growth

AQUAculture infrastructures for EXCELlence in European fish research towards 2020 — AQUAEXCEL2020

Deliverable D5.2
First prototype models for growth, feed intake and waste production

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Executive Summary

Write a short summary of your Deliverable. This summary must be 2 pages maximum but very informative (and accessible to non-researchers) and must include the following elements:

Objectives:
The purpose of this document is to describe the functionality and technical implementation of the AquaFishDEB model. This numerical model prototype is one of the main components in the AQUAEXCEL2020 virtual laboratory, which will be developed in WP5: "Virtual laboratories and modelling tools for designing experiments in aquaculture research facilities".

The main components are:

- Growth, nutrition and waste production models for different fish species
- Water quality and water treatment modelling
- Modelling of hydrodynamic flow fields in tanks and cages

The objective of the AquaFishDEB model is to predict growth, feed consumption and waste production for Atlantic salmon, seabream and trout. Specifically, the model predicts 1) fish growth for different feeds (quantity and composition) and water temperature and 2) oxygen consumption and waste production (nitrogen, CO_2, solids) at different fish sizes, temperatures, feed rations and diet compositions and allows predictions for fish groups.

Rationale:
One of the main research activities in AQUAEXCEL2020 is to develop a virtual laboratory system that enables virtual experiments in aquaculture research facilities. This system will feature a framework that allows the integration of mathematical models of different subsystems in common simulations, replicating the system operation of research laboratories.

Main Results:
The AquaFishDEB prototype model is developed and tested, and it is shown that this model component can be integrated with the other main components. The model is based on the Dynamic Energy Budget (DEB) theory for metabolic organization, a theory that provides the conceptual and quantitative framework to study the whole life cycle of an individual while making explicit use of energy and mass balances (Kooijman, 2010). The model covers all life stages of a fish (including larvae, juveniles and market size fish) and explicitly is tied with feed and temperature. It accommodates different feeding strategies (e.g., ad libitum or restricted, feeding frequency, adaptive feeding) and feed composition. The output of the model includes fish growth characteristics (number of fish, mean body-size, total biomass, feed intake, specific growth rate and feed conversion efficiency), waste production (faecal dry matter and nitrogen-loss, expressed in g/h or in g/Kg of feed, as well as non faecal nitrogen loss in g/h) and gaseous exchange (O_2 consumption and CO_2 production).

Authors/Teams involved:
The authors of this Deliverable are from the HCMR team (Konstadia Lika, Orestis Stavrakidis-Zachou, Nikos Papandroulakis). The NOFIMA group contributed with providing the data for Atlantic salmon and the WU team with providing nutrition data for rainbow trout and advices for the nutrient utilization module of the model.

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1. BACKGROUND

This document is part of the AQUAEXCEL2020, WP5/Joint Research Activity 1 – Virtual laboratories and modelling tools for designing experiments in aquaculture research facilities.

Experiments with fish usually involve extensive use of laboratory facilities and run for long periods of time. Both from an ethical perspective (3R's) and from a cost perspective, tools for design and planning of experiments are increasingly important. In aquaculture research as well as other domains, numerical models are increasingly used preparatory to the actual experiments.

One of the main research activities in AQUAEXCEL2020 is to develop a virtual laboratory system that enables virtual experiments in aquaculture research facilities. This system will feature a framework (see Bjørnson et al., 2016) that allows the integration of mathematical models of different subsystems in common simulations, replicating the system operation of research laboratories. The overall system architecture is shown in Figure 1.

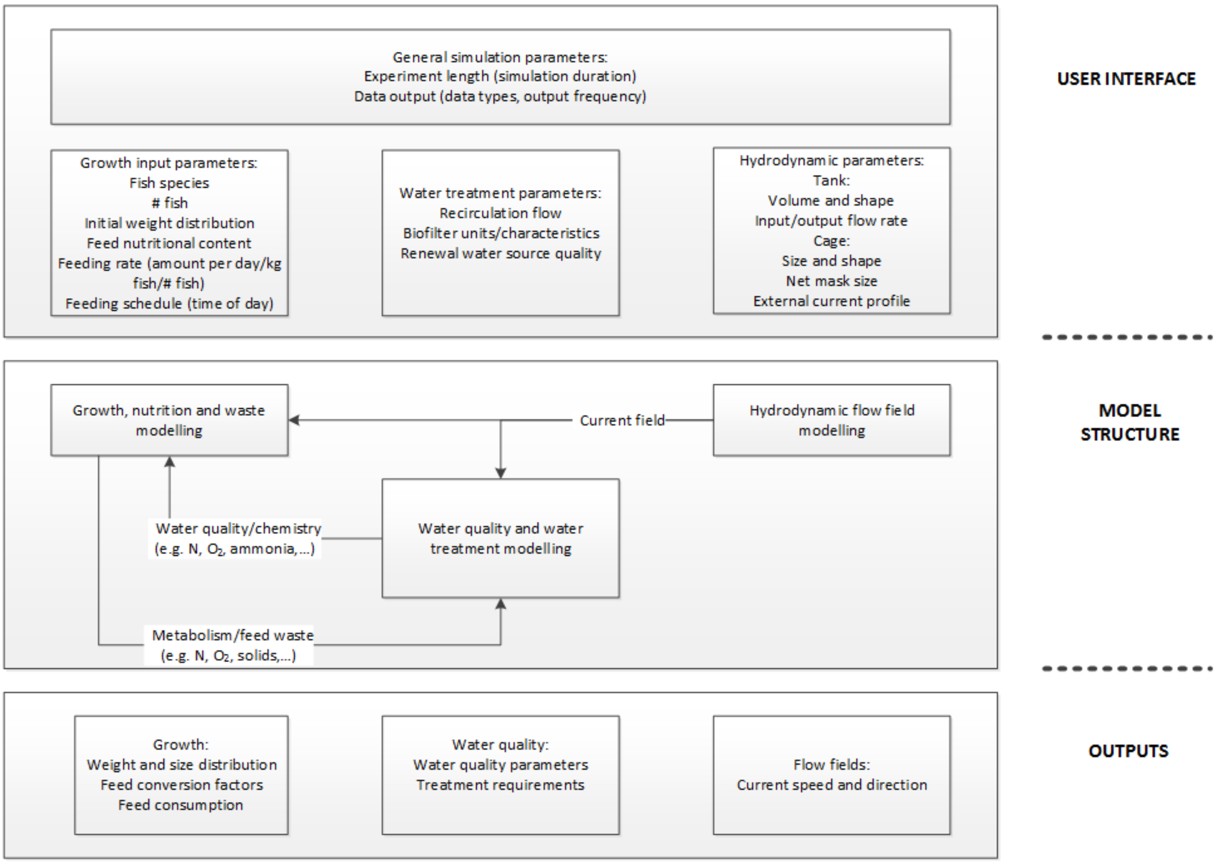

Figure 1. Virtual laboratory system architecture

This document describes the technical implementation and functionality of the AquaFishDEB model.

2. MODEL DESCRIPTION

Theoretical background

The Dynamic Energy Budget theory (DEB) provides the qualitative and quantitative framework to study individual metabolism throughout the entire life cycle of an organism via explicit use of energy and mass balances (Kooijman, 2010). Its ability to model the bioenergetics of organisms as a function of temperature and food quantity and quality throughout their life cycle has established the DEB theory as a widely applicable approach to study fish metabolism on both wild populations and farmed fish (e.g., Pecquerie *et al.*, 2009; Serpa *et al.*, 2013; Fore *et al.*, 2016).

An individual fish is described by three state variables: structure, reserve and maturity. The latter is expressed in terms of cumulative energy investment to maturation. Adults first accumulate energy for reproduction in a buffer; the emptying is controlled by buffer handling rules. Observable body mass has contributions from structure (V), reserve (E), and the reproduction buffer (E_R) for reproducing adults. DEB theory describes the interconnections among the processes of assimilation, maintenance, development, growth and reproduction of an organism throughout all stages of its life cycle, and in a dynamic environment. Life stage transitions occur when the cumulative investment into maturation reaches certain thresholds. The AquaFishDEB model is an extension of the standard model and assumes three life stages (larvae, juvenile and adult) as well as metabolic accelerated development for early stages which is an established practice for studying fish species in the DEB context (Lika *et al.,* 2014; Kooijman, 2014). The most important transitions include birth, which is marked by the start of exogenous feeding, metamorphosis as the completeness of metamorphosis, and puberty, denoted by developmental completeness and the start of allocation to reproduction. This approach allows to follow individual fish metabolism through all the stages that are relevant for aquaculture which may not be explicit. For instance, the on-growing stage of production usually contains fish that transition from the juvenile to adult stages before reaching harvest size.

An individual fish converts food to reserves (a process called assimilation) and allocates mobilized reserve to somatic and maturity maintenance, growth (i.e., increase in structural body mass) and maturation/reproduction. Food uptake depends upon food availability and fish size. Food uptake is converted into reserves with a constant efficiency, which is specific to each type of food. A fixed fraction κ of the mobilized energy is used for somatic functions, such as somatic maintenance and growth, while the remaining 1-κ fraction is allocated to maturation/reproduction, after subtraction of maturity maintenance costs.

One of the core assumptions of the theory is that each of the biomass components (structure, reserves and reproductive buffer) consists of a mixture of polymers such as proteins, lipids and carbohydrates which form generalized compounds of constant chemical composition. Consequently, all energy and mass fluxes can be described as a weighted sum of the three basic DEB fluxes namely, assimilation, growth and dissipation (metabolic work that converts reserve into mineral products in ways that do not lead to the production of new biological material). Therefore, identification of the chemical indices of the mineral and organic compounds found in the diet, the structure and the reserves, allows for the quantitative and qualitative assessment of metabolic waste output under various experimental scenarios.

Model interfaces

The developed prototype model is able to predict growth, feed consumption and waste production based on user input regarding fish and feed characteristics.

Input parameters

The inputs of the model include the name of the farmed species (Species name) and the physicochemical parameters of the tank water (Water type parameters), namely temperature (ºC), oxygen concentration (D.O. in mg l^{-1}), salinity and pH. Temperature affects the rates of the model, while oxygen concentration, salinity and pH act as red flags when their values fall outside the pre-specified ranges.

Fish size is given as the average initial wet weight (g) at the start of the experiment for a desired initial number of fish (Fish group size). Mortality is given as the percentage of the initial fish group size that is lost by the end of the experimental period (d). Feeding level can be assigned as ad libitum, referring to the maximum feed intake, or restricted, given as the amount of feed (g d^{-1}) equal to the input percentage of body weight (BW). In addition, restricted feeding allows for the adaptation of the % BW d^{-1}, through intermediate weighing at an interval (d) defined by the user. The number of rations fed daily as well as the interval between them (h) are also user-defined features. Feed composition is given in g of crude protein (CP), crude fat (CF), crude ash (CA) and nitrogen-free extract (NFE) per kg of feed dry matter, dry matter (DM) as g per kg of feed Fresh Weight and gross energy (GE) as kJ per g feed DM. The apparent digestibility is given as % of the DM/nutrient/GE retained by the fish after faecal loss has been accounted for. Alternatively, the model uses default values, which are the recommended FAO standard feeds based on the production stage and species.

Output parameters

The outputs of the model include information on the farmed species (Species name), the water temperature of the tank (ºC) and the duration of the experimental period in days. The number of fish (#) and the total fish biomass (g) are predicted as functions of time, taking into account the input mortality rate. The feed conversion ratio (FCR), specific growth rate (SGR) (d^{-1}), total feed intake (g h^{-1}) as well as waste production and gaseous exchange are also given as functions of time. Faecal dry matter and faecal nitrogenous loss are given in g per kg of feed and the total waste production as feacal and non faecal nitrogenous loss in g N h^{-1}. O_2 consumption and CO_2 production are predicted for the total fish biomass (g h^{-1}) as well as per kg of fish hourly (mg kg^{-1} h^{-1}).

Technical implementation

Model predictions are the end product of a two step modeling procedure (Figure 2). The first step involves the parameterisation of the DEB model for each species. The DEB parameters can either be retrieved from the AmP collection (AmP2018) for the species that are available or estimated as described in Marques *et al.* (2018) using the freely downloadable DEBtool software (http://www.bio.vu.nl/thb/deb/deblab/) and a number of zero- and uni-variate data sets. In the second step, the DEB parameters are used in the prototype AquaFishDEB model that simulates the dynamics for a group of fish exposed to the specified experimental conditions.

For the sake of simplicity, it is assumed that the inter-individual variability in the group of fish is small and, thus, the group consists of identical individuals that share the same parameter

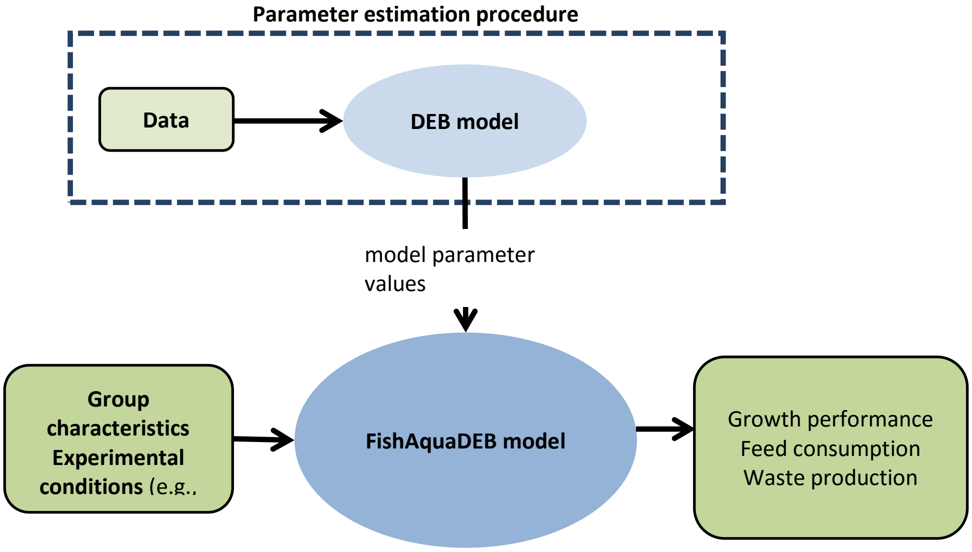

Figure 2. Schematic representation of the two-step procedure for the development of the *prototype* AquaFishDEB model.

values. Therefore, the number of fish and the mean individual biomass determine the total biomass.

Table 1 in the Appendix summarizes the dynamics of an individual fish. For a more comprehensive description of the DEB theory and a full list of the equations and the nomenclature used we refer to Kooijman (2010). The feeding rate depends on the feeding protocol (see *input parameters*). The model assumes that the elemental composition of structure and reserve remain constant while that of feed, and therefore feaces, may vary. Consequently, meticulous mass and energy balances yield the digestion efficiency κ_X of feed in terms of the digestibility κ_* of its components, where (*) denotes the macronutrients found in feeds (CP, CL, NFE). This requires prior knowledge of the composition and properties of structure and reserve. Information on the specific density of structure (d_V) and reserve (d_E), their respective molecular weights (w_V and w_E) and chemical potentials (μ_V and μ_E) was therefore extracted from literature for each species. Furthermore, a formula was developed to obtain the chemical indices of the organic compounds found in diet using the composition of feeds in macronutrients and simple transformations based on the generic macronutrient chemical formulas. The effect of temperature on metabolism is quantified via the Arrhenius relationship and the abstract state variables are linked to commonly measured quantities using the auxiliary DEB theory (Kooijman, 2010).

Table 2 in the Appendix summarizes the equations that produce the AquaFishDEB model outputs. The model, using the equations in Tables 1 and 2, generates individual and group outputs.
The first step of the modeling procedure has been accomplished for the three species. The DEB parameters for the rainbow trout model were retrieved from the AmP collection (AmP Oncorhynchus mykiss version 2017/10/30 bio.vu.nl/thb/deb/deblab/add_my_pet/). The DEB parameters for the seabream were estimated simultaneously from zero- and uni-variate data sets provided by HCMR and those for Atlantic salmon using data provided by NOFIMA and completed with literature data. Using the estimated parameters, predictions for growth and feed intake can be made, as shown in Figure 3. An illustrative example of model output for waste production is given in Figure 4.

The AquaFishDEB prototype model has been developed and tested for functionality towards its implementation in the virtual laboratory system (Figure 1) using data provided by WU for the rainbow trout and it has been shown that this model-component can be integrated with the other main components. The outputs of the AquaFishDEB model are given in the format specified by Task 5.2.

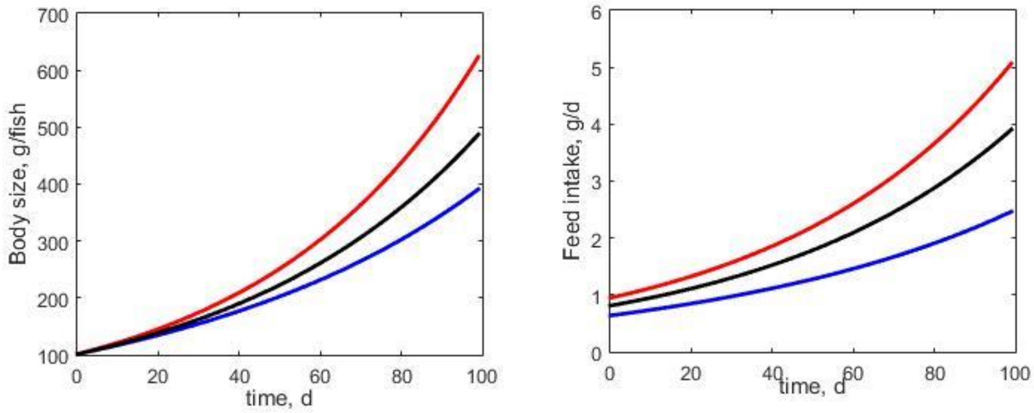

Figure 3. Model predictions of growth and feed intake for rainbow trout (blue), Atlantic salmon (red) and gilthead seabream (black) of initial weight 100 g grown for 100 days at temperatures typical for the species (15.5, 10, 17.5ºC, respectively). Feed composition: 40% CP, 20% CF,10% CA, 30% NFE.

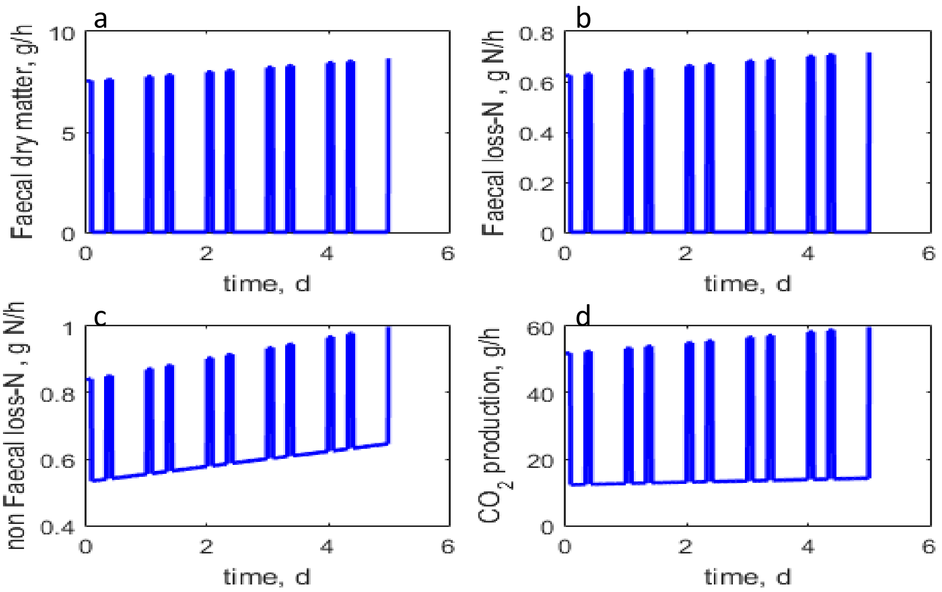

Figure 4. Waste production: a) Faecal dry matter b) faecal loss-N, c) non faecal loss-N and d) CO_2 production for 100 rainbow trout fish of initial weight 100 g, grown at 20ºC for five days. Feeding protocol: feeding level = ad libitum, number of daily rations = 2, feeding interval = 8h.

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Appendix

Table 1. State variables, energy fluxes, dynamics and parameters of the AquaFishDEB. Brackets [.] indicate quantities expressed per unit of structural volume and braces {.} per unit of structural surface area.

State variables		
V, $L = V^{1/3}$		Structural body volume, Volumetric structural length
E, $[E] = E\,/\,V$		Energy in reserve, Reserve density
E_H, E_R		Energy investment into maturation, - to reproduction
Fluxes		
$\dot{p}_X$		Feeding rate
$\dot{p}_A$		Assimilation rate: $\kappa_X \dot{p}_X$
$\dot{p}_C$		Reserve mobilization rate: $L^3[E](\dot{v}/L - r)$ with $\dot{r} = \frac{\frac{\kappa[E]\dot{v}}{L} - \dot{p}_S}{[E_G] + [E]\kappa}$
$\dot{p}_S$		Somatic maintenance rate: $[\dot{p}_M]L^3$
$\dot{p}_J$		Maturity maintenance rate: k_J min$\{E_H, E_H^p\}$
$\dot{p}_G$		Growth rate: $\kappa\dot{p}_C - \dot{p}_S$
$\dot{p}_R$		Energy flux to maturation/reproduction: $(1-\kappa)\dot{p}_C - \dot{p}_J$
$\dot{p}_D$		Dissipating power: $\dot{p}_S + \dot{p}_J + (1-\kappa_R)\dot{p}_R$
Dynamics		
$\frac{d}{dt}V = rV$		
$\frac{d}{dt}[E] = [\dot{p}_A] - [E]\dot{v}/L$		
$\frac{d}{dt}E_H = \dot{p}_R(E_H < E_H^p)$		
$\frac{d}{dt}E_R = \dot{p}_R(E_H \geq E_H^p)$		
Parameters		
Symbol	Units	
$\dot{v}$	cm d^{-1}	Energy conductance
κ	-	Allocation fraction to soma
κ_X	-	Digestion efficiency of food to reserves
κ_P	-	Faecation efficiency of food to faeces
κ_R	-	Reproduction efficiency
$[\dot{p}_M]$	J cm^{-3} d^{-1}	Volume-specific somatic maintenance rate
$[E_G]$	J cm^{-3}	Specific costs for structure
E_H^p	J	Maturity threshold at puberty
$\dot{k}_J$	d^{-1}	Maturity maintenance rate coefficient
μ_*	J mol^{-1}	chemical potentials of $*$ = X(feed), P(product), V(structure), E(reserves)
w_*	g mol^{-1}	molecular weights of $*$
d_*	g cm^{-3}	specific density of $*$
n_{NP}	-	chemical index of nitrogen in faeces

Table 2. Model equations that produce the output parameters. The equations use quantities defined in Table 1.

Wet weight (g)	$W_w = d_{Vw}\left(V + (E + E_R)\frac{w_{Ed}}{d_{Ed}\mu_E}\right)$
Group size	$\frac{dN}{dt} = mN$, with m the mortality rate
Feeding rate (g/d)	$\dot{J}_X = \frac{w_X}{\mu_X}\dot{p}_X$
Specific growth rate (1/d)	$SGR = \frac{1}{W_w}\frac{dW_w}{dt}$
Feed conversion ratio	$FCR = \frac{\dot{J}_X}{dW_w/dt}$
Faeces production (g/d)	$\dot{J}_P = \frac{w_P\kappa_P}{\mu_P}\dot{p}_X$
Faecal loss-N	$\dot{J}_{PN} = \frac{14 n_{NP}\kappa_P}{\mu_P}\dot{p}_X$
Non faecal loss-N	$\dot{J}_N = \eta_{ND}\dot{p}_D + \eta_{NG}\dot{p}_G$
Oxygen consumption	$\dot{J}_O = \eta_{OA}\dot{p}_A + \eta_{OD}\dot{p}_D + \eta_{OG}\dot{p}_G$
Carbon dioxide production	$\dot{J}_C = \eta_{CA}\dot{p}_A + \eta_{CD}\dot{p}_D + \eta_{CG}\dot{p}_G$

Glossary

AQUAEXCEL^{2020}: AQUAculture Infrastructures for EXCELlence in European Fish Research towards 2020

Definitions

Document information

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		CO Confidential, restricted under conditions set out in Model Grant Agreement		
		CI Classified, information as referred to in Commission Decision 2001/844/EC.		

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Issue Date	Revision N°	Author	Change
dd/mm/yyyy			Ex: first version/first review by WP leader etc/accepted version

Annex 1: Check list

Deliverable Check list (to be checked by the “Deliverable leader”)

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