321 | CTAT | 1.3326552516881693e-08 | True |
| | | | | | | | | 44. | 150076321 | CTAT | 0.0 | True |
| | | | | | | | | 52. | 123775551 | ATCT | 0.0 | False |
| | | | | | | | | 52. | 123775551 | ATCT | 4.0395699630552646e-09 | False |
| | | | | | | | | 48. | 123775551 | ATCT | 1.6158279656403555e-08 | False |
| | | | | | | | | 40. | 67841988 | TCTA | 5.896053288579334e-08 | True |
| | | | | | | | | 40. | 67841988 | TCTA | 0.0 | True |

Column 1 = reads count
Column 2 = length of STR (bp)
Column 3= repeat motif (bp)
Column 4 = hamming distance
Column 5 = chromosome
Column 6 = left flanking region stop
Column 7 = Marker name
Column 8 = Marker name
Column 9 = STR length of STR flank analysis
Column 10 = the start coordinates of the STR sequence in the genome
Column 11 = repeat motif
Column 11 = The difference in the STR start positions
Column 11 = STR length comparison of the STR length

6.1 Download the output tabular.

6.2 Perform subsequent analysis to distinguish between allele and stutter signals.

6.3 STRaM profiles collection and sample assessment