Standardized XML changes for version 3.0

Additional fields:

|  |  |
| --- | --- |
| New field | Purpose |
| Sampling Date | When was sample taken? |
| Date received | When was sample received at lab? |
| Sample Type Code | Allows mapping of codes within each lab to codes used by client |
| Account number | Who paid for the analysis? |
| Account name | “ “ |
| Requester\_ID | Who submitted the sample? |
| Recipient\_ID | Who should receive the sample? |
| Lot\_ID | Grouping multiple samples over time |
| Titanium | Added nutrient |
| DON\_3Ac15Ac | Some methods only quantify these together |
| T2HT2 | Some methods only quantify these together |
| HT2, FUM\_B1, FUM\_B2, FUM\_B3, FusarenonX, Nivalenol, Neosolaniol, DAS, Ochratoxin Z | Added mycotoxins |

Analysis ID convention

|  |  |  |  |
| --- | --- | --- | --- |
| XML 2.9 | XML 3.0 | Example | Purpose |
|  | PropertyID\* | 012345 | ?seeking clarification on customer request |
| Name | PropertyName | TFA | Maintains current mapping by name |
| Value | Result | 2.68 |  |
|  | Unit | %DM | Defines unit outside of name. |
|  | Operator\* | = | Analyses with LOD, LOQ, <,<=,=,>,=> |
|  | AnalyseDate\* | 4/6/2018 | Allows tracking of tests completed at different times. Rechecks? |
|  | MethodType | WC | WC, NIR, Calculation |
|  | MethodName\* | Jenkins 1 step GC | Allows communication of method if desired. Independent of method type so reference methods for NIR can be communicated |

\*optional

Digestibility convention

Nutrient\_Type\_Timepoint\_grindgrindtype

aNDFomD\_IV\_30h\_1c

|  |  |
| --- | --- |
| Nutrient | NDF, aNDF, aNDFom, NDR, aNDR, aNDRom, Starch, CP, ect… |
| Type | IV = in vitro, IS = in situ, CG = Combs\_goeser |
| Time point | In hours, no decimals (7h,24h,30h, ect..) |
| Grind | Screen size in mm, no decimals, As Is = AI |
| Grind type | Cyclone = c, wiley = w |

Eliminate iNDF since its measured as 96,120,240 time points?

D = digestibility (StarchD,aNDFomD,NDRD, ect)

u = undigested (uaNDFom,uNDR, ect)

Unit field needs to reflect method

Fatty acid convention

Need ability to identify:

* Chain length
* Number of double bonds
* Cis and trans isomers
* Location of doubles

C\_chainlength\_doubles\_ConfigLoc

|  |  |
| --- | --- |
| Portion | Example |
| C |  |
| chain length | 18 |
| doubles | 2 |
| Config | Cis,trans |
| LOC | 10,12 |

Calculations

Either eliminate or provide naming convention for differentiation.

* What does NDFkd mean in the context of different methods, systems for calculations, multiple digestibility pools?
* What does NEL mean in the context of different systems for calculation?
* What does DCAD mean in different calculations?

Suggested kd convention

Nutrient\_kd\_timepoints\_pools

aNDFom\_kd\_t1\_p1

|  |  |
| --- | --- |
| kd rates | Examples |
| nutrient | aNDFom, Starch, NDR, ect |
| number of time points included | 1,2,3 |
| number of digestible pools assumed | 1,2 |
| Example | aNDFom\_kd\_t2\_p1 |

Suggested energy convention:

Type\_system

NEL\_NRC01

|  |  |
| --- | --- |
| Type | NEL, NEM, NEG |
| System | ADF, NRC01, Milk06, Milk06np, Milk13, others? |
| Units | NEL, NEM, NEG, always Mcal/kg |
| TDN | energysystem unitless (%DM?) |
| milk/ton | energysystem kg/metric tonne? |

Alternatively add units as last segment of the tag, but then we have to support Mcal/kg, Mcal/lg, Mcal/CWT, MJ/kg

Milk/tonne in metric units won’t be popular, but it would be strange to do NEL, NEM, NEG metric and milk/ton English. We could do everything in English units, but scientific applications typically use metric.

Open questions:

* Can/should we incorporate limits on the number of characters in a field? This would apply to;
  + SampleIDLab
  + Expected text fields:
    - Description 1,2,3, ect
* Create list of methods: ID’s and names?
* Should all protein fractions be N based?
* Should we adopt water nutrients?