



**HAL**  
open science

## **TnSeek : analysing Tn-seq data for multiple conditions and multiple species**

Loïc Couderc, Erwan Gueguen, Maxime Brunin, Areski Flissi, Guillemette Marot, Guy Condemine, H el ene Touzet

### ► **To cite this version:**

Loïc Couderc, Erwan Gueguen, Maxime Brunin, Areski Flissi, Guillemette Marot, et al.. TnSeek : analysing Tn-seq data for multiple conditions and multiple species. Journ ees Ouvertes en Biologie, Informatique et Math ematiques (JOBIM 2022), Jul 2022, Rennes, France. hal-03827389

**HAL Id: hal-03827389**

**<https://hal.science/hal-03827389>**

Submitted on 24 Oct 2022

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destin ee au d ep ot et  a la diffusion de documents scientifiques de niveau recherche, publi es ou non,  emanant des  tablissements d'enseignement et de recherche fran ais ou  trangers, des laboratoires publics ou priv es.



Distributed under a Creative Commons Attribution 4.0 International License

# TnSeek : analysing Tn-seq data for multiple conditions and multiple species

Loïc Couderc<sup>1</sup>, Erwan Gueguen<sup>2</sup>, Maxime Brunin<sup>1</sup>, Areski Flissi<sup>3</sup>, Guillemette Marot<sup>4</sup>, Guy Condemine<sup>2</sup> and H el ene Touzet<sup>3</sup>

<sup>1</sup> Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, US 41 - UAR 2014 - PLBS - Plateforme bilille, F-59000 Lille, France

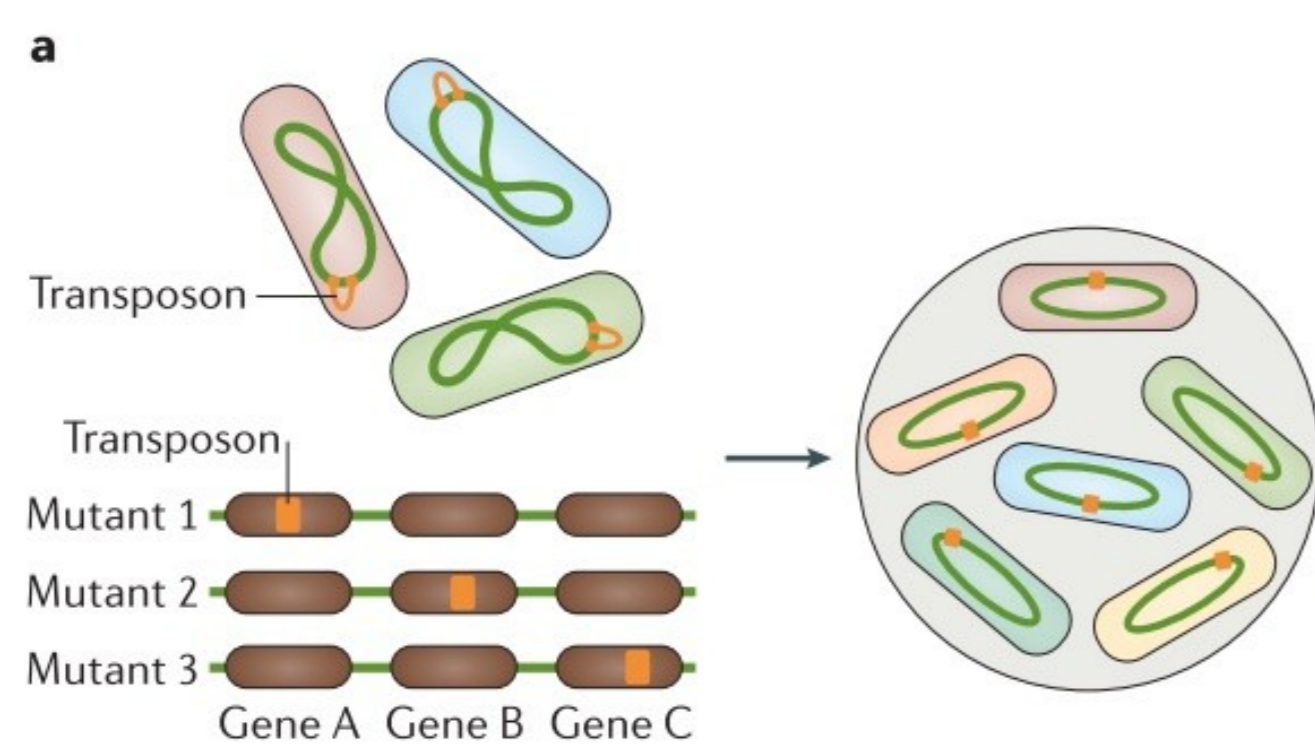
<sup>2</sup> Univ. Lyon, Univ. Lyon 1, UMR CNRS 5240, Villeurbanne, France

<sup>3</sup> Univ. Lille, CNRS, Centrale Lille, UMR 9189 CRISTAL, F-59000 Lille, France

<sup>4</sup> Univ. Lille, CHU Lille, ULR 2694 - METRICS - Inria MODAL, F-59000 Lille, France

## Tn-seq → Transposon sequencing

Tn-seq is a genome-wide screening method that rapidly identifies, on a large panel of strains, genes related to a specific phenotype or growth condition in bacteria. It consists in random transposon mutagenesis in parallel coupled with high throughput sequencing.



### Main steps

- creation of a pool of mutants by random insertion of a transposon
- growth (and selection)
- high-throughput sequencing of surviving cells

### Essential genes

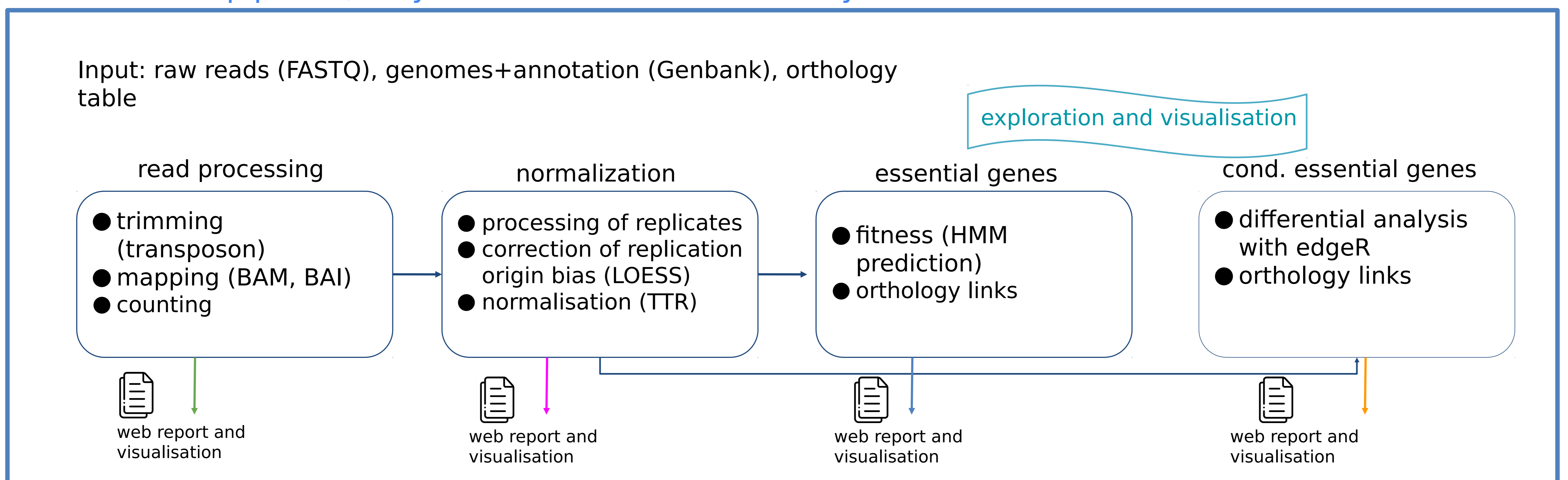
genes essential for growth under a given condition.

### Conditionally essential genes

genes that are required for growth under one condition but not another

Example of applications: identification of virulence factors of pathogenic bacteria, identification of genes involved in antibioresistance, ...

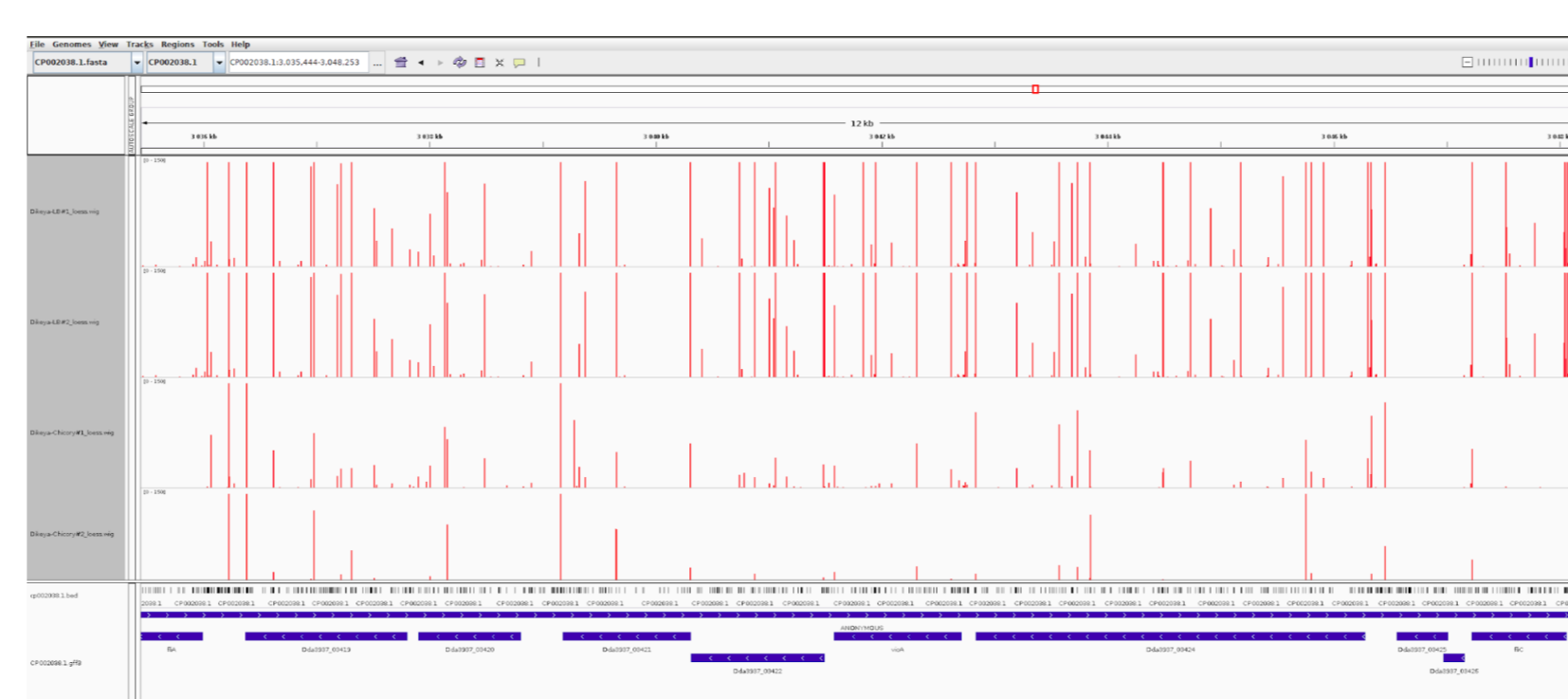
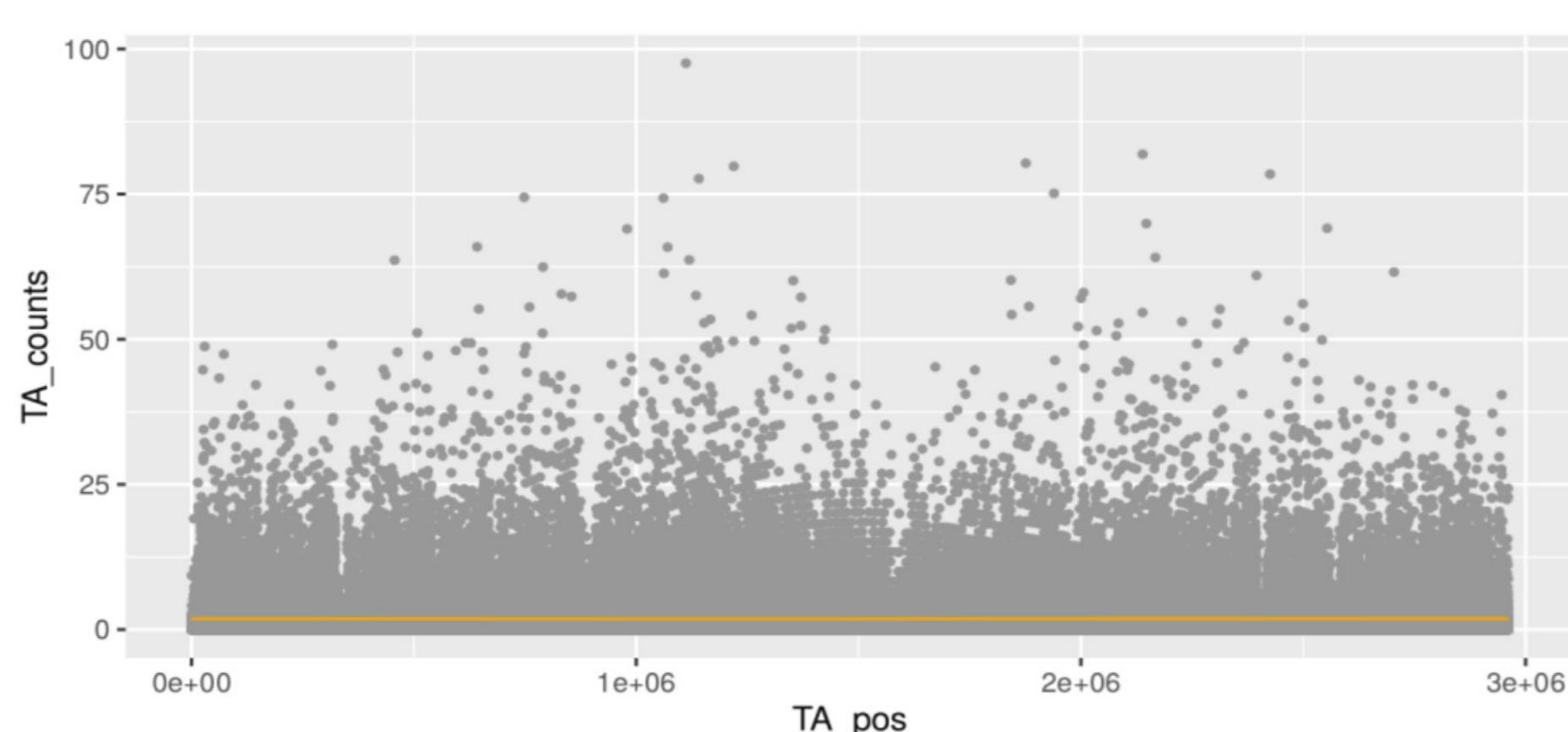
## TnSeek → our pipeline, any number of conditions + any number of strains



## TnSeek in practice → easy-to-install + easy-to-use

1. Download source at <https://gitlab.cristal.univ-lille.fr/bonsai/tNSEek>
2. Build the Docker image and run it
3. Connect to the Shiny server at <http://localhost:3838>

implemented in Python and R  
installation with docker  
reports in R markdown  
web application for exploration and visualization: R Shiny & SQLite



| genus           | strain                         | condition | genes | p-value | histogram | volcano                              | all conditions |
|-----------------|--------------------------------|-----------|-------|---------|-----------|--------------------------------------|----------------|
| Dickeya         | Dickeya_dadantii_3937          | water     | tsv   | graph   | plot      | tsv (Dickeya_dadantii_3937)          |                |
| Dickeya         | Dickeya_dadantii_3937          | planta    | tsv   | graph   | plot      | tsv (Dickeya_dadantii_3937)          |                |
| Dickeya         | Dickeya_zeae_A586              | water     | tsv   | graph   | plot      | tsv (Dickeya_zeae_A586)              |                |
| Dickeya         | Dickeya_zeae_A586              | planta    | tsv   | graph   | plot      | tsv (Dickeya_zeae_A586)              |                |
| Pectobacterium  | Pectobacterium_aquaticum_A212  | water     | tsv   | graph   | plot      | tsv (Pectobacterium_aquaticum_A212)  |                |
| Pectobacterium  | Pectobacterium_aquaticum_A212  | planta    | tsv   | graph   | plot      | tsv (Pectobacterium_aquaticum_A212)  |                |
| Danthoniartarum | Danthoniartarum_varensilia_479 | wester    | tsv   | graph   | plot      | tsv (Danthoniartarum_varensilia_479) |                |

