Fitting metabolic models to dissolved oxygen data: the Estuarine BAyesian Single-station Estimation method

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## Abstract

Continuous monitoring data for dissolved oxygen have been used to estimate the contribution of gross primary production and ecosystem respiration to net ecosystem metabolism. Most models for estimating metabolic processes make several assumptions on how biological and physical factors affect the expression of metabolism in dissolved oxygen concentrations, which can lead to poorly constrained errors that influence the interpretation of results. In estuaries, these methods can inform our understanding of spatial and temporal patterns in trophic state, yet very few models have been developed that address challenges of estimating metabolism in these dynamic systems. This paper describes the development, assessment, and interpretation of results from a new approach for estimating metabolic rates in estuaries, or the Estuarine BAyesian Single-station Estimation (EBASE) method. EBASE provides several advantages over existing models by 1) using a linear relationship between irradiance and production, 2) removing the temperature-dependency of respiration, and 3) applying a wind-based gas exchange formulation method applicable to estuaries. Moreover, the approach uses a Bayesian framework where critical model parameters are fit as a function of the data and informed using a set of prior distributions. We demonstrate that EBASE can reproduce known metabolic parameters from a synthetic time series created with continuous monitoring data from the Apalachicola estuarine reserve and provide a quantitative assessment of how the prior distributions affect the model results. The approach is also bench-marked with more conventional open-water methods for estimating metabolism, with critical differences attributed to formulation of the metabolic mass-balance equations and the underlying statistical framework (i.e., Bayesian vs simple integration). The EBASE approach is available using open source software and can be readily applied to multiple years of long-term monitoring data that are available in many estuaries. Overall, EBASE provides an accessible method to parameterize a simple metabolic model appropriate for estuarine systems and will provide additional understanding of processes that influence ecosystem status and condition.

*Key words*:

## 1 Introduction

* Overview of metabolism - importance
* Existing methods: Odum/WtRegDO, BASE, 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 EBASE mass balance equation is:

where the terms on the right side of the equation are gross primary production (P or ), ecosystem respiration (R), and gas exchange (D, remainder), respectively, modeled as a function of the change in dissolved oxygen () per unit time () of the input data. Production is modeled linearly as a function of surface irradiance (, Watts m) and (light efficiency, ). Respiration is modeled with the single parameter (). Gas exchange is modeled using the formulation in Wanninkhof (2014) as a wind-based parameterization for the gas transfer velocity (Ho et al. 2016) multiplied by the oxygen concentration gradient as the difference between the concentration measured in the surface water layer, (mmol m), and the saturation (or equilibrium) concentration, (mmol m), calculated from salinity (psu) and temperature (C) (Millero and Poisson 1981; García and Gordon 1992). The gas transfer velocity is modeled using wind speed squared at 10 meters above the water (, m s), water column depth ( in meters, as a fixed parameter or time series from a pressure sensor), and the Schmidt number () defined as the ratio of the kinematic viscosity of water to the molecular diffusivity of the gas for oxygen (from water temperature and salinity using the polynomial fit in Wanninkhof 2014). The parameter is estimated from the data and has units of . As such, the three parameters estimated by EBASE are , , and using the required input data that includes time series of dissolved oxygen, water temperature, salinity, PAR, wind speed, and water column depth (Table ).

The EBASE approach was based on several modifications to BAyesian Single-station Estimation (BASE) the mass balance equation described in Grace et al. (2015):

### 2.1 Changes to BASE

A common theory behind most gas exchange parameterizations for metabolism estimates is that the transfer of gases of relatively low solubility, like oxygen, is proportional to the concentration gradient in a thin film of water at the air–water interface. It is also assumed that the water at the top of the film is saturated with respect to the atmosphere, so that the concentration difference across the thin film can be approximated as the difference between oxygen concentration measured in the surface water layer, , and the saturation (or equilibrium) concentration , which is usually calculated as a function of water temperature and salinity (the negative sign is needed because positive flux is set to be from water to air):

The gas transfer velocity, , has dimensions of length over time and increases as the water column in the vicinity of the air–water interface becomes more turbulent. As such, is usually modeled as a function of measurable variables that can potentially predict turbulent mixing of the surface water, e.g., wind speed, current velocity, and water depth (Ho et al. 2016). also increases with temperature because the film of water at the air-sea interface becomes more thin as the random motion of gas and water molecules increases at higher temperatures and transfer of molecules across the film increases. This dependence of on temperature is usually modeled with the Schmidt number as in [Equation 1](#eq-ebase), which combines information on the viscosity of the fluid and the diffusivity of the gas.

Grace et al. (2015) used the following for the gas transfer in BASE:

where is the average water temperature over each 24-hour period in the oxygen time series and is the reaeration coefficient estimated from the data. [Equation 4](#eq-gasexbase) indicates that increases with temperature and depth. The temperature dependence is consistent with the known decrease of with the Schmidt number, but the depth dependence is difficult to justify. An expectation is that would increase as water depth decreases for a given current speed because turbulence generated at the sediment–water interface by currents would more easily reach the surface (Ho et al. 2016). Based on these differences, the wind-based parameterization for gas exchange was used for EBASE (Wanninkhof 2014). Additionally, was calculated using only temperature and salinity, removing the need for barometric pressure used in BASE.

The additional modifications to [Equation 2](#eq-base) for EBASE were removing the and parameters from the production (P) and respiration (R) components, respectively. The BASE method provides options to estimate both and from the data or to set as fixed values defined in the model file (, ). For EBASE, the temperature dependency of respiration is removed by setting = 1 and it is assumed that respiration is constant as in other methods (Odum 1956; Murrell et al. 2018). The parameter, which is dimensionless, is also set to 1 as in Holtgrieve et al. (2010), such that a linear relationship of production to was used. This removes the exponential dependence of production with increasing . Removing these components also improved model stability by creating more reasonable estimates for the other parameters.

### 2.2 EBASE model estimation

The remaining three parameters (light efficiency, ), (respiration, ), and () are estimated by likelihood given the observed data and prior distributions for the parameters. The JAGS software (as for BASE, Plummer et al. 2003) is used with the EBASE R package (described below, Beck et al. 2022; R Core Team 2022) to estimate the unknown parameters using Markov Chain Monte Carlo simulations in a Bayesian framework. At each time step, the change in oxygen concentration between time steps is calculated from the equation using model inputs and parameter guesses based on the prior distributions, and then a finite difference approximation is used to estimate modeled oxygen concentration. Estimations proceed using a forward in time integration where the dissolved oxygen at each time step is informed by parameter estimates from the preceding time steps. The estimated dissolved oxygen concentration is also returned, which can be compared to the observed values as one measure of model performance. All parameter inputs and outputs for EBASE are shown in Table . Areal rates for , , and () are returned for comparability of estimates across locations where water column depth may vary.

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 be changed based on previous knowledge of parameters specific to an ecosystem or as informed by other metabolic modeling approaches. Reasonable uninformed prior distributions for EBASE were chosen with mean values using approximate estimates from the literature (Wanninkhof 2014; Grace et al. 2015) and standard deviations that were sufficiently large to allow the Bayesian routine to search an unconstrained parameter space. The default priors for , , and are:

where indicates a normal distribution with mean and standard deviation and is 1 between and and 0 elsewhere; has the effect of truncating the normal distribution to minimum and maximum values. All prior distributions were constrained to positive values based on known physical constraints and requirements of the model formula in [Equation 1](#eq-ebase). Additionally, the prior distribution for was constrained to an upper limit of 0.502 (~twice the default mean). Initial development of EBASE showed that using an undefined upper limit of led to unstable and unreasonable parameter estimates. Examples of the prior distributions in Equations [5](#eq-aprior), [6](#eq-rprior), and [7](#eq-bprior) are shown in [Figure 1](#fig-priorplot).

For ease of application, an R package was developed to implement the EBASE methods described above (Beck et al. 2022). A detailed web page (<https://fawda123.github.io/EBASE/>) describes the required data inputs for estimating the metabolic parameters using the core R functions that pass inputs to the JAGS software. A JAGS model file is included with the package that implements [Equation 1](#eq-ebase), with options to supply a custom model file as needed. Users can also specify alternative prior distributions from those in Equations [5](#eq-aprior), [6](#eq-rprior), and [7](#eq-bprior) for each parameter. Functions are available for viewing model results, including a plot of the modeled dissolved oxygen with the observed, a time series plot of the primary metabolic estimates (P, R, and D, as areal rates with units ), and a time series plot of the credible intervals for the , , and parameters. An additional option allows the user to specify the model optimization period, where the time period can vary from a minimum of one day to the maximum of the entire length of the time series. This differs from the BASE approach where the optimization period is set at one day. Sensitivity of the EBASE method to different optimization periods is described in [Section 3.1](#sec-cmpmod). All results provided herein were generated using the EBASE R package.

## 3 Assessment

### 3.1 EBASE comparison with known results

A preliminary assessment of the ability of EBASE to produce reasonable parameter estimates for , , and ([Equation 1](#eq-ebase)) was conducted using a synthetic time series with actual data as inputs. These assessments evaluated if 1) EBASE estimates similar values for the known parameters in the synthetic time series, and 2) how the estimated values change with different model configurations. The synthetic time series used inputs from one year of continuous data from Apalachicola Bay, Florida. The input data were observations from the year 2012 at the Cat Point water quality monitoring station (29.7021 N, –84.8802 W) and included 15-minute observations of water temperature and salinity. 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, wind speed, and PAR. Missing observations in the water quality and meteorological data were filled using autoregressive modelling of the actual parameters versus time to create a complete dataset from January 1st to December 31st. A synthetic oxygen time series was then generated using the inputs from Apalachicola Bay ([Figure 2](#fig-synapa)a) and [Equation 1](#eq-ebase) as a forward calculating model with user-defined values for , , and . All metabolic rates for production, respiration, and gas exchange ([Figure 2](#fig-synapa)b and c) were also estimated with the synthetic time series. The only parameter that could not be created as a continuous time series was , which was set to 0.251 (Wanninkhof 2014). Accordingly, the synthetic dissolved oxygen time series and the observed water quality and meteorological data were used with EBASE to determine if reasonable estimates for the known parameters and metabolic rates were recovered.

Several configurations of the EBASE model can influence how the parameters and metabolic rates are estimated. Two types of sensitivity analyses were conducted to evaluate changes in the results returned by EBASE, where in all cases, the results were compared to the known values in the synthetic time series. First, results were compared to the known values after changing characteristics of their prior distributions. Second, results were compared using a model period of optimization for one, seven, and 30 days to assess how results varied based on the amount of data used for the Bayesian estimation. Details of these analyses are as follows.

The prior distributions for the EBASE parameters follow truncated normal distributions with defined means () and standard deviations ()(Equations [5](#eq-aprior), [6](#eq-rprior), and [7](#eq-bprior)). The sensitivity analysis evaluated changes in the distributions by varying the means and standard deviations from small to large to test the effect of changes in the central tendencies and more or less constrained ranges, respectively, on the priors. For each parameter, low and high values for the means and standard deviations were assessed as changes approximately equal to two orders of magnitude of the means and standard deviations of the known parameters of the synthetic time series. The only exception was the parameter where the low values created priors with a distribution close to zero and the high values were equivalent to a uniform prior distribution in the range of 0 to 0.502 (justification noted in [Section 2.2](#sec-ebasemod)). Each unique combination of low and high values for the means and standard deviations of each parameter were evaluated, creating 2 = 64 different combinations of prior distributions that were used with the synthetic time series in EBASE.

The optimization period used for a time series determines how much data are used to estimate the three EBASE parameters (, , and ). Unlike BASE, the EBASE software allows flexibility in the period of time used for optimization, with a minimum being one day and a maximum being the length of the time series. For a chosen optimization period, single estimates for , and are returned by the model. A short period of optimization (e.g., one day) 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, although at the risk of overgeneralizing metabolic rates if variation occurs at time scales less than the optimization period. Results from optimization periods of one, seven, and thirty days were compared for the synthetic one-year time series. Each optimization period was also evaluated for every unique combination of prior distributions, totaling 192 (64 times the three optimization periods) unique analyses for the assessment of changing priors of all parameters.

Changing the prior distributions affected the ability of EBASE to return the known parameters from the synthetic time series, with results varying by optimization period. [Figure 3](#fig-priorcomp) shows a summary of the comparisons of the synthetic data with EBASE for each unique combination of prior distributions and the three optimization periods of one, seven, and thirty days. The results are shown using Nash-Sutcliffe Efficiency (NSE) values (Nash and Sutcliffe 1970; Moriasi et al. 2007):

where is the estimate from EBASE or the synthetic times series for the optimization period , evaluated for each metabolic parameter, each unique combination of priors, and each optimization period. The value is the number of optimization periods in the one-year time series, i.e., for one day, for seven days, and for 30 days. All metabolic estimates were averaged within the number of days for each optimization period prior to calculating NSE values, if appropriate. The NSE value is conceptually similar to the coefficient of determination, but varies from to 1. Values in the positive range from 0 to 1 are desirable with 1 being a perfect fit, whereas values in the negative range indicate the mean of the synthetic data is a better predictor than EBASE.

Several conclusions can be made from the results in [Figure 3](#fig-priorcomp) following the patterns of the NSE values. Overall, most models regardless of optimization period or priors were able to reproduce the dissolved oxygen time series. The only models where the NSE values were less than zero for dissolved oxygen were those where of the parameter was low. However, substantial variation in NSE values was observed among all other parameters. Not considering dissolved oxygen, gas exchange () was estimated with the highest NSE, with a median value across all optimization periods and priors slightly larger than zero (median NSE = 0.03). Conversely, the parameter was reproduced the most poorly, with a median value across all optimization periods and priors less than zero (median NSE = -5.75). By optimization period, median NSE values across all parameters decreased slightly as the number of days used for model optimization increased (1 day = -2.17, 7 days = -3.01, 30 days = -3.28). The top three ranked models were identical for the seven and thirty day models and similar for models using the one day optimization period. Median NSE values across parameters for the top model in each optimization period were also similar (1 day = 0.76, 7 days = 0.55, 30 days = 0.77). For the seven day and thirty day optimization periods, the NSE values for all parameters were greater than zero for the top models, where two of the parameters in the top model for the one day optimization period has NSE < 0. Most parameters regardless of optimization period or priors had NSE < 0 (74%). As such, the prior combinations that produced the highest NSE values across all parameters were those where the values were high for each prior distribution, regardless of the values for , i.e., those with sufficient flexibility to search a larger parameter space regardless of produced metabolic parameter estimates most similar to the known values from the synthetic time series.

[Figure 4](#fig-priorsumcomp) provides an alternative summary of how the prior distributions influenced the ability of EBASE to reproduce the synthetic parameters. Median NSE values across all models and each optimization period for the different subsets of the prior combinations are shown. For example, the bottom left panel with the x-axis value for the parameter shows the median NSE values for all models using a one-day optimization period where the value for the prior distribution was low or high. The size of the points indicate the inter-quartile range of NSE values for each subset. As such, each set of points denoted by the x-axis parameters in each panel include median NSE values for all models by optimization period, but subset by the low/high or values for each parameter. Although most of the median NSE values are less than zero, indicating a poor ability of EBASE to reproduce the parameters, patterns emerge as to which characteristics of the prior lead to robust estimates. For example, large differences in the median NSE values are observed for low and high for the and parameters, with positive median NSE values and smaller IQR values when using a high value using the 7 and 30 day optimization periods. A similar, but smaller effect is seen for the value of the prior for the parameter. A conclusion similar to that for [Figure 3](#fig-priorcomp) is that large standard deviations in the prior distributions lead to more accurate estimates of metabolic parameters. Conversely, model results are less sensitive to low or high values for as the spread between median NSE values is less than those for . This suggests that EBASE model sensitivity is most influenced by of the prior distributions, i.e., larger values produce more accurate and less variable estimates regardless of .

The actual model results for the best and worst performing combinations of prior distributions for the one day, seven day, and thirty day optimization periods are shown in [Figure 5](#fig-optex) (all results are averaged at the time-step of the optimization period for comparability). The best performing models were those with the highest median NSE values across all parameter estimates in [Figure 3](#fig-priorcomp). The best performing models for each optimization period ([Figure 5](#fig-optex) a, c, e) showed similar results where the parameter estimates were similar to the synthetic time series, although more variation in the EBASE results were of course observed with the one day optimization period. However, the parameter was estimated with high variability for the one and seven day optimization periods ([Figure 5](#fig-optex) a, c, bottom row) and with a large positive bias for the 30 day optimization period ([Figure 5](#fig-optex) e, bottom row). These results were not unexpected because it was impossible to evaluate NSE estimates using a fixed value in the synthetic results and the accuracy was not considered in identifying the best performing model. Finally, the worst performing model for each optimization period ([Figure 5](#fig-optex) b, d, f) demonstrates the negative NSE values that were obtained (i.e., EBASE values much lower or higher than the synthetic values). The worst performing models were caused by constraining EBASE to a small parameter space using low or high values for combined with low values for .

### 3.2 EBASE and Odum comparison with real observations

Metabolic estimates from EBASE were further compared to those from existing methods to benchmark and evaluate potential differences from alternative model formulations used by each approach. The observed one-year continuous time series described above for water quality and weather data from Apalachicola Bay was used to compare metabolic estimates from EBASE and the Odum open-water method (Odum 1956). The Odum method used an approach described in Murrell et al. (2018) created for estuarine application that uses a gas-exchange approach from Thébault et al. (2008). For a better comparison with the EBASE methods, the gas exchange parameterization in the Odum method was modified to use the Wanninkhof (2014) approach and the parameter was fixed at 0.251 (as available in the WtRegDO R package, Beck 2021). An additional and fundamental difference between EBASE and the Odum method is that the former is likelihood based with metabolic rates estimated by fitting the model to the data, whereas the latter is strictly arithmetic based primarily on integration of the diel dissolved oxygen curve. Thus, potentially different results are expected between the approaches based on differences in formulation of the mass balance equations for metabolism, as well as alternative statistical approaches to estimating the parameters. Each comparison also evaluated differences in the metabolic estimates using the observed dissolved oxygen time series and a detided time series using weighted regression (Beck et al. 2015; Beck 2021). The latter comparison provided an assessment of metabolic rates that are expected to be minimally influenced by tidal advection, as a fundamental assumption of metabolic models using *in situ* dissolved oxygen time series from fixed monitoring stations. The prior distributions for EBASE were uninformed using the same large values from [Section 3.1](#sec-cmpmod) and moderate values ( = 0.2 for , = 20 for , = 0.251 for ). A one day model optimization period was used for EBASE for comparability with the Odum method.

The common set of metabolic parameters returned by the EBASE and Odum methods are net ecosystem metabolism (NEM), gross primary production (P), ecosystem respiration (R), and gas exchange (D). 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 metabolic estimates). Comparisons of the intercept and slope estimates to zero and one, respectively, were based on confidence intervals from the standard errors of each. Root mean square errors (RMSE) of each linear model were also evaluated. Results were assessed separately for estimates using the observed or detided dissolved oxygen time series.

[Figure 6](#fig-apacmpfig) and Table provide a comparison of the metabolic estimates from the EBASE and Odum methods. Correlations for all metabolic estimates, regardless of method or the input time series, were positive and significantly correlated, as expected. The intercept values were all significant, excluding P with the observed dissolved oxygen, suggesting some level of bias when comparing metabolic estimates between the methods. The slope estimates for R and D were significantly different for metabolic estimates from the observed dissolved oxygen, where all but R were significantly different using the detided dissolved oxygen. The RMSE values of each regression comparing the metabolic estimates between methods were generally lower in the detided results, excluding D which was higher with the detided dissolved oxygen relative to the observed. This result suggests that detiding the time series produces more comparable metabolic estimates between methods.

As noted in the previous paragraph, metabolic estimates between the methods were generally more similar based on RMSE results using the detided dissolved oxygen time series ([Figure 6](#fig-apacmpfig)b) than using the observed dissolved oxygen as input ([Figure 6](#fig-apacmpfig)a). This suggests that tidal effects on continuous monitoring data can severely violate assumptions required for methods of estimating ecosystem metabolism (as described in detail in Beck et al. 2015). These effects are easily identified with estimates from the Odum method as negative values for P and positive values for R, i.e., “anomalous” values. The effects of tidal advection on estimates from EBASE were more subtle as anomalous values cannot be returned based on constraints of the priors (i.e., none can be negative), although the range of values for the metabolic estimates was much larger with observed dissolved oxygen. Overall, the results suggest that detiding the dissolved oxygen time series prior to estimating metabolic rates produces more stable estimates with smaller ranges (Table ), regardless of the method used.

## 4 Discussion

EBASE provides several computational advantages over BASE implemented in the R package that was created for the purposes herein. Most importantly, EBASE was developed to allow different model optimization lengths, whereas the BASE method was developed to estimate results for only a single day. Allowing EBASE to incorporate more than a day of observations in the optimization can likely produce more accurate and precise estimates for the metabolic parameters. Physical and biological characteristics of an ecosystem that affect the metabolic rates are likely acting at time scales longer than a day, e.g., wind patterns that can affect gas exchange as manifested in the parameter may persist for several days. Exposing the model to additional observations may produce more stable results as the parameters for the best fit are estimated by the Bayesian routine as a function of the data that are evaluated each optimization period. However, we cannot provide a precise recommendation on the number of days to use for the optimization period as the exact length of time that ecosystem characteristics can affect metabolic rates may not be known and likely varies by location. Our example using the synthetic time series from Apalachicola Bay suggests that results were similar for the 7 and 30 day optimization period. As such, using one week of data for each optimization period is likely appropriate for this location. Using one day is not recommended given the issues stated above (i.e., unstable results), whereas an optimization period longer than a month may miss important events in the time series that can affect the metabolic estimates.

The EBASE R package can also accommodate missing observations in the input data. This allows the estimation of metabolic rates for time series that cover relatively long periods of time (e.g., more than year), when data gaps are likely to occur for several reasons (e.g., equipment malfunction, routine maintenance, etc.). The R package accommodates data gaps using linear interpolation for any required parameter used by EBASE. This allows the Bayesian routine to provide continuous estimates across the time series. The results are then post-processed such that any metabolic estimates that exceed a threshold for interpolated observations are removed from the output. The analyst can determine the appropriate length of time to use for excluding results based on interpolated values. The default setting for EBASE is 12 hours, where results for an entire optimization period are removed if any interpolated period exceeded 12 hours. Although this does not apply to the synthetic time series, some of the estimates using the 2012 observed data for Apalachicola Bay were excluded from the analysis. This feature allows EBASE to be used more readily because an analyst does not need to manually screen data that include missing values.

* Primary modifications (Production is linearly related to PAR (aPAR), not saturation point Respiration is constant (not temp dependent), Uses a gas exchange commonly used in oceanic systems (not littoral - streams/lakes as in Grace))
* Describe how EBASE deals with gaps and flexibility of the model to accommodate diff optimization periods
* b is sketchy, how to improve? Either fix or develop JAGS model further to include additional data, e.g. tidal height.
* detiding
* other main conclusions (from RGN comments on draft?)

## 5 Comments and Recommendations

## Acknowledgments

## Figures

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| Figure 1: The default prior distributions for , , and used in EBASE. All priors are normal distributions and truncated to positive values. is also truncated to a maximum of 0.502. |

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| Figure 2: Synthetic time series for one year of continuous data at Apalachicola Bay. Synthetic input to EBASE was the (a) dissolved oxygen time series, with results compared to the (b) synthetic parameter and (c) synthetic metabolic estimates for gross primary production (P), ecosystem respiration (R), and gas exchange (D). The parameter is shown as an areal value for comparison with the metabolic results. The parameter is also fixed at 0.251 and is not shown. |

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| Figure 3: Comparison of EBASE results to a synthetic time series created with known metabolic parameters. Results are compared for unique combinations of prior distributions and optimization period. The means () and standard deviations () are evaluated as low (L) or high (H) values (see text for details) and the optimization period is one day, seven days, or thirty days. The metabolic results for dissolved oxygen (DO), gross primary production (P), ecosystem respiration (R), gas exchange (D), and the parameter are evaluated based on Nash-Sutcliffe Efficiency (NSE) values between the EBASE results and synthetic values. NSE values from zero to one (green) indicate EBASE has recovered the synthetic parameters with values closer to 1 being a better approximation, whereas negative values indicate the mean of the synthetic data is a better predictor than EBASE. The color scale for NSE is also exponentially transformed to minimize the influence of large negative values on the visual display. The parameter is a fixed constant and was not evaluated. Rankings of each combination as the median NSE value across all parameters in a row are shown on the right, with the top three as black/bold and bottom three as black/italic. |

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| Figure 4: Summaries of median Nash-Sutcliffe Efficiency (NSE) values across all parameters for the comparisons of EBASE and synthetic model outputs separated by different combinations of prior values. Each result on the x-axis represents the median values for which the combination prior applies, e.g., all results from [Figure 3](#fig-priorcomp) where is high or low for the parameter using a one day optimization period. Point size represents the inter-quartile range of median NSE values for each result. |

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| Figure 5: Comparison of EBASE results for the best and worst performing models to a synthetic time series created with known metabolic parameters. The best and worst performing models for the one day (a, b), seven day (c, d), and thirty day (e, f) optimization periods are based on the EBASE results with prior distributions that produced the highest and lowest median Nash-Sutcliffe Efficenciy values across all parameter estimates ([Figure 3](#fig-priorcomp)). The results are averaged at the time step of the model optimization period. The parameter is fixed at 0.251 . |

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| Figure 6: Comparisons of daily metabolic estimates from the EBASE and Odum methods for one year of continuous monitoring data at Apalachicola Bay. Results for net ecosystem metabolism (NEM), gross primary production (P), ecosystem 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 areal as mmol O m d. Black lines show the 1:1 comparison and the red lines show the linear regression fit. |

## Tables

**Table** **:** EBASE model parameters showing the required input, parameters derived from the model input, and model output. The model notation for production, respiration, and gas exchange shows both the simple parameter name and the full model component used to estimate the parameter.

| Type | Description | Model notation | Units |
| --- | --- | --- | --- |
| Input |  |  |  |
|  | Dissolved oxygen |  |  |
|  | Water temperature | - |  |
|  | Salinity | - |  |
|  | Total photosynthetically active radiation |  |  |
|  | Wind speed | - |  |
|  | Water column depth |  |  |
| Input-derived |  |  |  |
|  | Wind speed at 10 meter height, squared |  |  |
|  | Schmidt number (from water temperature and salinity) |  | unitless |
|  | Dissolved oxygen at saturation (from water temperature and salinity) |  |  |
| Output |  |  |  |
|  | Dissolved oxygen (modelled) |  |  |
|  | Production |  |  |
|  | Respiration |  |  |
|  | Gas exchange |  |  |
|  | Light efficiency |  |  |
|  | b |  |  |

**Table** **:** Summary statistics of daily metabolic estimates comparing the EBASE and Odum methods for net ecosystem metabolism (NEM), gross primary 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 root mean square error (RMSE) 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 | Estimate |  |  | Slope |  |
| --- | --- | --- | --- | --- | --- |
| Observed |  |  |  |  |  |
|  | NEM | 0.35\*\* | -8.22\* | 0.78 | 46.56 |
|  | P | 0.46\*\* | 9.37 | 0.82 | 74.51 |
|  | R | 0.3\*\* | 22.97\* | 0.73\* | 95.84 |
|  | D | 0.68\*\* | 9.54\*\* | 0.67\*\* | 12.35 |
| Detided |  |  |  |  |  |
|  | NEM | 0.16\* | -22.49\*\* | 0.24\*\* | 21.15 |
|  | P | 0.71\*\* | 6.35\*\* | 1.23\*\* | 16.44 |
|  | R | 0.44\*\* | 28.09\*\* | 0.84 | 30.68 |
|  | D | 0.19\*\* | 21.6\*\* | 0.27\*\* | 20.03 |
| \* p < 0.05, \*\* p < 0.005 | | | | | |

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