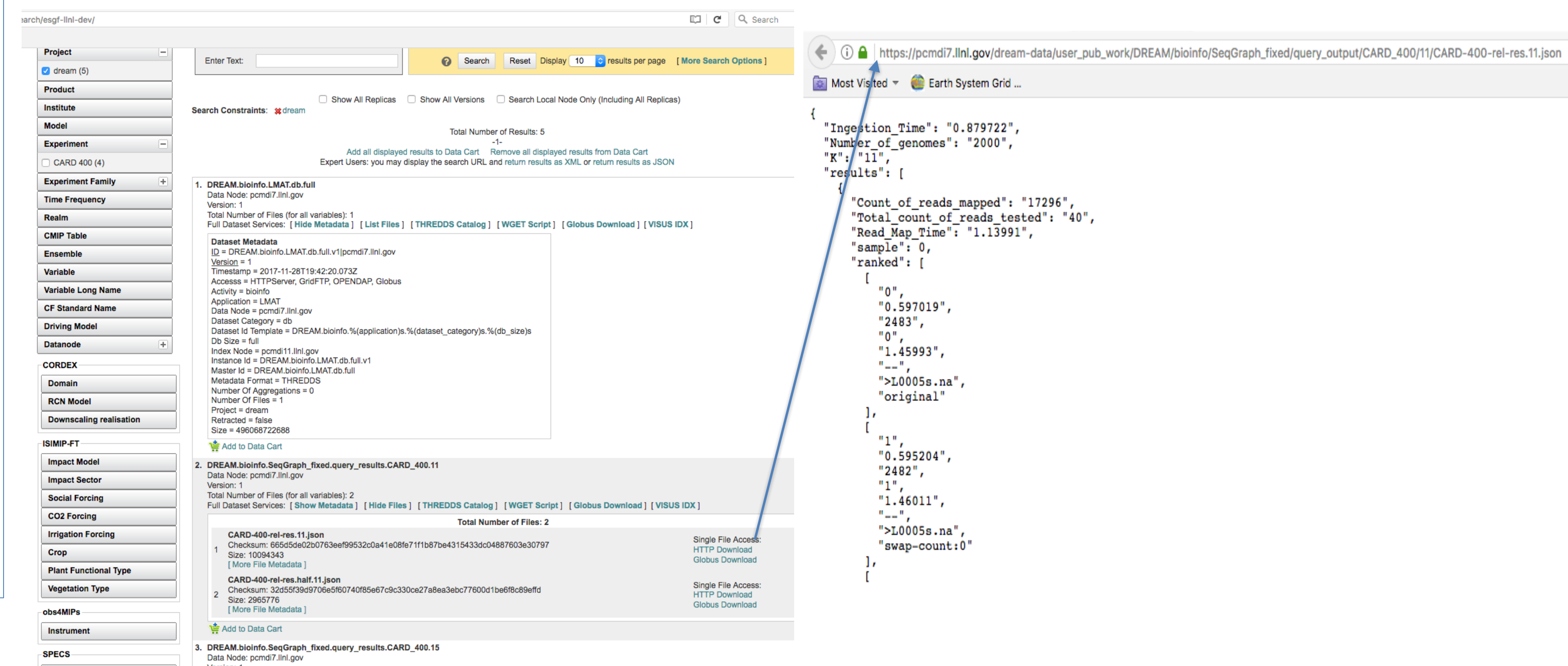


DREAM Data Services for Biological Data and Beyond

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- One of the many goals of the DREAM project is to explore enhancements needed for ESGF to enable publishing and access to data in scientific fields other than climate/weather
- THREDDS data server (TDS) has been very effective for serving NetCDF data published to ESGF
- Need a service more specific for alternate data (e.g. ASCII-based) in other domains
 - Example: FASTA format used in bioinformatics to represent genomic and protein sequences
- This service will allow a variety of content types to interoperate properly with a user's web browser



New tools:

- get_meta.sh
- create_dset.py
 - scripts to generate a generic mapfile with consistent directory_format to dataset_id mapping
- dream-data
 - Service supplies correct mime times for published files
 - eg. images, .pdf, .json
 - Flask module
 - <https://github.com/ESGF/esgf-dream-data-service>

➔ Benefit to input4MIPs: Example MPI-M “dataset” has .pdf, README, and code files

Steps taken for publishing to service:

- Modify esg.ini – use /dream-data/ for HTTPServer
- esg.dream.ini – use multiple_handler to accept non-netcdf data
- Generate mapfile with get_meta.sh + create_dset.py
- Reconfigure DRS when sub-project config changes, repeat

esg.dream.ini`

```
[project_dream]
# Define the categories to be used for this project:
# name | category_type | is_mandatory | is_thredds_property | display_order
categories =
project | enum | true | true | 0
activity | enum | true | true | 1
application | string | false | true | 2
dataset_category | string | false | true | 3
db_size | string | false | true | 4
experiment | string | false | true | 5
k_length | string | false | true | 6

category_defaults =
project | DREAM
activity | bioinfo

activity_options = bioinfo

#dataset_id = DREAM.bioinfo.%(application)s.%(dataset_category)s.%(db_size)s
dataset_id = DREAM.bioinfo.%(application)s.%(dataset_category)s.%(experiment)s.%(k_length)s

experiment_options =
dream | CARD_400 | 400 gene variants from CARD gene sequences

format_handler_name = multiple_built_in
project_handler_name = basic_built_in
las_configure = false
```

Future work:

- Add random access (FASTA and JSON)
- Content listing in service
- Support formats with metadata to be extracted (need to determine which)
- JSON input integrated into publisher for attribute and map specification
- Manage config externally (retire ini) using CV services and support mutable DRS projects