Travaux pratiques – Galaxy* (partie 4)

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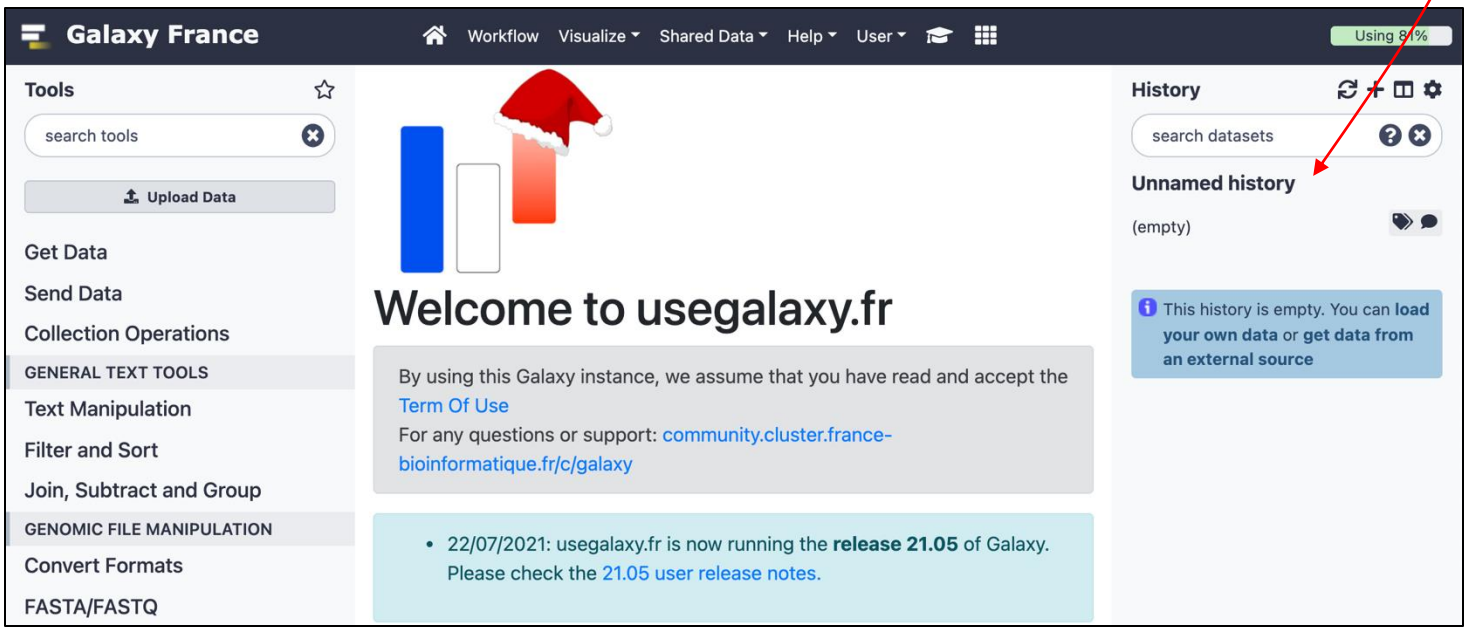
* Les captures d'écran ont été réalisées en 2022, il est possible que l'interface aujourd'hui soit légèrement différente.

Etape 1 : Connexion à Galaxy

- Se connecter à l'instance Galaxy « France » : https://usegalaxy.fr/

- Créer un nouvel historique de travail



Données utilisées pour le TP

cells

MDPI

Article

Characterization of the Radiation Desiccation Response Regulon of the Radioresistant Bacterium *Deinococcus radiodurans* by Integrative Genomic Analyses

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Abstract: Numerous genes are overexpressed in the radioresistant bacterium *Deinococcus radiodurans* after exposure to radiation or prolonged desiccation. It was shown that the DdrO and IrrE proteins play a major role in regulating the expression of approximately twenty genes. The transcriptional repressor DdrO blocks the expression of these genes under normal growth conditions. After exposure to genotoxic agents, the IrrE metalloprotease cleaves DdrO and relieves gene repression. At present, many questions remain, such as the number of genes regulated by DdrO. Here, we present the first ChIP-seq analysis performed at the genome level in *Deinococcus* species coupled with RNA-seq, which was achieved in the presence or not of DdrO. We also resequenced our laboratory stock strain of *D. radiodurans* R1 ATCC 13939 to obtain an accurate reference for read alignments and gene expression quantifications. We highlighted genes that are directly under the control of this transcriptional repressor and showed that the DdrO regulon in *D. radiodurans* includes numerous other genes than those previously described, including DNA and RNA metabolism proteins. These results thus pave the way to better understand the radioresistance pathways encoded by this bacterium and to compare the stress-induced responses mediated by this pair of proteins in diverse bacteria.

Keywords: radioresistance/desiccation; transcriptional regulator; *Deinococcus radiodurans*; ChIP-seq; RNA-seq; bioinformatic analyses

check for updates

Citation: Eugénie, N.; Zivanovic, Y.; Lelandais, G.; Coste, G.; Bouthier de la Tour, C.; Bentchikou, E.; Servant, P.; Confalonieri, F. Characterization of the Radiation Desiccation Response Regulon of the Radioresistant Bacterium *Deinococcus radiodurans* by Integrative Genomic Analyses. *Cells* **2021**, *10*, 2536. https://doi.org/10.3390/cells10102536

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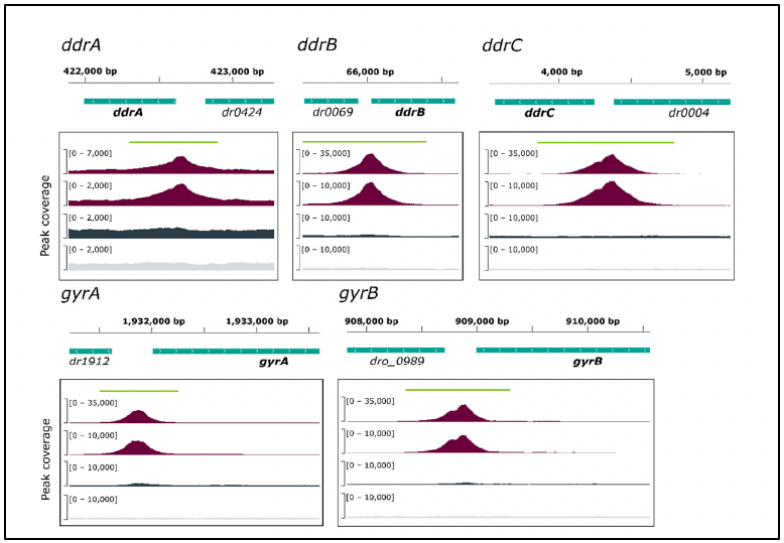
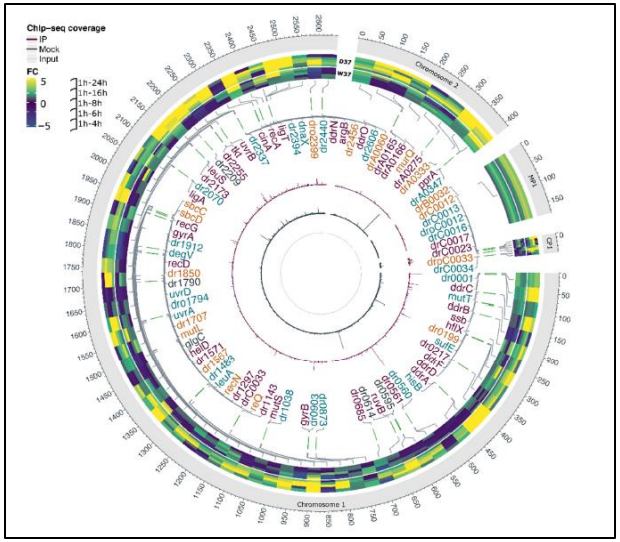
1. Introduction

Deinococcus radiodurans is one of the most resistant bacteria to genotoxic agent exposure and desiccation isolated to date [1–4]. Unlike radiosensitive organisms, once exposed to huge γ-ray doses, or after prolonged desiccation, *D. radiodurans* is able to reconstruct an intact genome in a few hours from several hundred DNA fragments [5]. Many factors contribute to the radioresistance of *D. radiodurans*, including efficient DNA repair mechanisms [5–8], a condensed nucleoid limiting the dispersion of genome fragments after irradiation [9,10], and the protection of proteins against oxidative damage [11]. Thus, the exceptional ability of this bacterium to overcome severe DNA damaging conditions is described as a combination of active and passive mechanisms acting in synergy within the cell, enabling survival following these stresses.

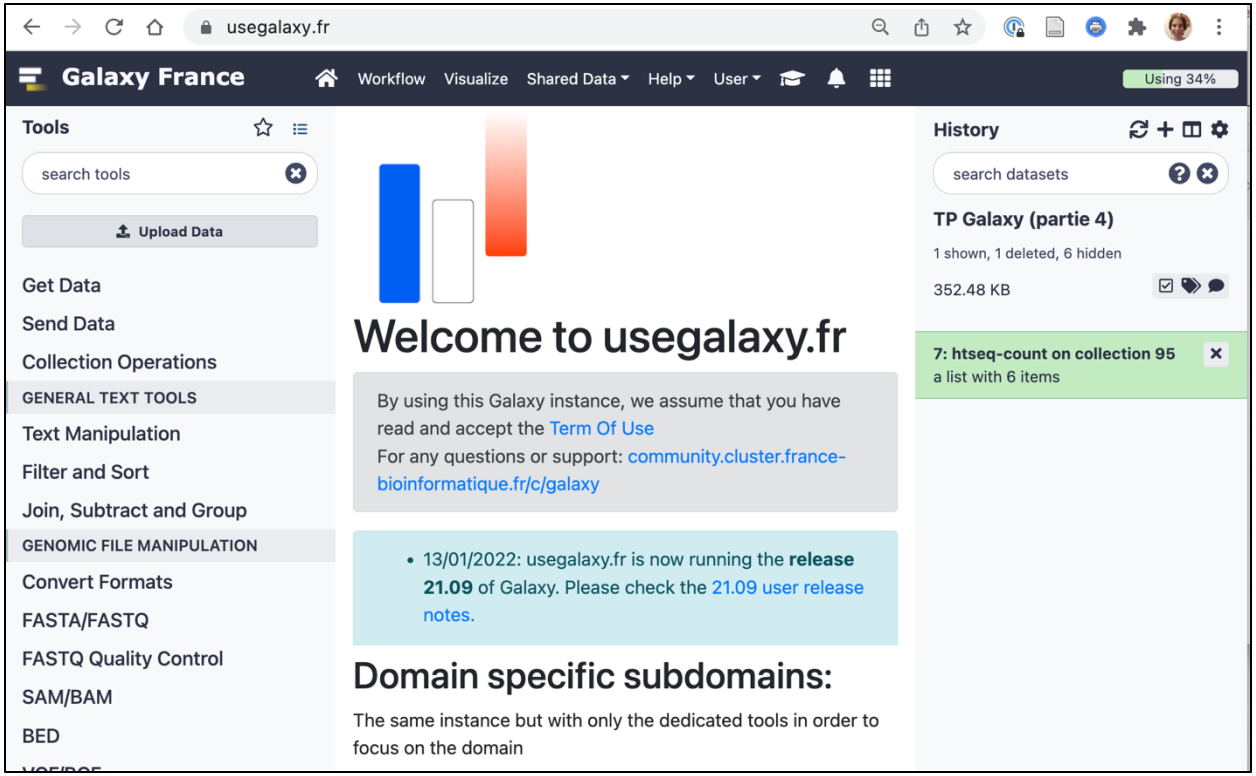
The exposure of *D. radiodurans* to γ-rays, or its recovery from desiccation, results in a rapid upregulation of the expression of numerous genes [12,13], even if constitutively expressed genes are also involved in the mechanisms of radioresistance. In many bacterial species, expression of DNA repair genes is under the control of LexA, the repressor of the well-known SOS response (for review [14]). *D. radiodurans* encodes two LexA homologs





Etape 2 : Importer les résultats des comptages (TP3)

- Récupérer dans votre nouvel historique de travail la collection des fichiers TXT :



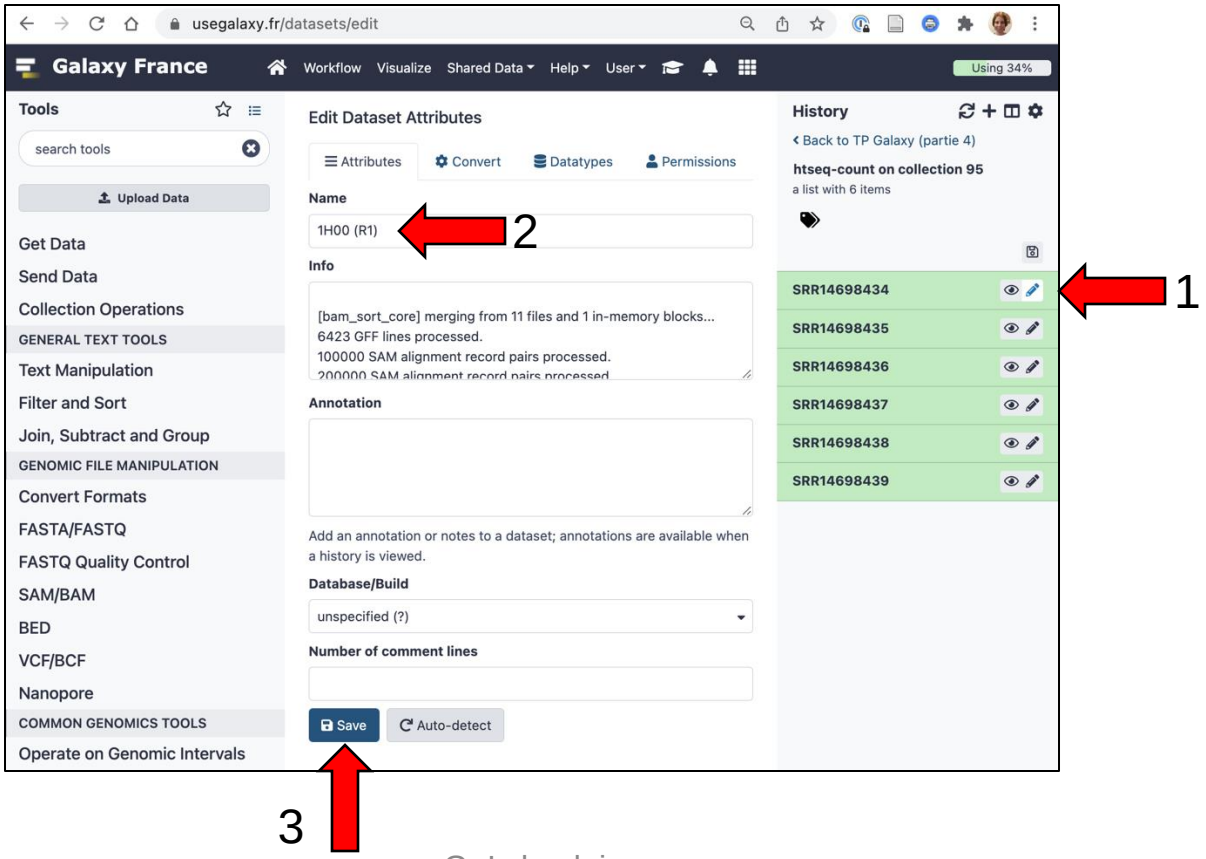
Etape 2 : Importer les résultats des comptages (TP3)

- Vérifier le contenu de la collection, les résultats pour les 6 échantillons suivant doivent être présents :

Run	Assay Type	strain	treatment	type-material	time_point
SRR14698434	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	1H
SRR14698435	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	1H
SRR14698436	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	1H
SRR14698437	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	4H
SRR14698438	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	4H
SRR14698439	RNA-Seq	ATCC 13939	37degreeC	type strain of Deinococcus radiodurans	4H

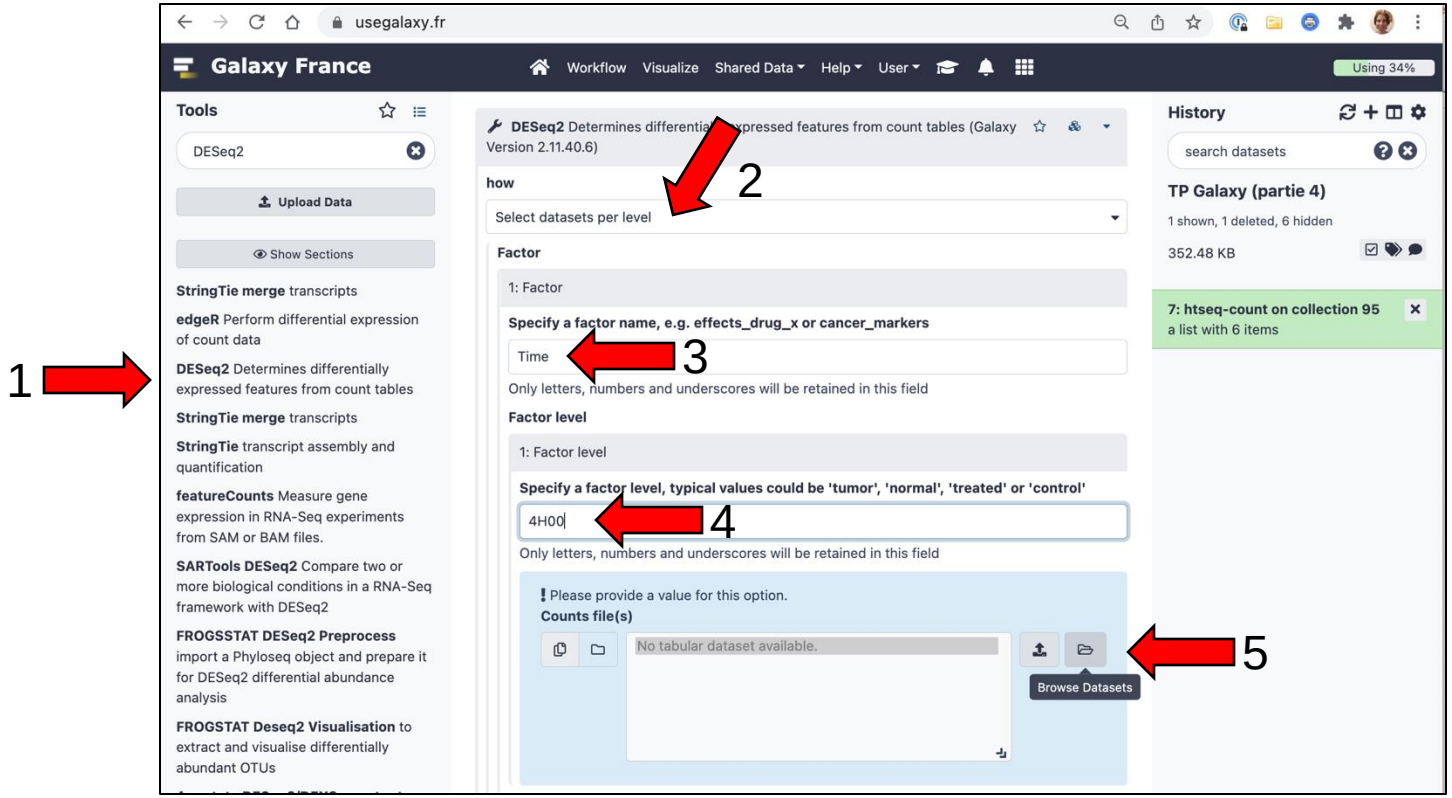
Etape 3 : Simplification des noms de fichiers

- Pour faciliter l'utilisation de DESeq2, renommer les fichiers par conditions (1H00 et 4H00) :



Etape 4 : Analyse différentielle

- Utiliser la méthode DESeq2 pour comparer les données de comptage entre les temps 4H00 et 1H00 :



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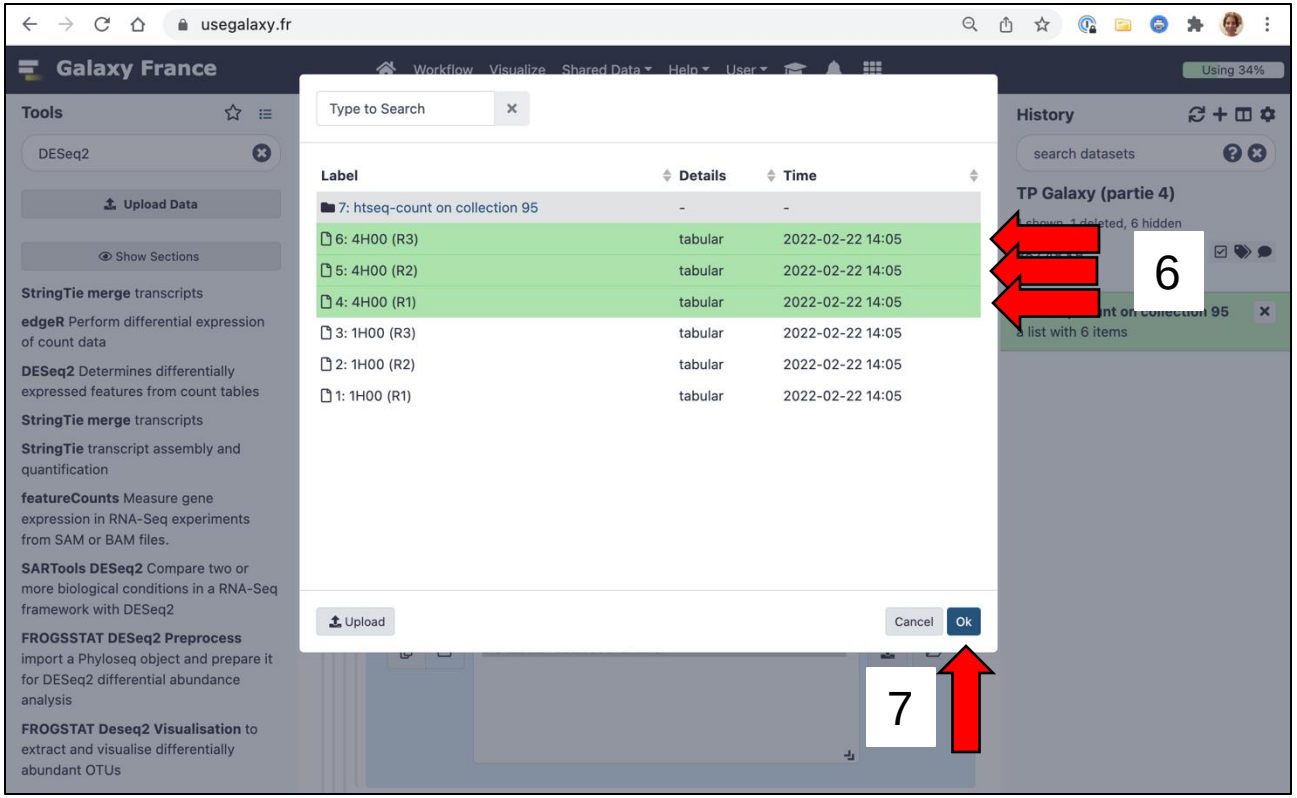

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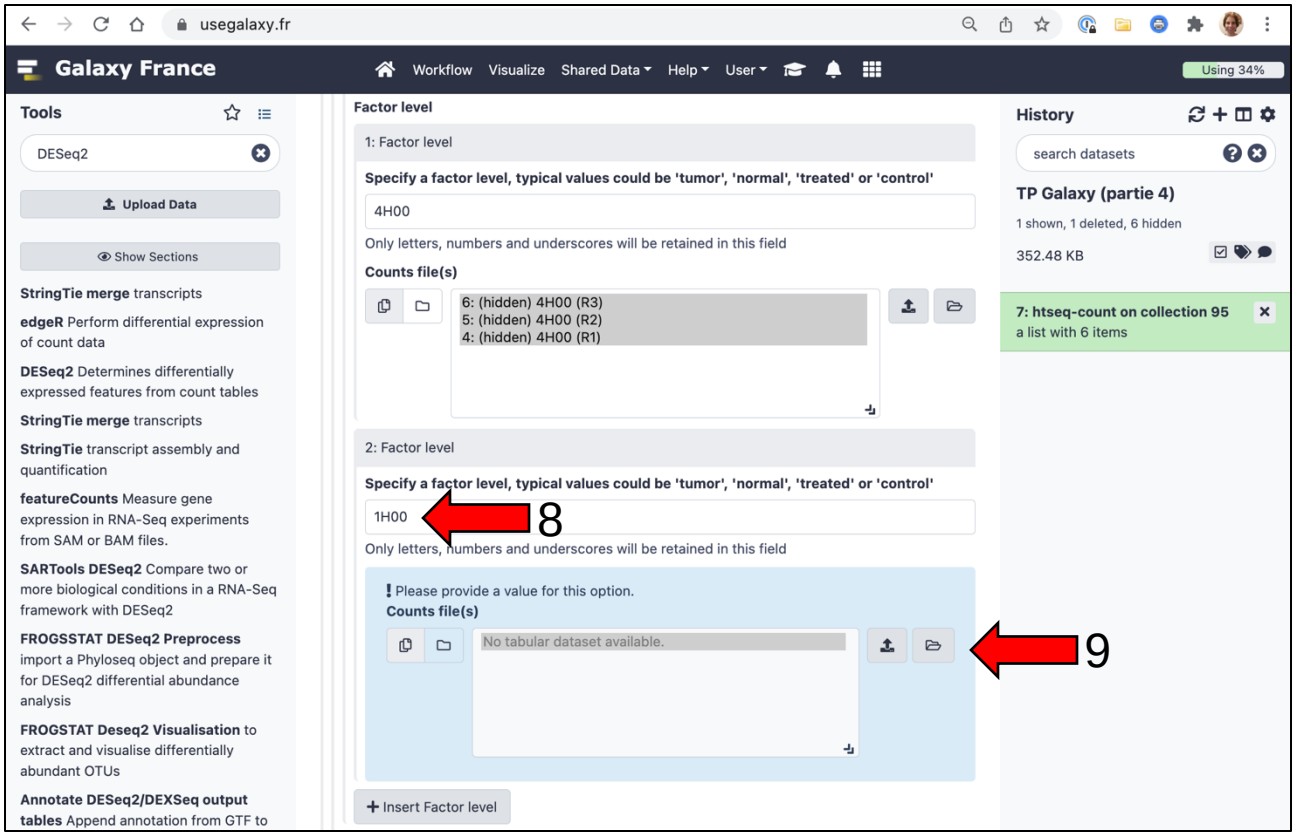

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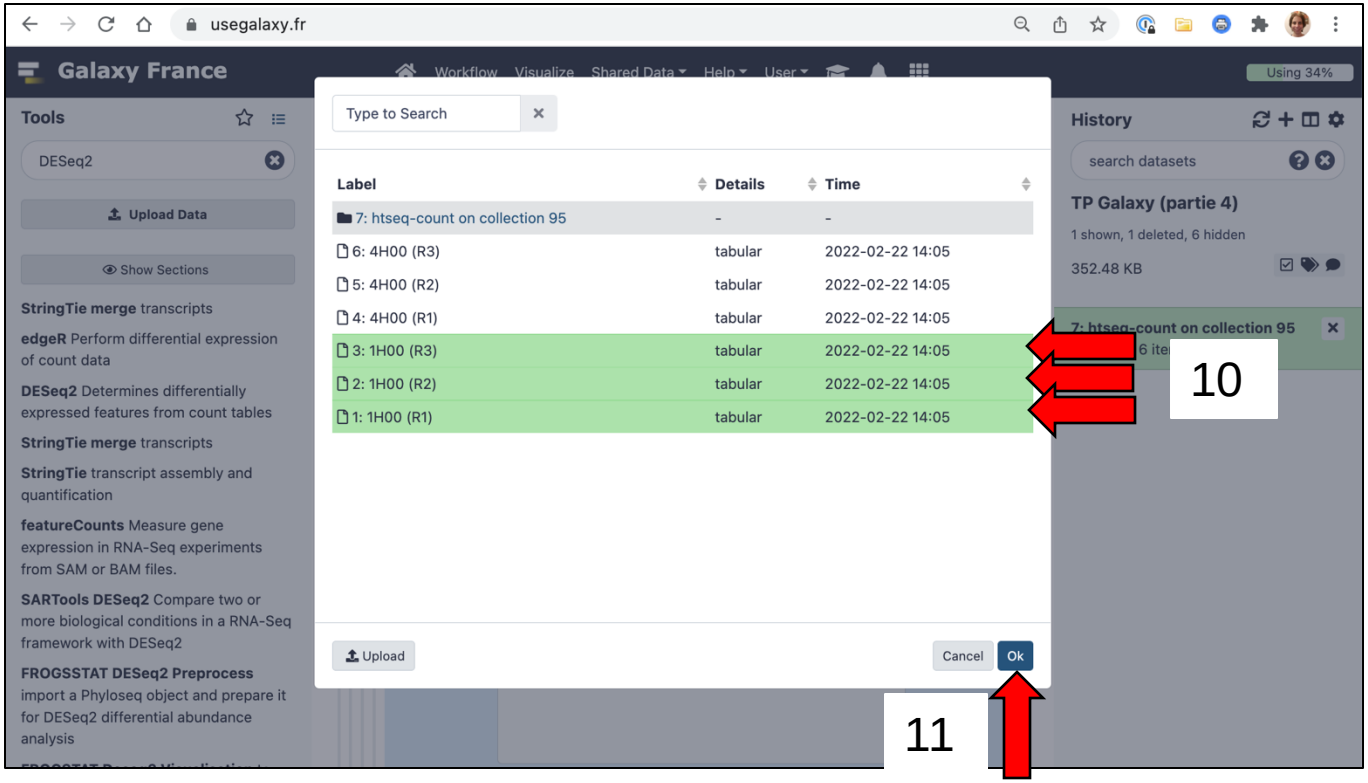

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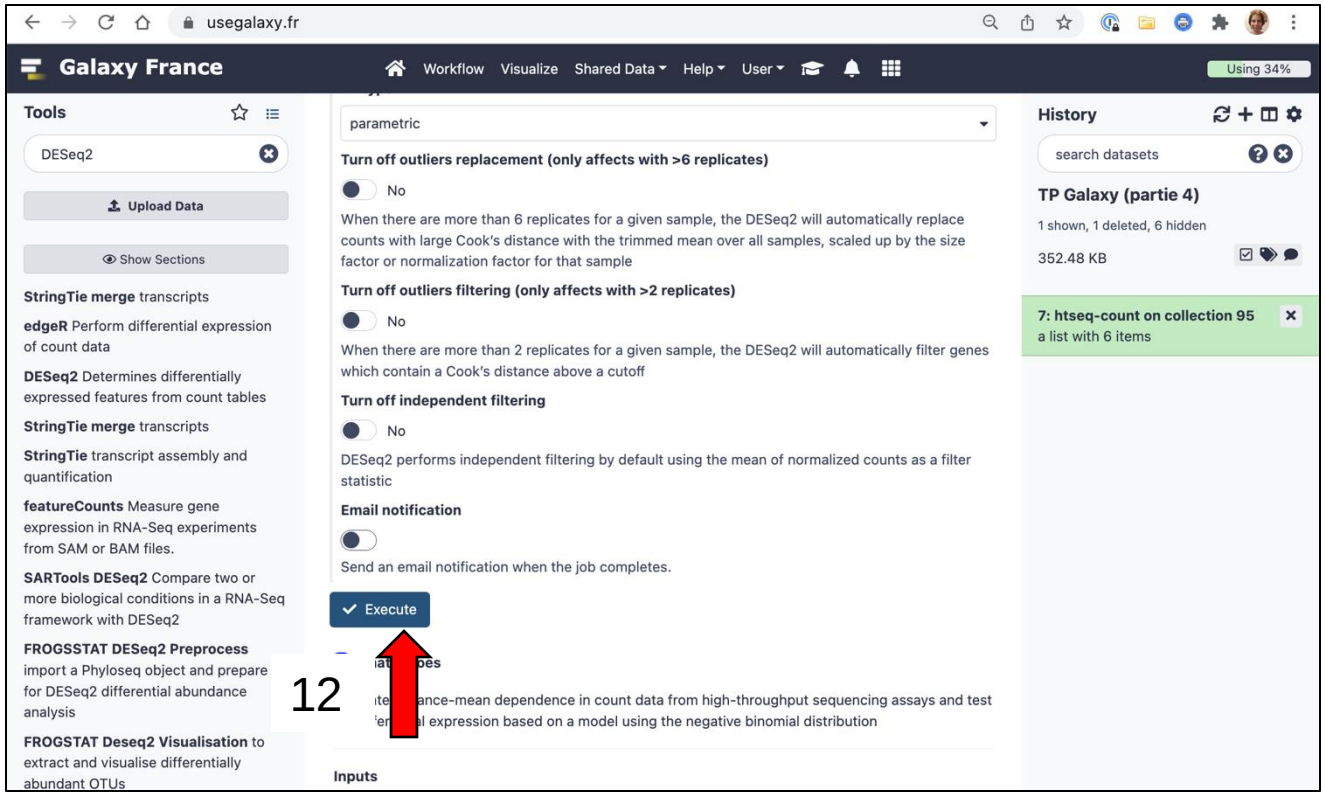
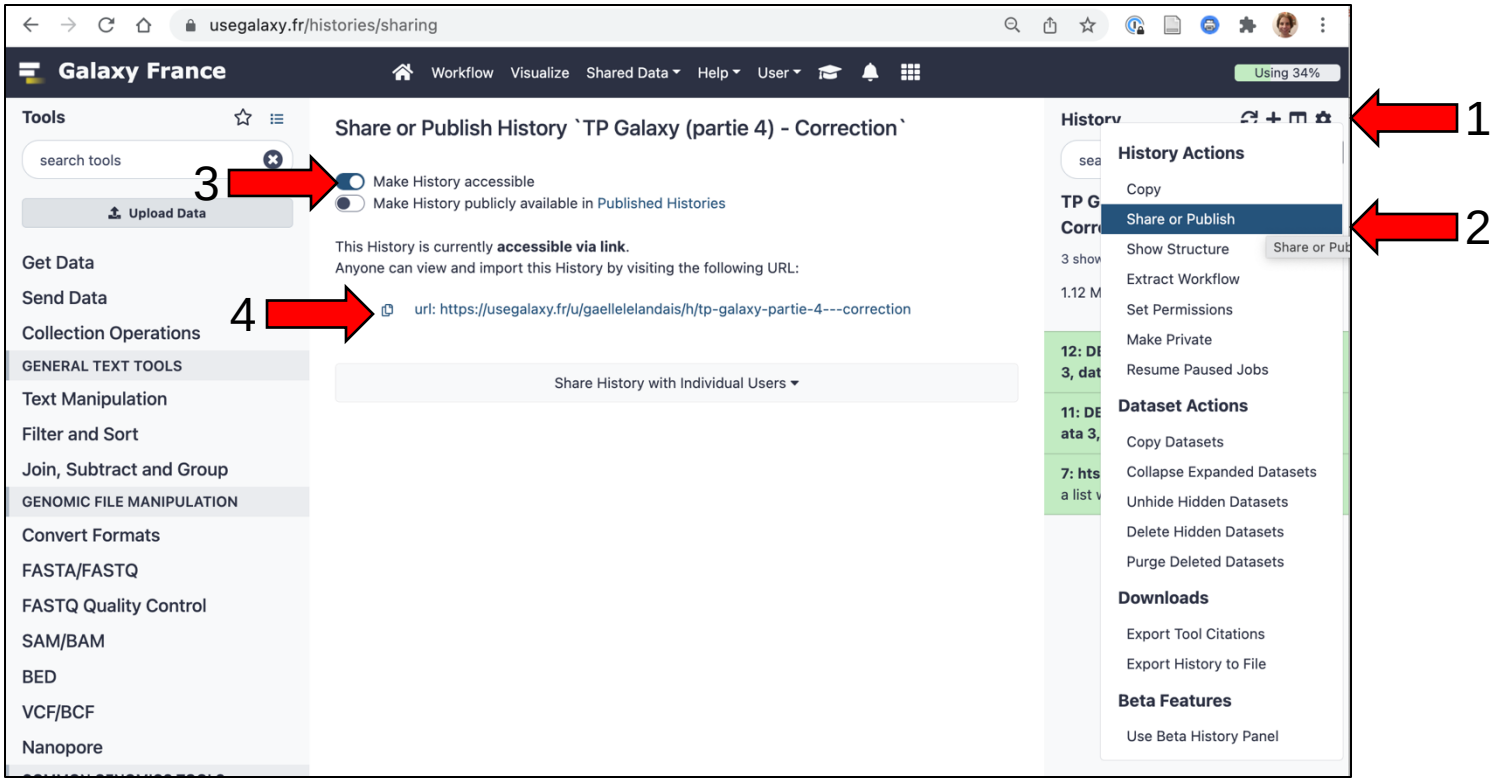


Etape 5 : Partager l'historique des résultats



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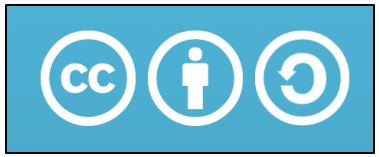

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