EBASE manuscript

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## Abstract

*Key words*:

## 1 Introduction

* Overview of metabolism - importance
* Existing methods: Odum/WtRegDO, BASEmetab, references in Grace et al. (2015), applications to lakes and streams
* Applications to estuaries - challenges
* Goals and objectives

## 2 Materials and Procedures

The Estuarine BAyesian Single station Estimation (EBASE) method provides a simple approach to quantify metabolic parameters from continuous dissolved oxygen time series. The estimates are based on a modified version of the mass balance equation described in Grace et al. (2015). The original mass balance equation is:

where the terms in the square brackets are production (P), respiration (R), and gas exchange (D) as a function of the change in dissolved oxygen () per unit time of the input data (). Five unknown parameters are estimated by the model: , , , , and . The required inputs are the time series of diel oxygen (, mmol/m), surface irradiance (, mol/m/s), water temperature (, C), and oxygen saturation (, mmol/m). Dissolved oxygen at saturation is calculated from the input data as a function of water temperature and salinity (psu) (García and Gordon 1992). [Equation 2](#eq-ts) is temperature scaled, as input to [Equation 3](#eq-co) that calculates the solubility of dissolved oxygen per volume of seawater at the given temperature. The coefficients are = 5.80818, = 3.20684, = 4.11890, = 4.93845, = 1.01567, = 1.41575, = -7.01211e-3, = -7.25958e-3, = -7.93334e-3, = -5.54491e-3, and = -1.32412e-7.

Dissolved oxygen saturation is then calculated by multiplying by the density of seawater given temperature and salinity ([Equation 4](#eq-csat)). The parameter (kg/m) is seawater density at zero elevation given temperature and salinity (Millero and Poisson 1981).

The first modification to [Equation 1](#eq-base) for EBASE is use of a wind-based parameterization for gas exchange that is more appropriate for estuaries (Wanninkhof 2014):

where is the wind speed at 10-m height and is the Schmidt number defined as the ratio of the kinematic viscosity of water to the molecular diffusivity of the gas for oxygen calculated as a function of water temperature and salinity using the polynomial fit of Wanninkhof (2014). The parameter () must be estimated from the data. The other variables are as defined as in [Equation 1](#eq-base).

The final modification to [Equation 1](#eq-base) for EBASE is a simplification to remove the and parameters. For EBASE, the temperature dependency of respiration is removed by setting = 1) and is also set as 1. This further simplifies [Equation 5](#eq-basewan) to:

As for BASE, the metabolic estimates in EBASE are defined by the change in dissolved oxygen over the time step , where gross production is provided by , respiration is provided by , and gas exchange is provided by the remainder (as in Wanninkhof 2014). Units for each of the metabolic estimates are .

The remaining three parameters (light efficiency, ), (respiration, ), and () are estimated by likelihood given the observed data with the JAGS model using prior distributions shown in the model file. At each time step, the change in oxygen concentration between time steps is calculated from the equation using model inputs and parameter guesses, and then a finite difference approximation is used to estimate modeled oxygen concentration. The estimated dissolved oxygen concentration is also returned, which can be compared to observed as one measure of model performance.

The metabolism estimates and their parameters returned by the Bayesian routine implemented in JAGS are affected by the prior distributions assigned to each. As for the BASE model, relatively uninformed prior distributions following a normal Gaussian distribution are used by default, although the priors can of course be changed based on previous knowledge of parameter specific to an ecosystem. The default priors were based on those that returned reasonable parameter estimates using a forward-feeding oxygen mass balance equation call FWOXY (ForWard OXYgen). For FWOXY, a dissolved oxygen time series is simulated by providing known parameter values in an equation similar to [Equation 6](#eq-ebase). All of the physical parameters are held constant, e.g., wind speed, temperature, and salinity. The other required inputs are the , , and parameters, which are set by the user. As such, the dissolved oxygen output simulated by FWOXY as change per unit time is modelled by EBASE using the constant physical parameters as input. Reasonable prior distributions by EBASE were identified based on the ability to return the known parameters from FWOXY:

The notation is JAGS model syntax indicating the distributions are truncated to a minimum (left) and maximum (right) value defined in the parentheses. All prior distributions were constrained to positive values based on requirements of the model formula in [Equation 6](#eq-ebase). Additionally, the prior distribution for was constrained to an upper limit of 0.504 (~twice the default mean). Wanninkhof (2014) states that the parameter typically does not vary by more than 20% and the standard deviation of the default prior is sufficiently high to expand beyond this range. Initial development of EBASE also showed that using an undefined upper limit of led to unstable and unreasonable parameter estimates. The density distributions for the default priors in EBASE are shown in [Figure 2](#fig-priorplot).

### 2.1 EBASE R package

For ease of application, an R package was developed to implement the EBASE methods described above.

## 3 Assessment

### 3.1 EBASE comparison with modelled observations

* Comparison with Odum and BASEmetab: Fwoxy Appalachicola

### 3.2 Sensitivity analyses

Several configurations of the EBASE model can influence how the metabolic rates are estimated. A simulated time series with known values for the , , and parameters that are returned by EBASE was used to determine if 1) EBASE estimates similar values, and 2) how the estimated values change with different model configurations. Two types of sensitivity analyses were conducted to evaluate changes in the parameters returned by EBASE, where in all cases, the parameters were compared to the known values in the simulated time series. First, parameter estimates were compared to the known values after changing characteristics of their prior distributions. Second, parameter estimates were compared using a model period of optimization for one day and one week of observations. Details of these analyses are as follows.

The standard prior distributions for the EBASE parameters follow normal distributions with defined means and standard deviations. The sensitivity analysis evaluated changes in the distributions by varying the standard deviations from small to large to test the effect of more or less constrained ranges, respectively, on the priors. For each parameter, low, medium, and high values for the standard deviation were assessed as 10%, 100%, and 1000% of the default values. Each unique combination of low, medium, and high values for the standard deviation of each parameter were evaluated, creating 3 = 27 different combinations of prior distributions that were used with the simulated time series in EBASE. Because initial assessments indicated that all parameter estimates were especially sensitive to changes in the prior distribution for the parameter, a second sensitivity analysis evaluated additional changes in both the mean and standard deviation of the prior. The mean of the prior was varied as 50%, 100%, and 200% (the upper limit used in the software) of the default and the standard deviation was varied as before. This resulted in 3 = 9 unique combinations of means and standard deviations for the prior that were evaluated.

The optimization period used for a time series determines how much data are used to estimate the three EBASE parameters (, , and ). Unlike BASEmetab, the EBASE software allows flexibility in the period of time used for optimization, with a minimum period of time being one day and a maximum period of being the length of the time series. For a chosen optimization period, a single estimate for and is returned by the model, whereas number of observations equal to the number of time steps in each optimization period are returned for the parameter (e.g., 96 values for 24 hour time period if the sampling interval is 15 minutes). Short periods of observation may return unstable parameter estimates if forcing factors (e.g., wind, temperature) that affect estuarine biogeochemical rates occur at time scales longer the chosen period of optimization for EBASE. As such, potentially longer optimization periods may return more stable and robust estimates given that more data are used for parameter estimation. An optimization period of one day was compared to results using an optimization period of seven days for the simulated one-year time series. Each optimization period was evaluated for every unique combination of prior distributions, totaling 54 unique analyses for the assessment of changing standard deviations of all parameters and 18 unique analyses for the assessment of changing the mean and standard deviation of only the parameter.

The metabolic estimates returned from each analysis were compared to the known values to identify priors the model was most sensitive to and if the conclusions varied by optimization period. Estimates for the modeled dissolved oxygen, gross production, respiration (), gas exchange (), and were compared to those from the simulated time series using coefficient of variation () and root mean square error () summaries of the 1:1 comparison of the estimated vs simulated values. For the one day optimization period, all parameter estimates returned at the time step of the input data (i.e., modeled dissoled oxygen, , and ) were daily-averaged for comparison. For the seven day optimization period, all parameter estimates and those from the known time series were weekly-averaged. Estimates for the parameter were evaluated only by visual comparison because a single value was used in the simulated time series, preventing the estimate of quantitative comparisons.

### 3.3 EBASE comparison with real observations

Metabolic estimates from EBASE were compared to those from existing methods to benchmark and evaluate potential differences from alternative model formulations used by each approach. An approximate one year continuous time series from Apalachicola Bay, Florida was provided as input to each method. The input data were 2012 observations from February 22nd to December 19th at the Cat Point water quality monitoring station (29.7021 N, -84.8802 W) and included 15 minute observations of dissolved oxygen (mg/L), water temperature (C), salinity (psu), and sonde depth (m). Continuous meteorological observations from the nearby East Bay station (29.7909 N, -84.8834 W, ~10km north of Cat Point) were combined with the water quality data at the same time step and included air temperature (C), wind speed (m/s), PAR (mmol/m as total per 15 minute observation), and barometric pressure (mb). The combined input data were provided to each method after converting the units as required (e.g., BASEmetab requires PAR as mol m s). Water column depth at Cat Point is approximately 1.8 m and all daily metabolic estimates returned by each method were converted to volumetric rates by dividing by the depth (mol O m d). Each comparison also evaluated metabolic estimates using the observed dissolved oxygen time series and a detided time series using weighted regression (Beck et al. 2015). The latter comparison provided an assessment of metabolic rates that are expected to be minimally influenced by tidal advection. All metabolic estimates were obtained using the default settings for each of the three methods, with an exception that the prior distribution for the reaeration coefficient () in BASEmetab was informed by results from the Odum output. Initial assessments indicated that unstable and inaccurate results are obtained from BASEmetab using an uninformed prior distribution for . All other prior distributions for BASEmetab and EBASE were set as the software default. A one-day model optimization period was used for EBASE.

The common set of metabolic parameters returned by the Odum, BASEmetab, and EBASE methods are net ecosystem metabolism, gross production, respiration, and gas exchange. Pairwise comparisons of the daily estimates returned by each method were evaluated using simple summary statistics including Pearson correlation coefficients and linear regression fits to evaluate potential biases in each method. For the latter analysis, differences in intercept estimates less than or greater than zero suggested a bias in magnitude, whereas differences in slope estimates less than or greater than one suggested a bias that depended on relative value of each observation (e.g., bias may differ between lower or higher values). Comparisons of the slope and estimates values to zero and one, respectively, were based on confidence intervals from the standard errors of each estimate. Results were assessed separately for estimates based on the observed or detided dissolved oxygen time series.

[Figure 1](#fig-apacmpfig) and Table provide a comparison of the EBASE metabolic estimates with those from the Odum and BASmetab methods.

### 3.4 Application to represenatiave NERR sites

## 4 Discussion

## 5 Comments and Recommendations

## Acknowledgments

## Figures

Figure 1: Fwoxy comparisons

Figure 2: Apalachicola comparisons

Figure 3: Sensitivity analyses

Figure 4: NERRS application

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| Figure 1: Comparisons of daily metabolic estimates from the Odum, BASEmetab, and EBASE methods for one year of continuous monitoring data at Apalachicola Bay. Results for net ecosystem metabolism (NEM), gross production (P), respiration (R), and gas exchange (D) are compared using the (a) observed and (b) detided dissolved oxygen time series as input to each model. All values are volumetric as mmol O m d and are grouped by the dry or wet season. Black lines show the 1:1 comparison, the blue line shows the linea regression fit, and the Pearson correlation values are shown in parentheses for each facet title. |

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| Figure 2: The default prior distributions for the , , and parameters used in EBASE. All priors are normal distributions and truncated to positive values. The parameter is also truncated to a maximum of 0.504. |

## Tables

Table 1: EBASE parameters and outputs

Table 2: Summary stats of Fwoxy comparison

Table 3: Summary stats of Apalachicola comparison

Table 4: Key parameters form NERRS application

**Table** **:** Summary statisics of daily metabolic estimates comparing Odum and BASEmetab to EBASE for net ecosystem metabolism (NEM), gross production (P), respiration (R), and gas exchange (D). Separate comparisons are made for estimates based on observed and detided dissolved oxygen. Summary statistics include Pearson correlation coefficients and intercept, slope, and residual standard deviation of a linear fit between the same metabolic estimates obtained from each method. Significance of the p-values for the intercept and slope indicates if the estimate is different from zero or one, respectively.

| Dissolved Oxygen | Comparison | Estimate | NA | Intercept | Slope | NA |
| --- | --- | --- | --- | --- | --- | --- |
| Observed |  |  |  |  |  |  |
|  | Odum v EBASE | NEM | 0.23\*\* | -11.4\*\* | 0.23\*\* | 26.26 |
|  |  | P | 0.28\*\* | 15.23\*\* | 0.56\*\* | 43.69 |
|  |  | R | 0.11 | -23.14\* | 0.65 | 54.12 |
|  |  | D | 0.74\*\* | 5.15\*\* | 0.65\*\* | 6.14 |
|  | BASEmetab v EBASE | NEM | 0.89\*\* | -8.14\*\* | 1.11\*\* | 15.12 |
|  |  | P | 0.47\*\* | 23.23\*\* | 0.69\*\* | 29.48 |
|  |  | R | 0.59\*\* | 22.38\*\* | 2.98\*\* | 36.93 |
|  |  | D | 0.57\*\* | 9.29\*\* | 0.48\*\* | 7.12 |
| Detided |  |  |  |  |  |  |
|  | Odum v EBASE | NEM | 0.74\*\* | -4.93\*\* | 1.03 | 7.77 |
|  |  | P | 0.52\*\* | 7.46\*\* | 0.93 | 10.73 |
|  |  | R | 0.53\*\* | -14.03\*\* | 0.87 | 15.72 |
|  |  | D | 0.8\*\* | 1.89\*\* | 1.04 | 6.66 |
|  | BASEmetab v EBASE | NEM | 0.59\*\* | -7.16\*\* | 0.52\*\* | 5.91 |
|  |  | P | 0.87\*\* | 2.79\*\* | 1.01 | 3.95 |
|  |  | R | 0.74\*\* | -9.54\*\* | 0.75\*\* | 7.59 |
|  |  | D | 0.54\*\* | 9.12\*\* | 0.42\*\* | 5.60 |
| \* p < 0.05, \*\* p < 0.005 | | | | | | |

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