RKI Report-file Elements

tags: nCoV2019 Sequencing

Source -Please check first

- https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/DESH/DESH.html
- https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/DESH/Cryptshare-Anleitung.pdf?__blob=publicationFile [v1.1 (2021-01-21)]

The report must contain following seven elements in this order:

1. IMS_ID
2. SENDING_LAB
3. DATE_DRAW
4. SEQ_TYPE
5. SEQ_REASON
6. SAMPLE_TYPE
7. OWN_FASTA_ID

In the following a short description of each element is given.

1. IMS_ID

Sequencing-based pseudonym as unique identifier for the aggregation in DEMIS ("Deutschen Elektronischen Melde- und Informationssystem für den Infektionsschutz").

Format: IMS-12345-CVDP-00001

- IMS: permanent prefix
- 12345: 5-digit identifier of the sequencing laboratory ("Untersuchungslabor"), analog to the already existing DEMIS-system (DEMIS-10001 to currently DEMIS-10563). The list is managed by the DEMIS-Geschäftsstelle. If you are not registered already pls reach out to demis@rki.de
- CVDP: 4-digit DEMIS-abbreviation, which is directly dedicated to the "Meldetatbestand". Later additional pathogen-abbreviations, aside from SARS-CoV-2, applied.
- 00001: Ongoing Number, which in phase 0 is autonmously continued by the laboratory (later in phase 1 the system will automatically gernerate it).

2. SENDING_LAB

12345: 5-digit identifier of the sending laboratory, analog to the already existing DEMIS-system.

ATTENTION: This only applys for laboratories, which don´t sequence on their own, but instead sent their samples to other laboratories for sequencing. In case that the sending lab is also the sequencing lab the digit from the IMS_ID and the SENDING_LAB-id can be identical.

3. DATE_DRAW

Date of the sample isolation n ISO8601 (YYYYMMDD)

4. SEQ_TYPE

Used sequencing-platform. "OXFORD_NANOPORE" is provided automatically as entry.

5. SEQ_REASON

Cause for the sequencing. Choose one entry from the following list:

Entry	Description
X	Unknown to the sequencing laboratory
N	No (e. g. random selection of a PCR-positive sample for sequencing)
Y	Yes, but the kind of mutation or variante is unknown (to the sequencing laboratory)
A	Yes, it exists evidence for the mutation/variante from previous diagnostic [spezifying in textfield after entry-letter]

Note for "A":

- Textfield, max. length 64 signs
- Mutation to specify in "[ ]", in case of multiple mutations divided by "/"
- Example entry: A[B.1.1.7/B.1.351]

6. SAMPLE_TYPE

Type of sample. Choose one entry from the following list:

Entry	Description
s001	Upper respiratory swab sample (specimen)
s002	Nasopharyngeal swab (specimen)
s003	Swab from nasal sinus (specimen)
s004	Anterior nares swab (specimen)
s005	Oropharyngeal aspirate (specimen)
s006	Nasopharyngeal aspirate (specimen)
s007	Lower respiratory sample (specimen)
s008	Bronchoalveolar lavage fluid sample (specimen)
s009	Sputum specimen (specimen)
s010	Specimen from trachea obtained by aspiration (specimen)
s011	Pleural fluid specimen (specimen)
s012	Specimen from lung obtained by biopsy (specimen)

Entry	Description
s013	Blood specimen (specimen)
s014	Plasma specimen or serum specimen or whole blood specimen (specimen)
s015	Whole blood sample (specimen)
s016	Stool specimen (specimen)
s017	Urine specimen (specimen)
s018	Lower respiratory fluid sample (specimen)
s019	Nasopharyngeal washings (specimen)
s020	Plasma specimen (specimen)
s021	Saliva specimen (specimen)
s022	Serum specimen (specimen)
s023	Specimen unsatisfactory for evaluation (finding)
s024	Swab of internal nose (specimen)
s025	Throat swab (specimen)
X	Unknown (to the sequencing laboratory)

Value Set is geared to SNOMED CT and SNOMED CT COVID-19 Related Content(https://simplifier.net/covid-19labormeldung/materialsarscov2)

7. OWN_FASTA_ID

Laboratory-internal identifier, which enables the distinct assignment of the FASTA-file to the sequence (given in the FASTA-header). Autoprovided by PoreCov-workflow, according to your sample-names.

NOTE: Used in phase 0 for the assignment of the metadata from the .csv-file to the sequence-data in the FASTA-file.