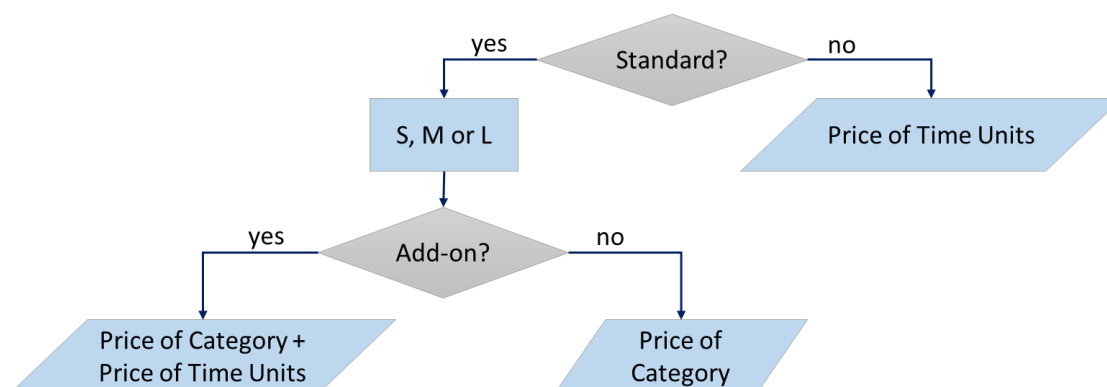


## Cost Calculation: Overview

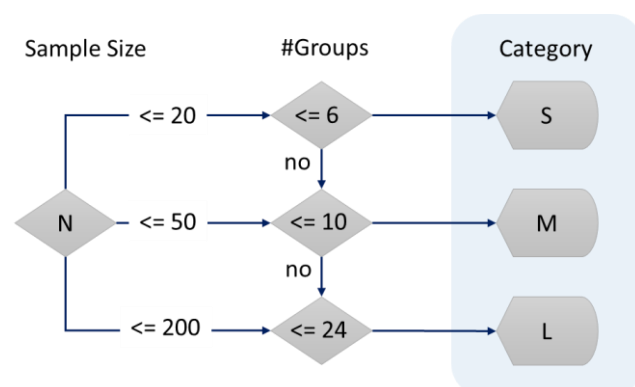
A fixed price is charged for standard –omics bioinformatics analyses and the price of any other custom analysis is based on the working time (**Figure 1**).

**Figure 1: Flowchart**



Standard –omics analysis like RNA seq or MS proteomics include processing, quality control and statistical analyses. There are 3 categories of standard analysis packages. The category depends on the sample size and the complexity of the experimental design, i.e. the number of groups (**Figure 2**).

**Figure 2: Guideline to determine category of standard package**



Final costs are calculated using the following fixed prices for each category (standard project) and for each working time unit (custom analysis and add-on package, **Table 1**).

**Table 1: Package and unit prices**

Category	Price [Euro]
S	600
M	1000
L	1800
1 unit (1 day)	400
½ unit (½ day )	200

# Cost Calculation: Details

A **standard package** includes

- standard bioinformatics data processing, quality control, statistics and visualisations (e.g. multiqc, PCA, heatmap, profile plot, volcano plot, Venn diagram and result table)
- a meeting to define the analysis and one to handover the results
- a period of one month to answer questions after handover of results

**Add-on** packages need to be defined if

- multiple meetings or milestones are required for the successful completion of the analysis
- additional custom visualizations or analyses are requested
- questions are raised later than one month after completion of the analysis

Add-on packages are priced by working time as multiples of half or full time units (minimum ½ unit).

**Custom analysis** (likewise add-on packages) are priced by working time as multiples of half or full time units (minimum 1 unit). Any complex analysis which requires an iterative process will be split into milestones and costs are calculated and billed per achieved milestone.

**Other:** Recurrent bioinformatics tasks are priced by number of occurrences or samples.

## Examples

**Example 1:** RNA seq data set with 3 treatment and 1 control group. Each group contains 4 replicates, thus there are 16 samples. All samples are aligned, quantified and statistical results are calculated for the 6 pairwise group comparisons. Quality control reveals one sample outlier which needs to be removed from the data set and the analysis has to be repeated. In total there are two meetings: one meeting to receive the data and one to deliver and explain all results and visualisations. A **standard analysis package of category S** for 600 Euro is billed. (Table 1 & Figure 2).

**Example 2:** The same 16 samples as in Example 1 are subsequently measure with MS proteomics. Again a standard analysis package of **category S** (600 Euro) is charged for the analysis of the MS proteomics data. In addition, a straightforward cross-correlation analysis of the transcriptomic and proteomic results including statistics and visualizations is requested and requires one day of bioinformatics analysis. For this **add-on package 1 working time unit** (400 Euro) will be billed on top of the 2 standard packages.

**Example 3a and 3b:** Data set as in Example 2 but a batch effect is identified.

- a) The batch effect can easily explained by the experimental protocol and can be addressed in the statistical model. **No add-on package** is required.
- b) Additional meetings, communication and bioinformatics efforts are needed to understand and to minimize the impact of the batch effect on the analysis results. An add-on package may be billed in accordance to the extra time spent on the analysis.