Creating (meta)data

Step 1: create metadata	*Step 2: update metadata*	*Step 2: add data*	*Step 3: QC (meta)data*
Create metadata	Update metadata	Upload data	QC and correct (meta)data
Google sheets, PlutoF	Google sheets, PlutoF	PlutoF	Google sheets, PlutoF
Stations, HQ	Stations, Sequencing scientist	Stations	Data managers
Observatory, unit, event, sample	ENA and omics details, update after events	Unit and event images, observations	All metadata and file names

Harvesting and combining (meta)data

Step 4: harvest metadata	*Step 5: QC metadata*	*Step 6: combine metadata*
Harvest metadata from Google sheet, PlutoF	QC and correct metadata	Combine metadata
Github	GitHub	GitHub
Data managers	Data managers	Data managers
All metadata and download URI for files	Consistency checks; feeds into step 3	One set of CSVs with all ARMS metadata and file URIs

Creating ARMS LOD

Step 7: add semantics	*Step 8: create LOD*	*Step 9: create RO-Crates*
Add semantics to CSVs	CSV	Create RO-crates per repo
GitHub	GitH	GitHub
Data managers	Data	Data managers
Metadata descriptions for each ARMS CSV	Interoperable, machine-accessible	Interoperabe, machine-accessible

Not yet done

PEMA bioinformatics

Step 1: upload PEMA	*Step 2: QC PEMA*	*Step 3: Describe PEMA*	*Step 9: create RO-Crates*
Upload PEMA I/O	QC PEMA metadata	Describe PEMA files	Create RO-crates per repo
GitHub, MDA	GitHub	GitHub	GitHub
PEMA scientist	Data managers	PEMA scientist, data managers	Data managers
Selected PEMA input and output	Consistency check with event, sample metadata	To make reusable	Interoperabe, machine-accessible

Publishing

Step 1: Create DwC	*Step 2: first QC*	*Step 3: second QC*	*Step 4:create new repos*	*Step 5: submit to IMIS*
ARMS metadata to DwC format	QC, correct DwC	QC, correct DwC	Copy subset of all data to GH repos, creat RO-Crates	IMIS dataset metadata record; request DOI
GitHub	GitHub	IPT	GitHub	IMIS
Data managers	Data managers	Data managers	Data managers	Data managers
Convert ARMS metadata to DwC	QC in-house	Using EurOBIS IPT tool	For ARMS sample, ENA, PEMA (meta)data submitted to EurOBIS	Using IMIS submission tool

Step 1a: define DwC	*Step 1b: Combined CSV to DwC*	*Step 1c: PEMA info to DwC*
Define DwC occurrence, emof, DNA extension	Extract metadata from CSV	Extract metadata from PEMA outputs
GitHub	GitHub	GitHub
Data managers + EurOBIS consultants	Data managers	Data managers
Decide columns, content, occurrence IDs	Script to extract and reformat	Script to extract and reformat