



Vivaldi Project

Data management plan

Mussel hemocytes stimulation in vitro

Mytilus galloprovincialis

Hemocytes

In vitro stimulation

31/07/2018

DATA MANAGEMENT PLAN

Template sheet for each dataset

Partner name	CSIC
Data category	Transcriptome (host)
Concerned WP	WP2
Name of the VIVALDI referent(s)	Transcriptome: Beatriz Novoa & Paola Venier
Reference of the dataset <i>Please refer to the DMP table to find the appropriate reference.</i> <small>Ex: Genome-Patho/SubTaskN*/Pathogen/PartnerN*</small>	Transcriptome-host/2.4.1/mussel_in vitro/CSIC
Description of the data	Raw data without trimming in fastq format Transcriptomic information Processed data will be a de novo assembled fasta transcriptome
Type	Sequences
Period and frequency of data collection	Hemolymph from raft mussels were withdrawn and pooled, set in 6 well plates and stimulated with different molecules. Samples were collected 8h after the stimulation and RNA was extracted.
Geographical site of data collection (if applicable)	The mussels origin was the Ría de Vigo (raft mussels). The experiment was carried out in lab controlled conditions.
Description of the material from which the dataset is generated <i>Information will be obtained from individuals, which can come from natural/hatchery population and/or from family produced in hatchery. Animals can be infected (naturally or experimentally). DNA extraction can be done from the whole animal, tissue.</i>	Transcriptomic information has been obtained from hemocytes treated in vitro. RNA was extracted following the Maxwell (promega) protocol. Each sample (below, correspondence with the sampling table) belongs to a pool of 25 mussels (3 replicates) and a specific stimulation (4 different stimulus + a control): CSIC-2.1.1.1_2017 CSIC-2.1.2.1.1_2017 CSIC-2.1.2.1.2_2017 CSIC-2.1.2.1.3_2017 CSIC-2.1.2.1.4_2017 CSIC-2.1.2.1_2017 CSIC-2.1.2.2.1_2017 CSIC-2.1.2.2.2_2017 CSIC-2.1.2.2.3_2017 CSIC-2.1.2.2.4_2017 CSIC-2.1.3.1_2017 CSIC-2.1.2.3.1_2017 CSIC-2.1.2.3.2_2017 CSIC-2.1.2.3.3_2017 CSIC-2.1.2.3.4_2017
Protocols <i>Example: 16S ribosomal RNA gene sequencing by NGS</i> Please refer to the DMP table* for more examples	Quality control of samples and preparation of the libraries was performed in Macrogen Korea mRNA sequencing by Illumina paired-end, TruSeq Stranded mRNA LT, HiSeq 4000

<p>Nature of the collected/generated data <i>Example: Raw dataset in .blc/.fastqc/.fasta formats for genomic information, and processed data set will be .vcf/.bed formats.</i> Please refer to the DMP table* for more examples</p>	<p><i>Raw data without trimming in fastq format</i> <i>Transcriptomic information</i> <i>Processed data will be a de novo assembled fasta transcriptome</i></p>
<p>Coverage (if applicable) <i>Example: random genomic regions covered at 50 X</i> Please refer to the DMP table* for more examples</p>	<p><i>Approximately 90x: an average of 70 million reads per sample</i></p>
<p>What are the prerequisites allowing to use the data as such? <i>Example: Any person able to use .fastqc file and .fasta file</i> Please refer to the DMP table* for more examples</p>	<p><i>Any person who can deal with fasta quality files</i></p>
<p>Sharing of main data</p>	<p><i>Saved and shared after publication</i> <i>Accession number to download the raw reads will be available at NCBI SRA after publication (BioProject PRJNA470760)</i></p>
<p>Archiving and preservation <i>Example: data will be stored on a hard drive + online back up and then will be released on public database (Sinoe, Dryad) after publication.</i> Please refer to the DMP table* for more examples</p>	<p><i>Data will be stored in our hard disks and in NCBI SRA repository.</i> <i>It is foreseen to have another copy in an internal server of CSIC.</i> <i>Data will be of public accession after publication (BioProject PRJNA470760)</i></p>
<p>List, description and storage of associated data (metadata) <i>Examples: environmental data, mortality monitoring, genotyping...</i></p>	<p>NA</p>
<p>Sharing of metadata (if relevant)</p>	<p><i>No relevant</i> NA</p>

*To access the [DMP table](#), please login on the VIVALDI online platform

Once completed, this sheet has to:

1. Be sent to the referent(s) identified above for a final check
2. Be uploaded on the [VIVALDI online platform](#)

