



# GeT : 4-site core-facility for all in Genomics and Transcriptomics

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GeT is a cutting-edge 4-site core-facility in Toulouse (France), providing the academic and private scientific communities with technologies and expertise in the area of genomics and transcriptomics. It takes place in the GenoToul multidisciplinary life sciences facility, and works with Agrogenomics, Environment, Microbiology, Human Health, Animal Health and Toxicology research communities.





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## GeT : 4-site core-facility for all in Genomics and Transcriptomics

A comprehensive portfolio of sequencers at GeT core facility

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## **Tools dedicated to traceability and making data available**

We thank the GenoToul bioinformatics facility for its support in computing resources and data storage, and for helping us processing the data and making available all the needed software and infrastructure.

We thank the IG facility for its support in development of NGL.

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•*e-SIToul system* which has been developped for more than 15 years. It is a traceability system managing users, machines, projects,

 NGL (https://github.com/institut-de-genomique/NGL), developed by CEA CNRGH-Genoscope and also deployed by GeT. It is a LIMS composed of modules :

•NGL-Data is the interface between e-SIToul & NGL-SQ : It extracts relevant data from e-SIToul, transforms it and loads NGL-



•NGL-SQ is designed to trace runs from Illumina, Nanopore and

- •NGL modules currently under evaluation :
- •NGL-Bi stores quality control results on reads ans allows to
- •NGL-Sub allows raw read submission to international sequence

•nG6 [1] a user-friendly information system able to manage large sets of sequencing data, allowing the users to access bioinformatics analysis (primary and secondary analysis) and to download their data. The Genotoul Bioinformatics Platform and GeT developed it. Since 2012, GeT has developed jFlow pipelines to perform quality controls on various types of projects such as





# **Bioinformatics analysis**

A team of bioinformaticians is dedicated also to analyse data from research projects in the fields of transcriptomics, Single cell analysis, micro RNA and assembly of small genomes ...





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#### **Genotional Bioinformatics developments MATRiX: a Shiny application to explore transcriptomic datasets**

Statistical analyses **define arbitrary filtering criteria** to select relevant genes. Hence, biologists are led to reconsider these criteria according to their own scientific question. Thus, the data generated are **difficult to exploit** notably for scientists not familiar with bioinformatics.

In order to allow biologists to **explore** their datasets in **autonomy** and generate graphical representations, we have deployed a **turnkey** solution built with the Shiny framework [1]

This open source project is available at: https://forgemia.inra.fr/GET\_TRiX/matrix

- Import datasets (microarray, RNAseq) with statistical result table
- Explore and Analyze data
- Export publishable quality graphics
  - png, eps, svg, pdf
- ✓ Built into a single web application
  - Interactive and responsive user-friendly interface
  - Open source and open access code (GPL-3)
  - An instance available to GeT-TRiX users since January 2019

#### Explore data/results









www.matrix.toulouse.inra.fr



[1] RStudio, Inc. shiny : Easy web applications in R, 2014.