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## 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 » : <u>https://usegalaxy.fr/</u>
- Créer un nouvel historique de travail

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#### Données utilisées pour le TP

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#### Article

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

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RNA-seq; bioinformatic 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 radionesistance pathways encoded by this bacterium and to compare

Keywords: radioresistance/desiccation; transcriptional regulator; Deinococcus radiodurans; ChIP-seq;

the stress-induced responses mediated by this pair of proteins in diverse bacteria.

#### check for updates

Clustions: Engénico, N., Z. Kavarovic, Y.; Lelandaris, G.; Coste, G.; Bouthier de Bioru, C.; Berkhälkou, E.; Servand, P.; Confalomeri, F. Characterization of the Radiation Desizeation Response Regular on the Radiaconsistant Backeriann Driftocencer and/advances Integrative Genomic Analyses. *Cells* 2021, 10, 2506. https://doi.org/ 10.3309/cells102056

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Copyright © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). 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 y-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 mech-anisms [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  $\gamma$ -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

Cells 2021, 10, 2536. https://doi.org/10.3390/cells10102536

https://www.mdpi.com/journal/cells





(automatisation des analyses)

Cliquer sur l'onglet « Workflow »



(automatisation des analyses)

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

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(automatisation des analyses)

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(automatisation des analyses)

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

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#### 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.

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#### 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).



11/02/2025

### Fin de la partie 5 ©



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