Travaux pratiques – Galaxy* (partie 5)

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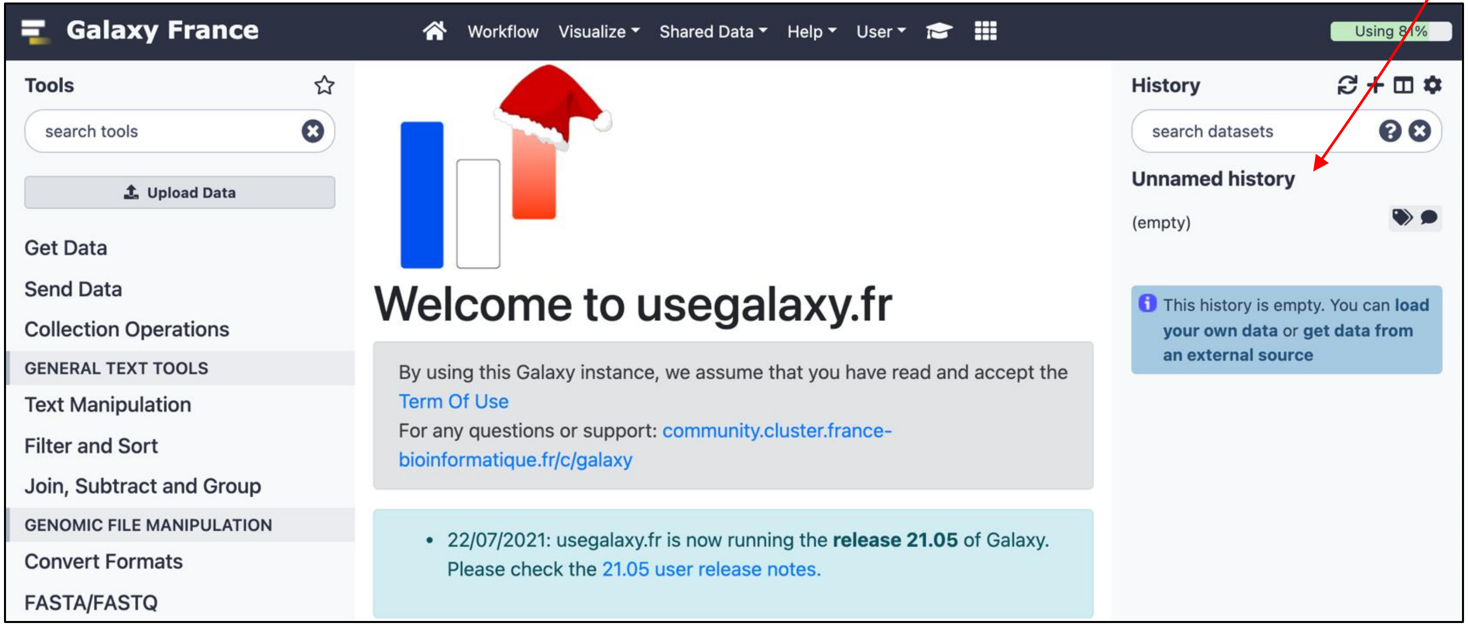
* Les captures d'écran ont été réalisées en 2022, il est possible que l'interface aujourd'hui soit légèrement différente.

Etape 1 : Connexion à Galaxy

- Se connecter à l'instance Galaxy « France » : https://usegalaxy.fr/
- Créer un nouvel historique de travail



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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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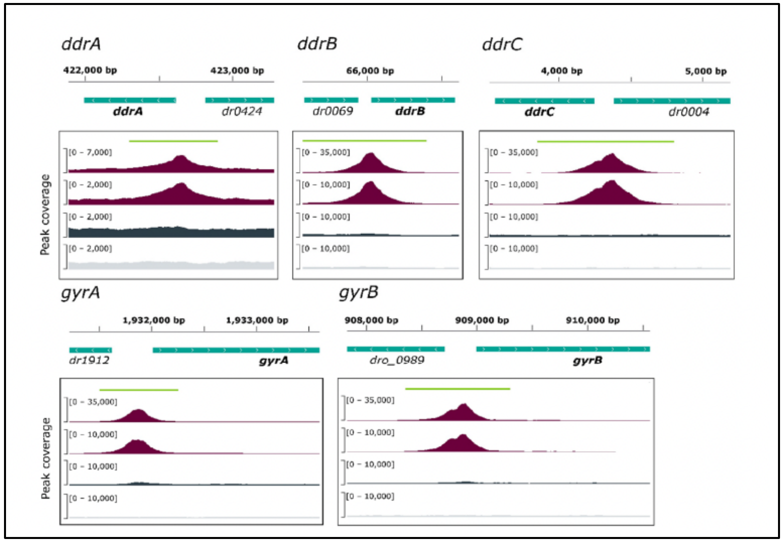
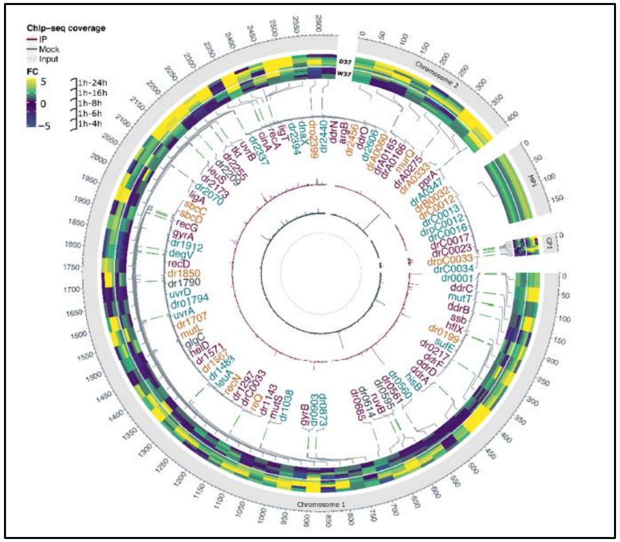
1. Introduction

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 : Créer un workflow
(automatisation des analyses)

- Cliquer sur l'onglet « Workflow »

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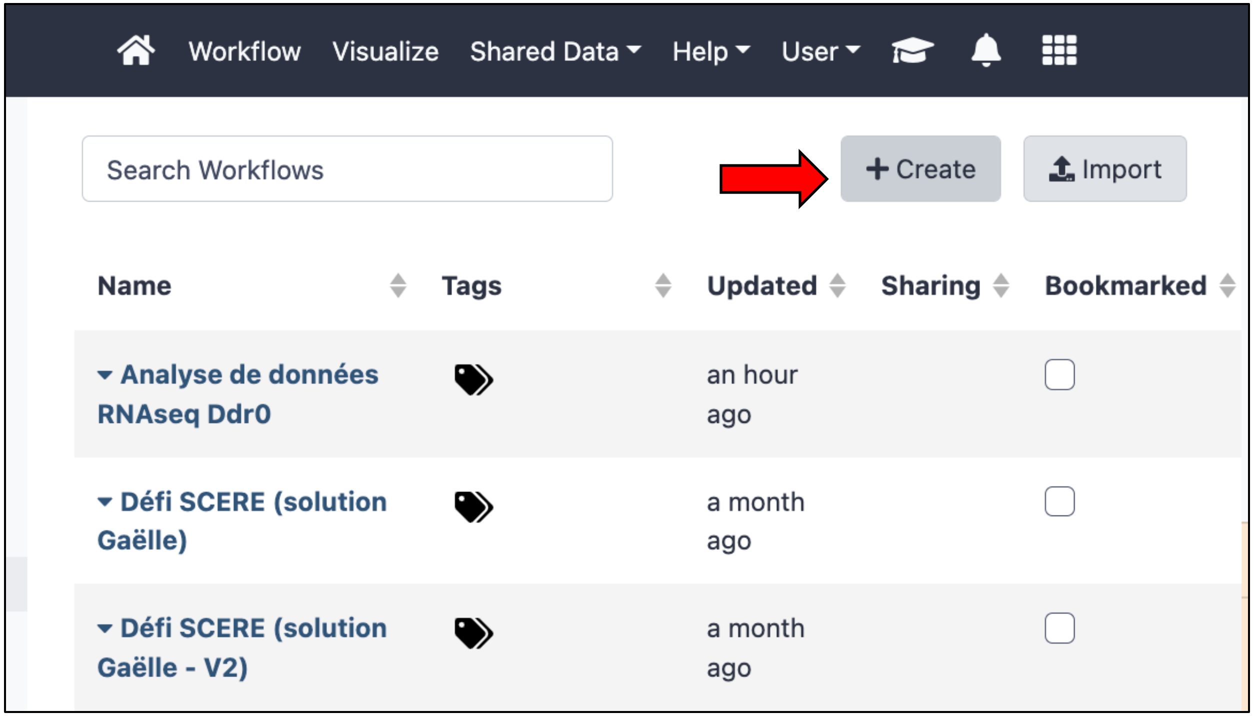
Etape 2 : Créer un workflow

(automatisation des analyses)

- Cliquer sur l'onglet « Workflow », puis sur le bouton « Create » :

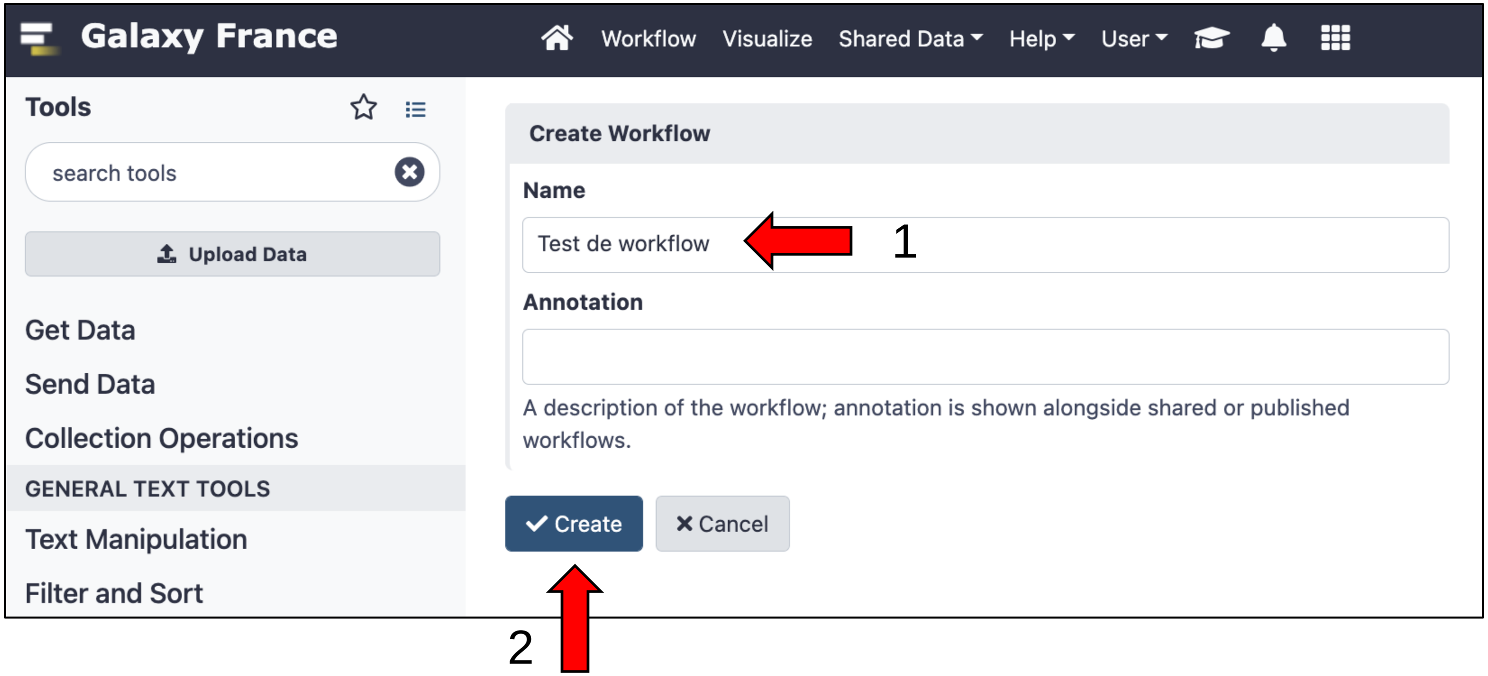


Name	Tags	Updated	Sharing	Bookmarked
Analyse de données RNAseq Ddr0		an hour ago		☐
Défi SCERE (solution Gaëlle)		a month ago		☐
Défi SCERE (solution Gaëlle - V2)		a month ago		☐

Etape 2 : Créer un workflow

(automatisation des analyses)

- Nommer votre workflow, puis cliquer sur le bouton « Create » :



Create Workflow

Name

Test de workflow

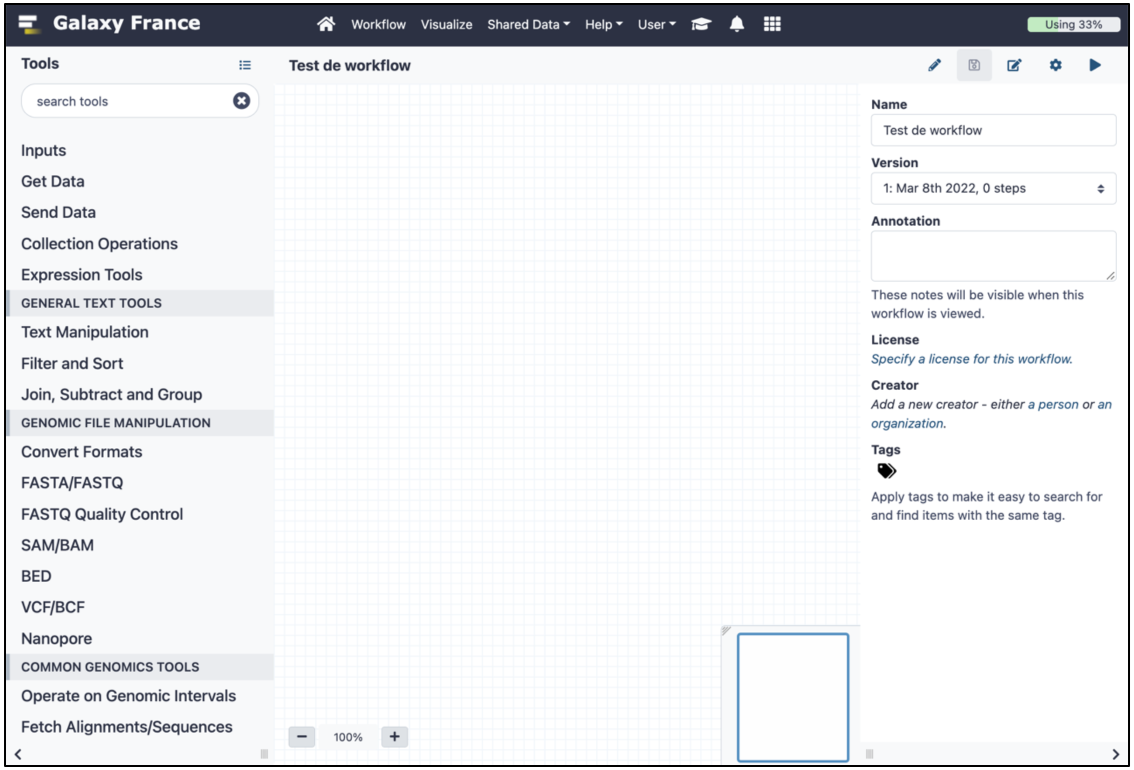
Annotation

A description of the workflow; annotation is shown alongside shared or published workflows.

Etape 2 : Créer un workflow

(automatisation des analyses)

- L’interface graphique de création d’un workflow doit être affichée, comme ci-dessous :



Test de workflow

Name
Test de workflow

Version
1: Mar 8th 2022, 0 steps

Annotation

These notes will be visible when this workflow is viewed.

License
Specify a license for this workflow.

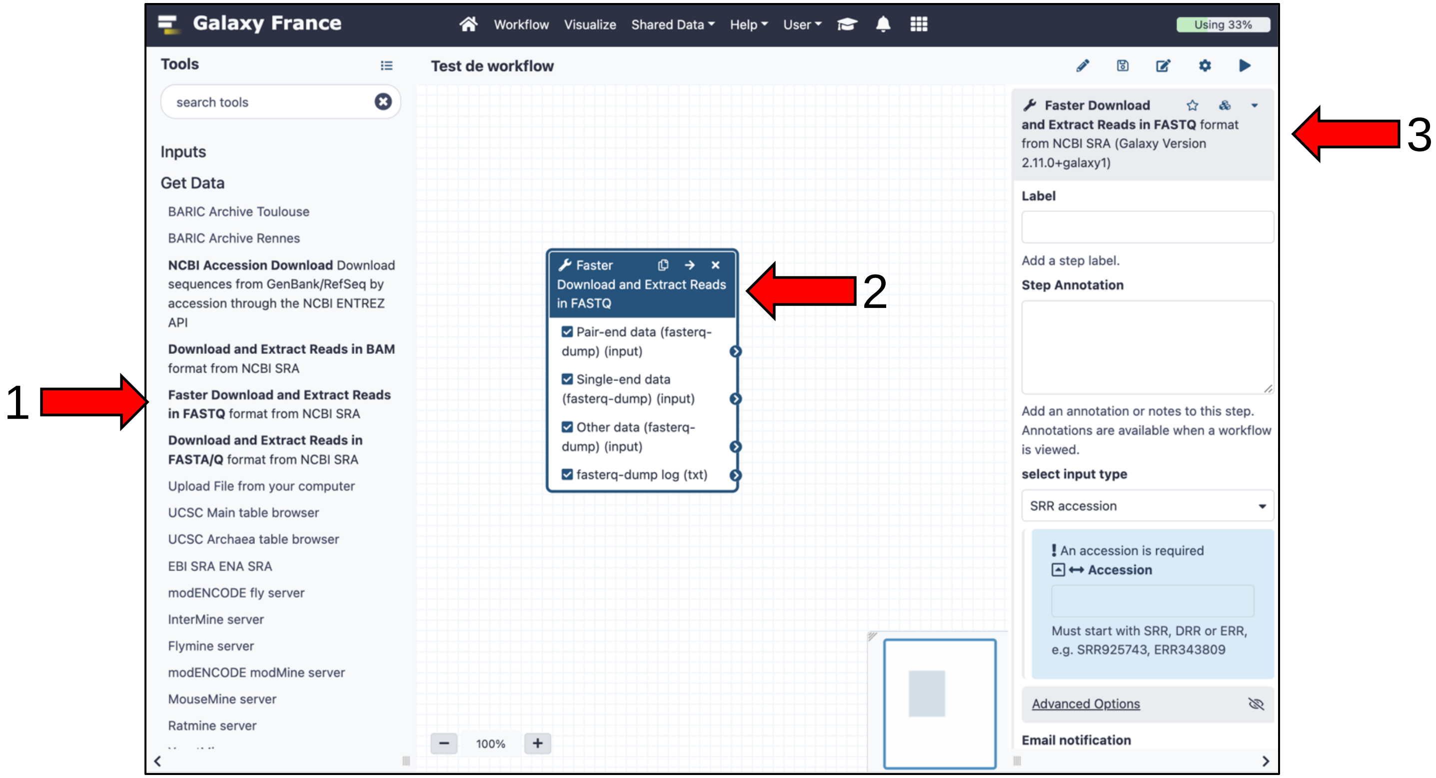
Creator
Add a new creator - either a person or an organization.

Tags

Apply tags to make it easy to search for and find items with the same tag.

Etape 3 : Ajouter des outils d’analyse (automatisation des analyses)

- Les outils s’ajoutent un par un. Ils sont sélectionnés dans le menu « Tools » et placés sur la page du milieu. Les paramètres des outils peuvent être modifiés dans le menu de droite.



Add a step label.

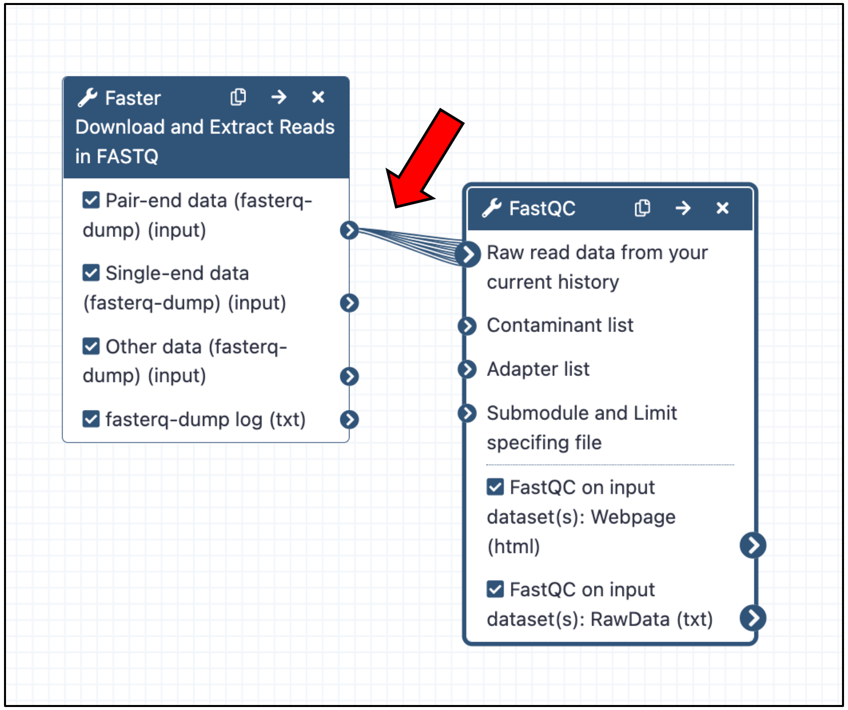
Add an annotation or notes to this step. Annotations are available when a workflow is viewed.

! An accession is required

Must start with SRR, DRR or ERR, e.g. SRR925743, ERR343809

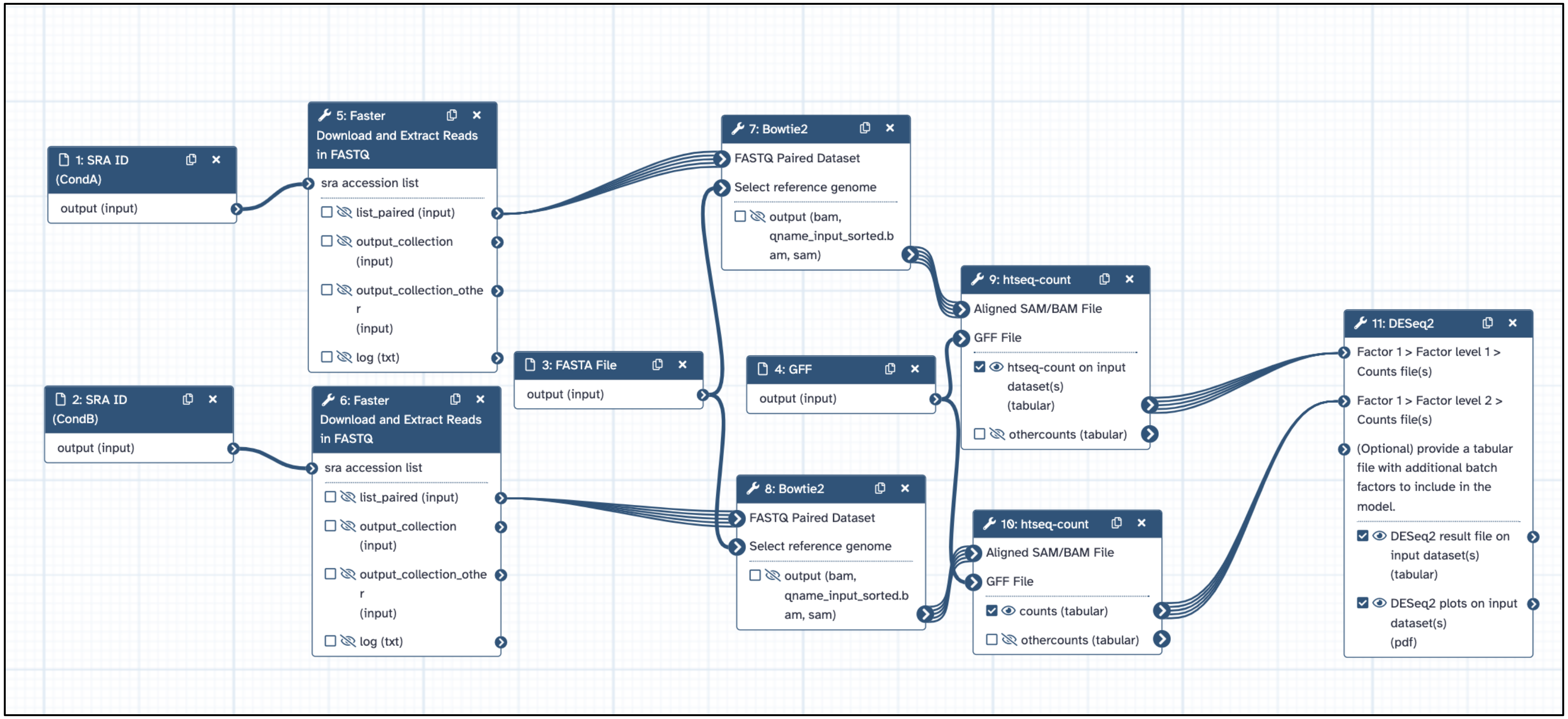
Etape 4 : Connecter des outils d’analyse (automatisation des analyses)

- Une fois ajoutés, les outils se connectent les uns aux autres. Ainsi, les fichiers de sortie (résultats d’un outil) sont utilisés comme fichiers d’entrée d’un autre outil.



Etape 5 : Automatiser les TP1, 2, 3 et 4 !

- Créer un workflow qui reproduit l'ensemble des analyses des précédents TP (récupération des fichiers FASTQ, alignement sur le génome de référence, quantification des expressions des gènes, analyse différentielle).



Fin de la partie 5 ☺

Gaëlle LELANDAIS

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