**Supplementary File 1**

Below arethree examples illustrating the structure and coding scheme of the SARS-ANI Dataset. These examples intend to facilitate the comprehension of the data as well as the coding of potential relationships between events.

# Example 1

The two following SARS-CoV-2 animal events occurred in the United States (**country\_name**), in one household (**living\_conditions =** *pet* AND event 2 is related to event 1, see **related\_to\_other\_entries** = “living together”) where three dogs were living (**number\_susceptible** **=** *3*). The first dog was tested by PCR (**test =** *PCR*) because it had contact with a human diagnosed with COVID-19 (**reason\_for\_testing =** *confirmed human case*); the infection was confirmed on 2020-06-25 (**date\_confirmed**): the dog showed symptoms that were not related to SARS-CoV-2 infection (**symptoms =** *unrelated symptoms*) and died from a cause not related to its SARS-CoV-2 status (**outcome**  = *death not related to Sars-CoV-2*). This case was reported (**date\_reported**) on 2020-07-02 by the OIE-WAHIS.

Almost two months later (**date\_reported** = *2020-08-27*), a second dog of this household (counting at that time two dogs, **number\_susceptible** = *2*) which had contact with the dog described in event 1 (**related\_to\_other\_entries** = *living together* AND **reason\_for\_testing =** *confirmed animal case*) was tested for SARS-CoV-2 by virus neutralization test (**test**). The dog was asymptomatic (**symptoms =** *subclinica*l) andwas isolated (**control\_measures**). Outcome of the infection was not reported (outcome = *NS*).

Summary: These events describe one outbreak of SARS-CoV-2 in a multi-dog household following contact with a COVID-19-infected person and in which 2/3 dogs were infected (for clarity purpose, not all fields of the dataset are shown below).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **ID** | **species** | **epidemiological\_unit** | **number\_cases** | **number\_susceptible** | **number\_tested** | **number\_deaths** |
| event 1 | dog | animal | 1 | 3 | 2 | 0 |
| event 2 | dog | animal | 1 | 2 | 1 | 0 |
|  |  |  |  |  |  |  |
| **country\_name** | **date\_confirmed** | **date\_reported** | **date\_published** | **related\_to\_other\_entries** | **related\_ID** | **test** |
| United States | 2020-06-25 | 2020-07-02 | 2020-07-03 | new | NA | PCR |
| United States | NS | 2020-08-27 | 2020-08-27 | living together | event 1 | virus neutralisation test |
|  |  |  |  |  |  |  |
| **sampling\_type** | **reason\_for\_testing** | **symptoms** | **outcome** | **living\_conditions** | **source\_of\_infection** | **control\_measures** |
| NS | confirmed human case | unrelated symptoms | death not related to Sars-CoV-2 | pet | human | NA |
| NS | confirmed animal case | subclinical | NS | pet | animal | isolation |

# Example 2

The three following events occurred in a zoo (**living\_conditions)** in the United States (**country\_name**). A tiger living with four other animals from the same species (**number\_susceptible** = 1+4 = *5*) was confirmed positive with SARS-CoV-2 by PCR (**test** = *PCR*) on 2020-04-03. Event 1 described infection in one animal (**epidemiological\_unit** = *anima*l). Date of reporting (**date\_reported**) and publishing (**date\_published**) are similar (*2020-04-06*). Condition of this tiger improved (**outcome** = *improved condition*).

Later in the month, two other events were reported in which SARS-CoV-2 infection was diagnosed by PCR (**test** = *PCR*) in the four other animals living with the tiger reported in event 3 (**related\_to\_other\_entries** = *living together*). For both events, **date\_confirmed** is not specified (*NS*), **date\_reported** = *2020-04-17* and **date\_published** = *2022-05-25*. For one animal (event 4), no information is available regarding the outcome of the infection (**outcome** = *NS*). For the three other animals described in event 5, the outcome of the infection is reported (**outcome** = *improved condition*). Because these three tigers were reported together and showed the same event and patients attributes (e.g. **date\_reported**, **test**, **outcome**), they are entered as one event in the dataset (**epidemiological\_unit** = *group*).

Summary: These three events describe one outbreak (occurrence of one or more cases in an epidemiological unit, which is here the enclosure of the tigers in the zoo), which started on 2020-04-03 and included five cases of SARS-CoV-2 infection (for clarity purpose, not all fields of the dataset are shown below).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID** | **species** | **epidemiological\_unit** | **number\_cases** | **number\_susceptible** | **number\_tested** |
| **event 3** | tiger | animal | 1 | 5 | 1 |
| **event 4** | tiger | animal | 1 | 5 | NS |
| **event 5** | tiger | group | 3 | 5 | NS |
|  |  |  |  |  |  |
| **number\_deaths** | **country\_name** | **date\_confirmed** | **date\_reported** | **date\_published** | **related\_to\_other\_entries** |
| 0 | United States | 2020-04-03 | 2020-04-06 | 2020-04-06 | new |
| 0 | United States | NS | 2020-04-17 | 2020-04-25 | living together |
| 0 | United States | NS | 2020-04-17 | 2020-04-25 | living together |
|  |  |  |  |  |  |
| **related\_ID** | **test** | **outcome** | **living\_conditions** | **source\_of\_infection** | **variant** |
| NA | PCR | improved condition | zoo | NS | NA |
| event 3 | PCR | NS | zoo | NS | NA |
| event 3 | PCR | improved condition | zoo | NS | NA |

# Example 3

The three following events report an outbreak that occurred in free ranging (**living\_conditions** = *wildlife*) white-tailed deer (**species**) in Canada (**country**) that were tested during a surveillance/monitoring programme (**reason\_for\_testing**). The animals were sampled as part of the same epidemiological investigation but not necessary at the same geographic location (**epidemiological\_unit** = *survey group*). Event 7 is an *update of* (**related\_to\_other\_entries**) event 6 (**related\_to\_other\_entries** = *update by*) and event 8 (related to event 7, see below) should also be considered as an *update of* event 6.

Events 6 and 7 report infections in more than one animal (**epidemiological\_unit** = *survey group*) while event 8 reports infection in one single animal (**epidemiological\_unit** = *animal*) related to the group described in event 7 (**related\_to\_other\_entries** = *same study*). Event 7 and 8 are distinguished because the tests conducted in the animal in event 8 differed from those performed on the four animals described in event 7.

Date at which infection was confirmed (**date\_confirmed)** is not specified in any events (*NS*); only event 6 was reported by the OIE-WAHIS (**date\_reported** = *2022-01-20*). The follow-up events (events 7 and 8) were published ~1.5 month after event 6. Most likely, this difference is due to the time required for laboratory analyses (events 7 and 8 present more sample and test types and provide identification of the SARS-CoV-2 variant involved).

Summary: These three events describe one outbreak (occurrence of one or more cases in an epidemiological unit, which is here the surveyed animals) which was reported for the first time by OIE-WAHIS and published on 2022-01-20 and was subsequently updated on 2022-03-03 in ProMED-mail, probably following more laboratory investigations. The outbreak included five confirmed cases of SARS-CoV-2 in white-tailed deer in Canada. The five animals did not die following SARS-CoV-2 infection (**number\_deaths** = *0* AND **outcome =** *death not related to Sars-CoV-2*). Indeed, they died from hunting, which this is not specified in the dataset but can be found in the reports (for clarity purpose, not all fields of the dataset are shown below).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID** | **species** | **epidemiological\_unit** | **number\_cases** | **number\_tested** | **number\_deaths** |
| event 6 | white-tailed deer | survey group | 5 | 213 | 0 |
| event 7 | white-tailed deer | survey group | 4 | 213 | 0 |
| event 8 | white-tailed deer | animal | 1 | 213 | 0 |
|  |  |  |  |  |  |
| **country\_name** | **date\_confirmed** | **date\_reported** | **date\_published** | **related\_to\_other\_entries** | **related\_ID** |
| Canada | NS | 2022-01-20 | 2022-01-20 | updated by | event 7 |
| Canada | NS | NA | 2022-03-03 | update of | event 6 |
| Canada | NS | NA | 2022-03-03 | same study | event 7 |
|  |  |  |  |  |  |
| **test** | **sampling\_type** | **test\_2** | **sampling\_type\_2** | **test\_3** | **sampling\_type\_3** |
| PCR | NS | NA | NA | NA | NA |
| PCR | lymph node (post mortem) | PCR | nasal swab | gene sequencing | nasal swab |
| PCR | nasal swab | gene sequencing | nasal swab | NA | NA |
|  |  |  |  |  |  |
| **reason\_for\_testing** | **symptoms** | **outcome** | **living\_conditions** | **variant** |
| surveillance/monitoring | subclinical | death not related to Sars-CoV-2 | wildlife | NA |
| surveillance/monitoring | subclinical | death not related to Sars-CoV-2 | wildlife | Ontario WTD lineage |
| surveillance/monitoring | subclinical | death not related to Sars-CoV-2 | wildlife | Ontario WTD lineage |