

# syntool-meta2sql

The syntool-meta2sql command reads the metadata.json files produced by syntool-ingestor to obtain information about the ingested granules and to generate the SQL statements used to register the granules in the Syntool database.

```
syntool-meta2sql [--init-only] [--chunk_size CHUNK_SIZE]
                 [--product_id PRODUCT_ID] OUTPUT_PATH -- INPUT
```

Parameter	Format	Description
OUTPUT_PATH	path	Path of the SQL file where results will be written to. If "-" is used, then the SQL statements will be printed to standard output instead.
--chunk_size	integer	Max number of datasets exported with one INSERT SQL statement.
--product_id	string	Override the identifier of the product read in the input files.
--init-only		Produce the SQL statements to initialize the tables of an empty SQL database.

## Examples

Print SQL statements generated from metadata files listed by the find command, with INSERT statements limited to 100 entries:

```
find ingested_dir -mindepth 2 -maxdepth 2 -name "metadata.json" \
| syntool-meta2sql --chunk_size=100 - --
```

Save SQL statements generated from a fixed list of metadata files, with an override of the product identifier:

```
syntool-meta2sql --product_id=3857_dummy /tmp/dummy.sql -- \
dataset1/metadata.json dataset2/metadata.json
```

Save SQL statements required to initialize the MySQL database:

```
syntool-meta2sql --init-only /tmp/syntool_init.sql
```