

# Inverse Oxygen Model

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## Oxygen process model

Start with a mass balance equation for oxygen concentration  $C$ :

$$\frac{\delta VC}{\delta t} = - \left( \frac{\delta q_x}{\delta x} + \frac{\delta q_y}{\delta y} + \frac{\delta q_z}{\delta z} \right) + S$$

where:  $V$  = volume  $C$  = concentration  $q$  = mass fluxes due to advective and dispersive transport  $S$  = sinks and sources

Assume: Uniform flow/well mixed water column:

$$\begin{aligned} \frac{\delta q_x}{\delta x} + \frac{\delta q_y}{\delta y} &= 0 \\ \frac{\delta VC}{\delta t} &= - \frac{\delta q_z}{\delta z} + S \end{aligned}$$

Integrate with respect to  $z$  and define fluxes per unit ground area  $A$  assuming the channel is rectangular with a depth of  $D$

$$\frac{\delta D\bar{C}}{\delta t} = q(D) - q(0) + \int_0^D S dz$$

where:  $\bar{C}$  is the depth-averaged concentration,  $q(D) = k(C_{sat} - \bar{C})$  is the exchange of oxygen with the atmosphere  $B(t) = -q(0) + \int_0^D S dz$  represents biological production and consumption of oxygen

So we can describe the biological time series as a function of  $\bar{C}(t)$ , depth, discharge, and riverbed slope using empirical equations:

$$B(t) = \frac{d(D\bar{C})}{dt} - k(C_{sat} - \bar{C})$$

## Example Stream:

## New Hope Creek

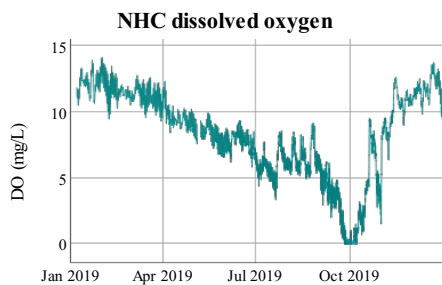
```
##
## -- Column specification -----
## cols(
```

```

## .default = col_double(),
## DateTime_UTC = col_datetime(format = ""),
## site = col_character(),
## Nitrate_mgL = col_logical(),
## Light_lux = col_logical(),
## Light2_lux = col_logical(),
## Light3_lux = col_logical(),
## WaterTemp2_C = col_logical(),
## underwater_lux = col_logical(),
## SpecCond_uScm = col_logical(),
## solar.time = col_datetime(format = "")
## )
## i Use 'spec()' for the full column specifications.

## Warning: 105418 parsing failures.
## row      col      expected actual
## 1674 Nitrate_mgL 1/0/T/F/TRUE/FALSE 0.1341 'C:/Users/Alice Carter/git/nhc_50yl/NHC_2019_metabolism/d
## 1675 Nitrate_mgL 1/0/T/F/TRUE/FALSE 0.1324 'C:/Users/Alice Carter/git/nhc_50yl/NHC_2019_metabolism/d
## 1676 Nitrate_mgL 1/0/T/F/TRUE/FALSE 0.1289 'C:/Users/Alice Carter/git/nhc_50yl/NHC_2019_metabolism/d
## 1677 Nitrate_mgL 1/0/T/F/TRUE/FALSE 0.1163 'C:/Users/Alice Carter/git/nhc_50yl/NHC_2019_metabolism/d
## 1678 Nitrate_mgL 1/0/T/F/TRUE/FALSE 0.1369 'C:/Users/Alice Carter/git/nhc_50yl/NHC_2019_metabolism/d
## ....
## See problems(...) for more details.

```



$$/dx + dq_y/dy + dq_z/dz) + S$$

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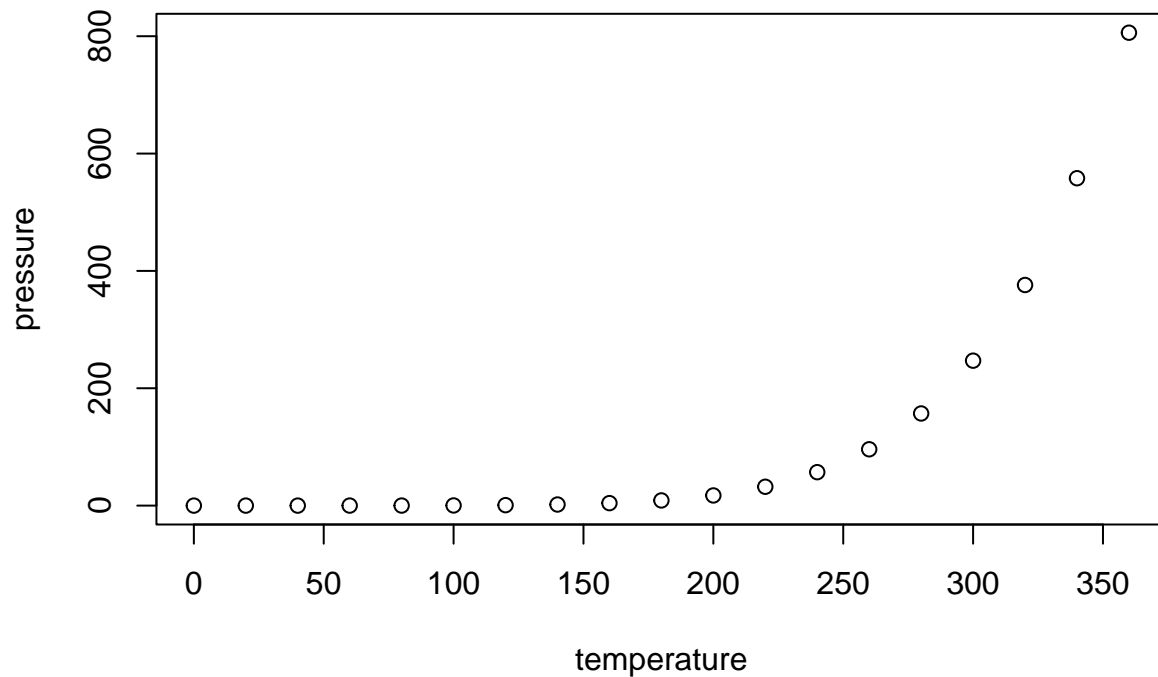
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.    : 2.00
## 1st Qu.:12.0    1st Qu.: 26.00
##  Median:15.0    Median : 36.00
##   Mean  :15.4    Mean   : 42.98
## 3rd Qu.:19.0    3rd Qu.: 56.00
##   Max.  :25.0    Max.    :120.00
```

## Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.