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import eatpy

# Make the model diagnostic for total chlorophyll available by adding it to the model state.
# This enables us to assimilate chlorophyll observations.
experiment = eatpy.models.GOTM(diagnostics_in_state=["total_chlorophyll_calculator_result"])

# Set up ensemble data assimilation using the Error Subspace Transform Kalman Filter
# (Nerger et al., 2012; https://doi.org/10.1175/MWR-D-11-00102.1)
filter = eatpy.PDAF(eatpy.pdaf.FilterType.ESTKF)

# Identify biogeochemical state variables by checking for an underscore in their name.
# (FABM variable names contain at least one underscore; GOTM physical variable names do not)
bgc_variables = [v for v in experiment.variables if "_" in v]

# Restrict the filter to operating on temperature, salinity and all biogeochemical state variables.
# Notably, other physical variables such as water velocities and turbulent quantities are
# thus not affected by assimilation.
experiment.add_plugin(eatpy.plugins.select.Select(include=["temp", "salt"] + bgc_variables))

# Log-transform all biogeochemical variables. Any associated observations have already been
# log-transformed in preprocessing (therefore, transform_obs=False)
experiment.add_plugin(eatpy.plugins.transform.Log(*bgc_variables, transform_obs=False, minimum=1e-12))

# Link remotely sensed surface temperature and chlorophyll observations to their model
# equivalents. In both cases, the value in the top layer of the model is used.
# This is the *last* model layer in GOTM, specified by index -1.
experiment.add_observations("temp[-1]", "cci_sst.dat")
experiment.add_observations("total_chlorophyll_calculator_result[-1]", "cci_chl.dat")

# Run the experiment
experiment.run(filter)
```