```
# * Adapt variable names below to your biogeochemical model (here: PISCES)
# * Make modelled chlorophyll and light are available to EAT by calling eatpy.models.GOTM
    with argument diagnostics in state=[CHL NAME, LIGHT NAME]
# * Link the new chlorophyll metric to observations with
    experiment.add observations(CHL NAME + " 10D", <FILE>)
CHL NAME = "total chlorophyll calculator result"
LIGHT NAME = "optics etot ndcy"
class ChlorophyllUptoOpticalDepth(eatpy.Plugin):
    def initialize(self, variables: Mapping[str, Any], ensemble size: int):
        # Get references to variables with chlorophyll, light, layer thickness
        self.chl = variables[CHL NAME]
        self.light = variables[LIGHT NAME]
        self.h = variables["h"]
        # Add a new variable for chlorophyll averaged over the first optical depth
        variables[CHL NAME + " 10D"] = self.chl sf = {
            "long name": "chlorophyll averaged over 1st optical depth",
            "units": self.chl["units"],
            "length": 1,
        }
    def before analysis(self, *args, **kwargs):
        # Obtain model values for chlorophyll, light, layer thickness.
        # All three have shape (nensemble, nlayer)
        chl = self.chl["data"]
        light = self.light["data"]
        h = self.h["data"]
        # Select only layers with light exceeding 1/e of surface value,
        # as representative for water-leaving irradiance (https://doi.org/10.1364/ao.14.000413)
        # Average chlorophyll over these layers, accounting for variable layer thickness
        select = light > np.exp(-1.0) * light[:, -1:]
        chl int = (chl * h).sum(axis=1, where=select)
        h int = h.sum(axis=1, where=select)
```

Plugin that calculates chlorophyll averaged over the first optical depth

To use it: