

1 Bayesian calibration for the Arctic sea ice biomarker IP₂₅

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4 **Key Points:**

- 5 A new ln(IP₂₅) index is proposed for fully quantitative sea ice reconstruction based on
IP₂₅ and associated phytoplankton biomarkers.
- 6 Using a pan-Arctic core-top biomarker database, a Bayesian model is developed to cal-
ibrate the proxy nonlinearly to sea ice concentration.
- 7 The calibration considers the non-stationary proxy seasonality and the influence of salin-
ity for more accurate palaeoclimate inference.

Abstract

Sea ice plays multiple important roles in regulating the global climate. Rapid sea ice loss in the Arctic has been documented over recent decades, yet our understanding of long-term sea ice variability and its feedbacks remains limited by a lack of quantitative sea ice reconstructions. The sea ice diatom-derived biomarker IP₂₅ has been combined with sterols produced by open-water phytoplankton in the PIP₂₅ index as a sea ice proxy to achieve semi-quantitative reconstructions. Here, we analyse a compilation of over 600 published core-top measurements of IP₂₅ paired with brassicasterol and/or dinosterol across (sub-)Arctic oceans to calculate a new ln(PIP₂₅) index that correlates non-linearly with sea ice concentration. Leveraging sediment trap and sea ice observational studies, we develop a spatially varying Bayesian calibration (*BaySIC*) for ln(PIP₂₅) to account for its non-stationary relationship with sea ice concentration and other environmental drivers (e.g. sea surface salinity). The model is fully invertible, allowing probabilistic forward modelling of the ln(PIP₂₅) index as well as inverse modelling of past sea ice concentration with bi-directional uncertainty quantification. *BaySIC* facilitates direct proxy-model comparisons and palaeoclimate data assimilation, providing the polar proxy constraints currently missing in climate model simulations and enabling, for the first time, fully quantitative Arctic sea ice reconstructions.

Plain Language Summary

A lipid termed IP₂₅ is produced by microorganisms residing in Arctic sea ice and deposited in underlying sediments. By measuring its concentration in sediment cores, palaeoclimatologists can interpret past sea ice conditions at the core locations. When multiple cores across the Arctic are analysed, palaeo sea ice extents can be reconstructed. This study refines the quantitative relationship of this proxy with sea ice, taking into account seasonal biases and other influencing environmental factors. A Bayesian (probabilistic) approach is used to quantify the uncertainties in the calibration. The new model enables quantitative Arctic sea ice reconstructions and helps us understand its long-term variability.

1 Introduction

Sea ice is a key component of the climate system, affecting planetary albedo (Curry et al., 1995), air-sea gas and heat exchanges (Ivanov et al., 2019; Rysgaard et al., 2011), and the thermohaline circulation (Mauritzen & Häkkinen, 1997), with impacts extending far beyond the polar regions. In recent decades, rising temperatures in the Arctic, caused by anthropogenic greenhouse gas emissions and amplified by the ice-albedo feedback, have led to rapid sea ice loss (Stroeve & Notz, 2018), yet our understanding of its long-term variability remains limited by our short-term observations (de Vernal et al., 2020). Furthermore, future projections for the Arctic Ocean suggest that it will become practically ice-free in summer at least once before the year 2050 under all emission scenarios, but the multi-model spread in simulated sea ice extent remains wide (Notz & SIMIP Community, 2020). To better understand changes in sea ice and associated feedbacks, as well as to improve predictions, quantitative palaeo sea ice reconstructions are needed.

Numerous proxies in marine sediment cores have been used to infer past sea ice conditions (e.g. de Vernal, Gersonde, et al., 2013), among which IP₂₅ (Ice Proxy with 25 carbon atoms) is one of the most commonly employed. The highly branched isoprenoid (HBI) monoene is produced by sympagic diatoms during the spring sea ice algal bloom and released into the water column in early summer when sea ice melts (Belt et al., 2007, 2008, 2013; Brown et al., 2011, 2016). Having been detected in sediments across the Arctic, IP₂₅ has been used as a proxy for seasonal sea ice in palaeo reconstructions extending as far back in time as the late Miocene (Stein et al., 2016). Within the Arctic and sub-Arctic regions, the absence of IP₂₅ has been attributed to two opposing scenarios. On the one hand, it may reflect year-round ice-free conditions, which do not support the growth of IP₂₅ producers (Belt et al., 2007; Belt & Müller, 2013; Müller et al., 2011). On the other hand, perennial sea ice cover has been hypothesised to hinder diatom growth by reduced light penetration through thick and dense ice (Belt et al., 2007; Belt & Müller, 2013; Müller

60 et al., 2009, 2011). This would limit the presence of IP₂₅ close to the ice edge or in the marginal
61 ice zone (MIZ; Müller et al., 2009, 2011).

62 To differentiate between the two contrasting sea ice conditions that preclude IP₂₅ produc-
63 tion, pelagic phytoplankton biomarkers have been used as indicators of (seasonal) open water con-
64 ditions (e.g. Müller et al., 2009, 2011; Navarro-Rodriguez et al., 2013; Volkman, 1986; Volkman
65 et al., 1998). These include brassicasterol (24-methylcholesta-5,22E-dien-3 β -ol) and dinosterol
66 (4 α ,23,24-trimethyl-5 α -cholest-22E-en-3 β -ol), which are mainly derived from diatoms, hapt-
67 ophytes, cryptophytes, and dinoflagellates during the summer phytoplankton bloom (e.g. Goad
68 et al., 1983; Volkman, 1986; Volkman et al., 1993, 1998). Müller et al. (2011) first proposed cou-
69 pling them with IP₂₅ in the PIP₂₅ (phytoplankton-IP₂₅) index to achieve quantitative sea ice re-
70 constructions. The index is calculated as follows:

$$\text{PIP}_{25} = \frac{[\text{IP}_{25}]}{[\text{IP}_{25}] + c \text{ [phytoplankton biomarker]}}, \quad (1)$$

71 where c is conventionally taken as the ratio of the mean IP₂₅ and phytoplankton biomarker con-
72 centrations of the sediment samples under study. This factor was introduced to compensate for
73 the substantial difference between the concentrations of IP₂₅ and phytoplankton biomarkers: the
74 former is typically lower, ascribed to its source-specificity in contrast to the multiple origins of
75 the latter (Müller et al., 2011; Navarro-Rodriguez et al., 2013).

76 The PIP₂₅ index is, by definition, limited between 0 and 1. As described by Belt and Müller
77 (2013), high PIP₂₅ values result from high IP₂₅ and low sterol concentrations, indicative of pre-
78 dominantly ice-covered conditions; conversely, low PIP₂₅ values arise from low IP₂₅ and high
79 sterol concentrations, which suggest mostly ice-free conditions. Intermediate PIP₂₅ values are
80 taken to represent ice-margin conditions. In addition to distinguishing between opposite sea sur-
81 face conditions, the sterols serve a second role in the PIP₂₅ index as proxies for productivity in
82 the surface ocean (Müller et al., 2011; Belt & Müller, 2013). By normalising IP₂₅ against pri-
83 mary productivity, PIP₂₅ indices can be compared across different Arctic regions.

84 To realise the full potential of the PIP₂₅ index in quantitative Arctic sea ice reconstructions,
85 a robust calibration is needed. Since the initial [calibration correlation reported](#) by Müller et al. (2011),
86 numerous studies have been undertaken to improve and validate the model's applicability in dif-
87 ferent regions (e.g. Kolling et al., 2020; Navarro-Rodriguez et al., 2013; Stoyanova et al., 2013;
88 Xiao et al., 2013, 2015) and in deep time (e.g. Hoff et al., 2016; Knies et al., 2014; Kremer, Stein,
89 Fahl, Bauch, et al., 2018; Kremer, Stein, Fahl, Ji, et al., 2018; Stein & Fahl, 2013; Stein et al., 2016,
90 2017), yet problems associated with the c factor and regional variability persist, hindering the
91 wider use of this proxy. Furthermore, while possible influences of other environmental variables
92 (e.g. salinity) on biomarker production and preservation have been acknowledged (Belt, 2018;
93 Ribeiro et al., 2017; Xiao et al., 2013, 2015), they have rarely been included in calibrations, po-
94 tentially underrating the aptness of PIP₂₅ for reconstructing sea ice conditions (Su et al., 2022).
95 As new biomarker datasets continue to be published and our understanding of the proxy system
96 evolves, existing calibrations need to be revisited to take into account such evidence and insights,
97 which may further help address previously identified issues.

98 At the same time, recent advances have been made in proxy system model (PSM) devel-
99 opment using Bayesian statistical methods, with forward and inverse models developed for sev-
100 eral commonly used marine geochemical palaeoclimate proxies (e.g. Malevich et al., 2019; Tier-
101 ney & Tingley, 2014, 2018; Tierney et al., 2019). The probabilistic approach employed by these
102 models enables more rigorous quantification of calibration uncertainties and their propagation
103 into proxy estimates or climate reconstructions. In addition, such PSMs facilitate proxy-model
104 comparisons (e.g. Hoem et al., 2022) and palaeoclimate data assimilation (e.g. Osman et al., 2021),
105 allowing the use of proxy data to validate or constrain model simulations.

106 Here, we develop a Bayesian calibration for IP₂₅ (and associated phytoplankton biomark-
107 ers) to model the relationship between the sea ice proxy and environmental factors using recently

108 compiled pan-Arctic biomarker, sea ice and oceanographic variable datasets, with The Bayesian
 109 framework supports uncertainty quantification and propagation to model predictions in both the
 110 forward and inverse directions. The model, called *BaySIC* (Bayesian Sea Ice Concentration),
 111 is amenable to incorporating additional core-top data as they become available, as well as other
 112 environmental drivers that may be identified in future investigations. We demonstrate its appli-
 113 cations with examples and discuss implications for palaeo-sea ice reconstruction.

114 **2 Data Compilation**

115 **2.1 Biomarkers in Surface Sediments**

116 We update the pan-Arctic surface biomarker database of Kolling et al. (2020) (Belt et al.,
 117 2013, 2015; Méheust et al., 2013; Müller et al., 2011; Navarro-Rodriguez et al., 2013; Pieńkowski
 118 et al., 2017; Smik et al., 2016; Xiao et al., 2013, 2015) with paired IP₂₅-brassicasterol and -dinosterol
 119 core-top measurements from recent literature (Harning et al., 2023), including the location (wa-
 120 ter depth, latitude, longitude), total organic carbon (TOC) content, and concentrations of the biomark-
 121 ers normalised to gram of sediment (µg/gSed) and/or TOC (µg/gTOC). The expanded database
 122 consists of 644 surface sediment samples collected between 38.00°N and 89.98°N and across the
 123 full range of longitudes (figure 1; dataset S1). Samples within the same sea ice grid cell (see sec-
 124 tion 2.2) are averaged to avoid overrepresenting densely sampled areas. This results in 551 ef-
 125 fective core-top samples with paired IP₂₅-brassicasterol measurements and 432 with paired IP₂₅-
 126 dinosterol measurements for our calibration model.

127 A dataset published by Stoynova et al. (2013) was excluded from the Kolling et al. (2020)
 128 database as it was obtained with different biomarker extraction solvents and method, and con-
 129 tained measurements inconsistent with those of other studies in the same area (e.g. Navarro-Rodriguez
 130 et al., 2013; Xiao et al., 2015). More recently, a dataset for the East Siberian Sea was made avail-
 131 able by Su et al. (2022). However, it records distinct brassicasterol and dinosterol distributions,
 132 with the former more closely resembling the IP₂₅ distribution. The authors hypothesised that the
 133 divergence emerged from differential impacts of estuarine turbidity on the respective sterol pro-
 134 ducers, but this is not observed in other datasets from river mouth settings (e.g. Xiao et al., 2013,
 135 2015). In comparing the brassicasterol/dinosterol ratio of each dataset, we find that the Su et al.
 136 (2022) data deviates from the rest of the database (figure S1). Since the cause of this discrepancy
 137 remains conjectural, we refrain from incorporating this dataset into our database.

138 As biomarker concentrations are affected by sedimentation rates, it has been recommended
 139 that they be normalised to TOC contents prior to comparisons across space and time (Müller et
 140 al., 2011). The PIP₂₅ index approach further circumvents comparing absolute concentrations by
 141 considering relative concentrations. When calculating PIP₂₅, the same normalisation should be
 142 applied to both the phytoplankton biomarker and IP₂₅ concentrations. Since the normalisation
 143 factors are cancelled out in the ratios (Belt, 2018), PIP₂₅ indices computed from measurements
 144 normalised in either way are directly comparable. However, as the biomarker concentrations are
 145 typically several magnitudes lower when normalised to gram of sediment rather than TOC con-
 146 tent, the reported measurements are less precise, especially near the detection limit. We there-
 147 fore use measurements reported in µg/gTOC where available for our calibration.

148 Both brassicasterol and dinosterol are commonly used as the phytoplankton biomarker in
 149 the PIP₂₅ index (P_B IP₂₅ and P_D IP₂₅, respectively) and, in general, their distributions are similar
 150 across the Arctic (figure 1). However, the sources of brassicasterol are more diverse than those
 151 of dinosterol: the former is produced by a range of marine and freshwater phytoplankton as well
 152 as higher plants (Volkman, 1986), while the latter is mainly synthesised by marine dinoflagel-
 153 lates (Nichols et al., 1984; Volkman et al., 1993, 1998). Brassicasterol found in marine sediments
 154 may have been transported by rivers from a lacustrine or terrestrial origin (Fahl et al., 2003; Hörner
 155 et al., 2016), thus appearing in higher concentrations than expected for the local sea surface con-
 156 ditions. Brassicasterol may also originate from sea ice diatoms (Belt et al., 2013, 2018), poten-
 157 tially undermining its role as an open ocean proxy. We develop calibrations for both P_B IP₂₅ and

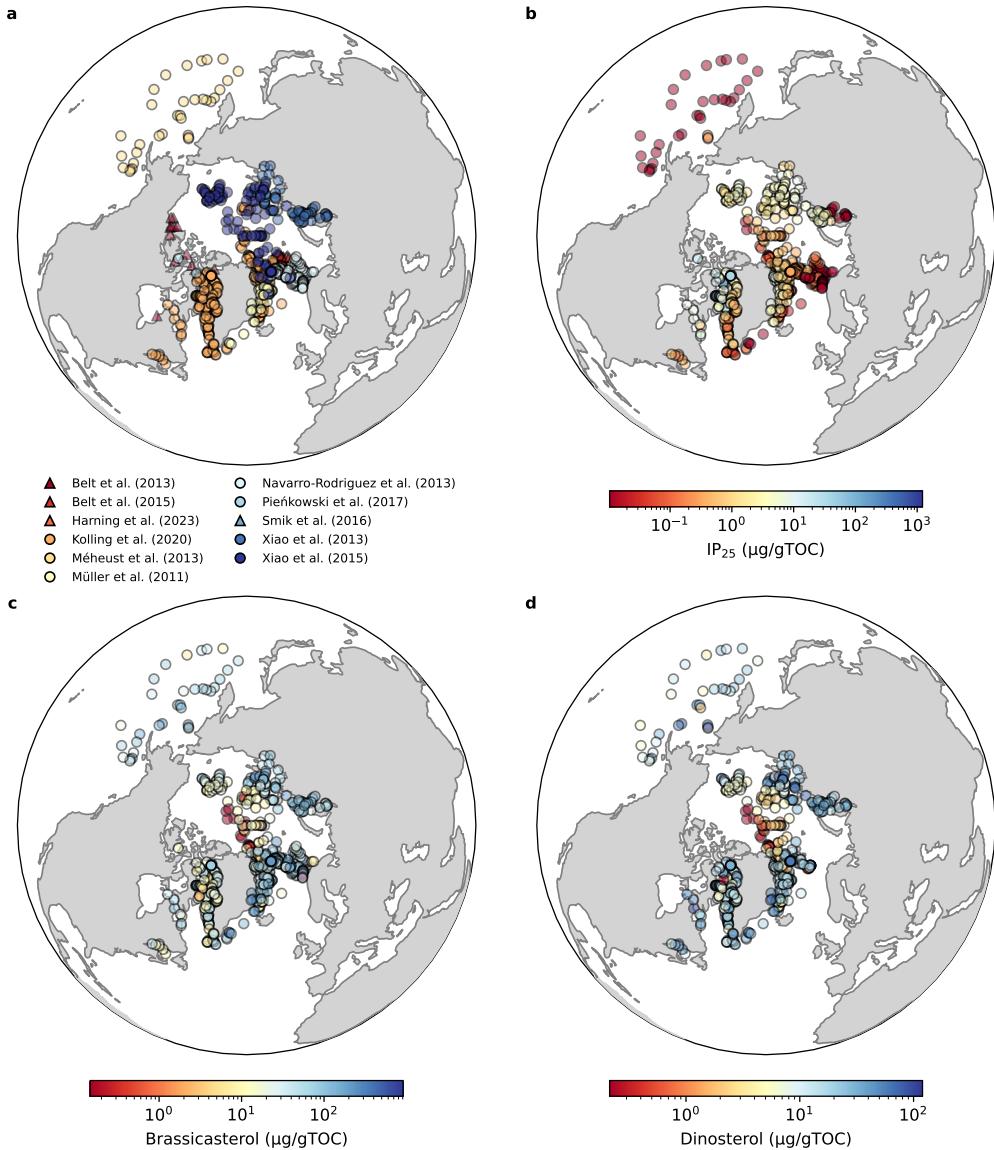


Figure 1. Locations of published core-top paired IP₂₅ and brassicasterol and/or dinosterol measurements, coloured by (a) study of origin, and concentration of (b) IP₂₅, (c) brassicasterol, and (d) dinosterol, normalized to total organic carbon content (µg/gTOC). In (a), triangle = concentration normalised to gram of sediment only, and circle = concentration normalised to TOC content also available.

158 P_DIP₂₅ but, due to the broader and more variable sources of brassicasterol, focus the discussion
 159 on the latter.

160 We note that the sterol extraction method (with dichloromethane/methanol) used across all
 161 studies has recently been suggested to underestimate concentrations (Köseoglu, 2019) (figure S2).
 162 However, since sterol data obtained with the more comprehensive method (using potassium hy-
 163 droxide) remain limited, and as only relative concentrations are of importance for their role as
 164 a normalisation factor in the PIP₂₅ index, measurements acquired with the conventional method
 165 are used here for the calibrations in order to investigate Arctic-wide trends and to maintain con-
 166 sistency across datasets. Should sufficient data collected with the saponification step become avail-
 167 able in the future, the calibrations may be updated to correct for any inaccuracies in the existing
 168 core-top sterol concentrations.

169 2.2 Sea Ice

170 Sea ice concentrations (SIC) corresponding to the core-top measurements are taken from
 171 the NOAA/NSIDC Climate Data Record of Passive Microwave Sea Ice Concentration, Version
 172 4 (Meier et al., 2021). The data are on a 25 km × 25 km grid and represent the percentage of ocean
 173 surface area covered by sea ice. For each core location, the monthly SIC from January 1979 to
 174 December 2022 in the nearest grid cell are drawn. The great-circle distance between each biomarker
 175 measurement and SIC observation is less than 100 km in all but seven cases. Among these, six
 176 samples are taken from locations in the North Pacific Ocean beyond the data coverage. The matched
 177 SIC data indicate year-round ice-free conditions, as expected for these localities; thus, the sam-
 178 ples are retained in our analysis. The remaining sample in Lake Melville is paired with SIC data
 179 for the ocean and is consequently excluded from the database. Climatologies are created by com-
 180 puting the mean monthly SIC from 1979 to 2000 and from 1979 to 2022. In each case, the in-
 181 terquartile range (IQR) is also computed as a non-parametric measure of year-to-year sea ice vari-
 182 ability.

183 Complementary SIC datasets are obtained from the Gridded Monthly Sea Ice Extent and
 184 Concentration product, Version 2 (Walsh et al., 2019), which combines various historical sources
 185 such as ship reports, maps by oceanographers, charts from meteorological institutes, etc. to pro-
 186 vide an Arctic-wide SIC record from 1850 onwards. The data are on a 1/4° × 1/4° grid, and the
 187 same procedures are followed to produce climatologies for the core locations. Since the prod-
 188 uct builds on more complete sea ice observations from 1953, we generate climatologies from 1950
 189 to 2000 and from 1950 to 2017.

190 2.3 Sediment Trap Time Series

191 To explore proxy seasonality, we also collate measurements of IP₂₅ fluxes in nine sediment
 192 traps deployed across the Arctic (Bai et al., 2019; Belt et al., 2008; Gal et al., 2022; Koch et al.,
 193 2020; Luostarinen et al., 2023; Nöthig et al., 2020; Rontani et al., 2016) (figure 2). Where mul-
 194 tiple traps positioned at the same location are found, data from the deepest one are taken to more
 195 closely reflect the fluxes that eventually reach the sediments. Each trap has a different sampling
 196 period, ranging from one month to a year (see table S1 for details). We focus on the spring and
 197 summer months, when IP₂₅ is produced and released. Since the time series are approximately
 198 normally distributed, we fit a normal probability density function (PDF) to each of them to fa-
 199 cilitate composite analysis. Monthly SIC during the sampling period are extracted from the NOAA/NSIDC
 200 record. In each case, data from grid cells within a 100 km radius of the trap location are com-
 201 piled to assess regional sea ice variability and to account for lateral advection (Salter et al., 2023).
 202 For sediment traps in the eastern Fram Strait, the source areas simulated by Salter et al. (2023)
 203 spanned sea ice conditions from completely ice-free to mostly ice-covered at any given time
 204 during the sampling period. To avoid dilution of the seasonal signal by lateral transport, we
 205 exclude data from this area, including those previously collected by Lalande et al. (2016), from
 206 our composite analysis.

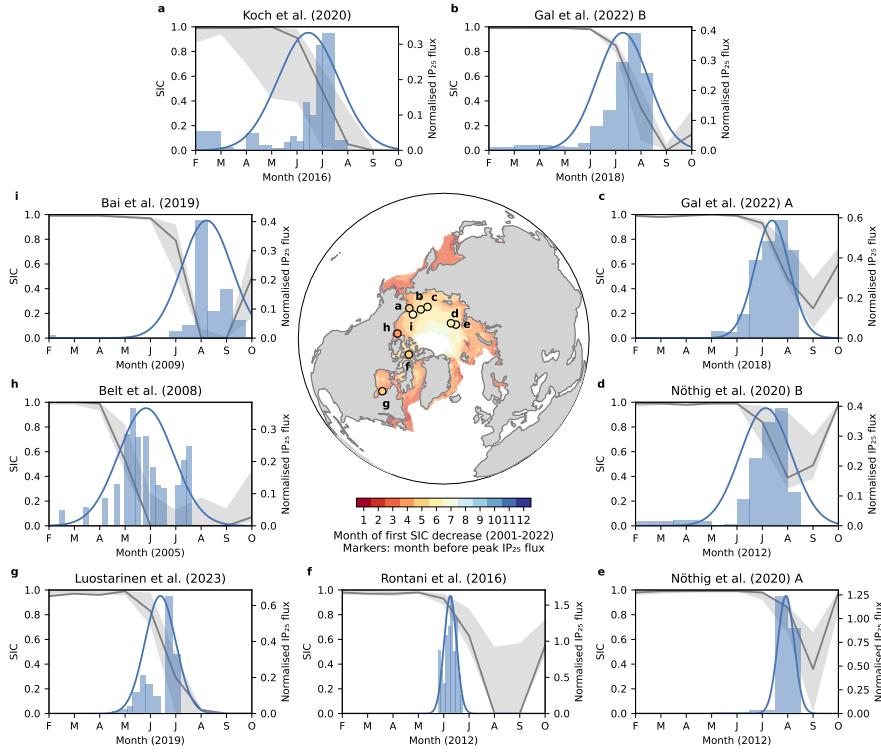


Figure 2. (a-i) Sediment-trap IP₂₅ flux time series and the fitted normal probability density function, as well as the corresponding sea ice concentration (SIC) trend and uncertainty associated with lateral transport (range of SIC found within a 100 km radius). The map shows the location of each sediment trap coloured by the corresponding timing of the peak IP₂₅ flux, and spatial variations in the timing of the first SIC decrease (2001-2022, matching the sampling periods of the sediment traps).

207 **2.4 Oceanographic Variables**

208 Environmental parameters such as temperature, salinity, and nutrient levels may promote
 209 or limit productivity, exerting additional influence on biomarker concentrations. To test for any
 210 such effects, measurements of these variables are acquired from World Ocean Atlas 2018 (Boyer
 211 et al., 2018; Garcia et al., 2019; Locarnini et al., 2019; Zweng et al., 2019). Temperature and salin-
 212 ity data are available at quarter-degree grid resolution, while silicate, nitrate, and phosphate data
 213 are available at one-degree grid resolution. Each core location is matched to the nearest grid cell
 214 to derive the monthly climatologies. For temperature and salinity, these are averages of six decadal
 215 means from 1955 to 2017; for the nutrients, these are averages of all available data. Data from
 216 the top 10 m of the water column (at 0 m, 5 m, and 10 m water depth) are averaged to represent
 217 sea surface conditions.

218 **3 Data Exploration**219 **3.1 Nonlinearity of the PIP₂₅ Index**

220 Following previous studies (e.g. Müller et al., 2011; Navarro-Rodriguez et al., 2013; Kolling
 221 et al., 2020), we investigate the relationship between PIP₂₅ and SIC by assessing their correla-
 222 tion across space in contemporary records. Existing calibrations have sought to establish a pos-
 223 itive linear relationship between the two by invoking the balance factor, *c*; however, complica-
 224 tions arise with its use. For example, the factor has been found to vary both as a function of core
 225 section and location (e.g. Belt et al., 2015; Navarro-Rodriguez et al., 2013), such that the PIP₂₅
 226 value for a given sediment sample changes with the particular dataset under consideration. This
 227 necessitates the recalculation of PIP₂₅ in each investigation that expands a previous dataset, which
 228 affects the inferred SIC. As Belt and Müller (2013) pointed out, the approach is particularly prob-
 229 lematic for applications on geologic time scales, as the *c* factor may change significantly with the
 230 length of the core under study. Furthermore, the factor is susceptible to negative impacts of out-
 231 lying biomarker measurements (Navarro-Rodriguez et al., 2013). Due to these unresolved issues,
 232 the PIP₂₅ index has thus far remained a semi-quantitative proxy for sea ice.

233 Another difficulty in applying linear calibration models for past sea ice reconstruction lies
 234 in the highly variable slope and intercept across different regions (e.g. Müller et al., 2011; Smik
 235 et al., 2016; Xiao et al., 2015). To aid interregional comparisons, Xiao et al. (2015) proposed Arctic-
 236 wide *c* values (0.11 for P_DIP₂₅), which were subsequently updated by Kolling et al. (2020) us-
 237 ing a larger dataset (0.203). Although similar values (0.238) can be calculated for our expanded
 238 database, marked regional differences persist in the linear correlation with SIC (not shown), pre-
 239 venting a pan-Arctic calibration. More generally, we show that the relationship between PIP₂₅
 240 and SIC remains nonlinear following correction across a broad range of *c* factors (figures 3a and
 241 S3). Thus, while the exact value taken for such a uniform factor may be revised by future core-
 242 top studies, it is unlikely that the relationship can ever be fully linearised.

243 In light of the problems associated with the *c* factor, we omit its use to develop a robust cal-
 244 ibration. To reduce the positive skewness of the PIP₂₅ data (calculated without *c*), we transform
 245 the ratio using the natural logarithmic function. The index then becomes:

$$\ln(\text{PIP}_{25}) = \ln\left(\frac{[\text{IP}_{25}]}{[\text{IP}_{25}] + [\text{phytoplankton biomarker}]}\right), \quad (2)$$

246 where the phytoplankton biomarker is either brassicasterol or dinosterol. Our dataset contains
 247 samples where IP₂₅ and/or the sterols are not detected. Although the biomarkers are recorded as
 248 absent in these cases, they may be present at concentrations below their respective limits of de-
 249 tection, which are expected to vary between laboratories but are rarely reported. Thus, the min-
 250 imum non-zero IP₂₅ concentration in the dataset, taken as the best approximation of the detec-
 251 tion limit, is added to all IP₂₅ measurements to enable the log transformation. The same treat-

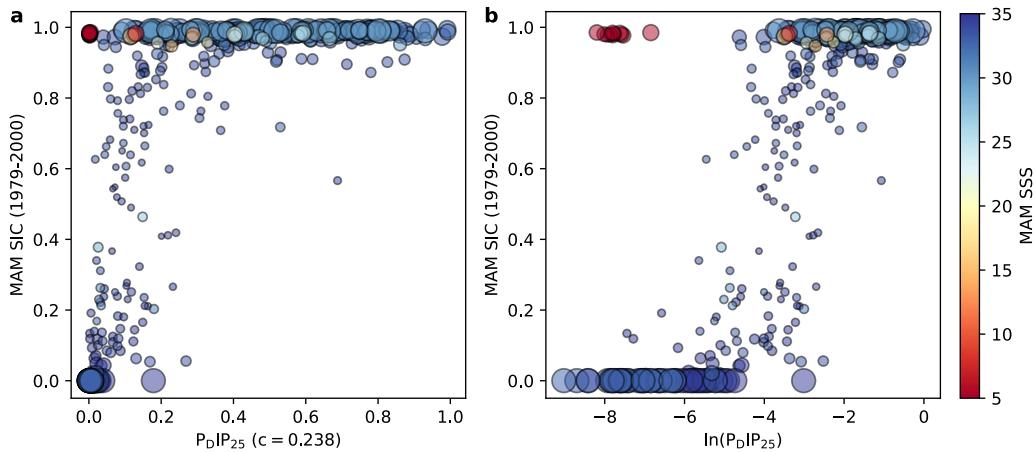


Figure 3. Mar-Apr-May sea ice concentration (SIC), 1979-2000, vs. (a) P_{DIP25} calculated with the c factor and (b) $\ln(P_{DIP25})$, coloured by sea surface salinity (SSS). Bubble size is inversely proportional to the interquartile range of the SIC over the 22-year calibration period.

ment is applied to brassicasterol and dinosterol measurements to maintain consistency in the ratio.

Using our expanded database, which includes samples from permanently ice-free and ice-covered regions in the sub-Arctic and central Arctic, we find that the new $\ln(P_{DIP25})$ index exhibits a sigmoidal (i.e., logistic-like) relationship with SIC: as $\ln(P_{DIP25})$ approaches 0, SIC tends to 1; likewise, as $\ln(P_{DIP25})$ approaches negative infinity, SIC tends to 0 (figure 3b). The suitability of the logistic function in describing the relationship can be understood intuitively, as SIC values are inherently limited between 0 and 1. There is a clear transition from SIC = 0 to 1 at $\ln(P_{DIP25}) \sim -4$, which mirrors the relatively narrow MIZ in nature. As illustrated subsequently, this abrupt shift can be well-characterised by logistic regression coefficients, enabling more effective differentiation between ice-free and ice-covered conditions based on $\ln(P_{DIP25})$ values. Nevertheless, some variability is still evident in the core-top data. This may be partly attributable to the inherent ambiguity of the P_{DIP25} ratio: the same value can be derived from coevally high or low concentrations of P_{DIP25} and sterols, caused by different sea ice conditions (Müller et al., 2011). To mitigate this, it has been recommended that individual biomarker records be interpreted along with P_{DIP25} (Belt & Müller, 2013; Müller et al., 2012).

3.2 Uncertainties in SIC Observations

As the proxy signals are taken to reflect the dominant sea ice conditions over the calibration period, $\ln(P_{DIP25})$ is compared against the climatological mean SIC. However, near the ice edge, the year-to-year variability in SIC can be significant: a location may be completely ice-covered in one year and ice-free in the next. In such cases, the core-top $\ln(P_{DIP25})$ value represents a mixture of variably recorded opposing sea ice conditions, and its relationship with the corresponding mean SIC value is uncertain. To incorporate this source of uncertainty in the calibration, we calculate the IQR of the SIC data over the calibration period as a non-parametric measure of its year-to-year variability (figure 3). Data points with high IQR values (high SIC variability) are associated with more uncertainties and thus are considered less reliable in the regression.

Although the core tops mostly sample the same sediment interval (1 cm, with exceptions in datasets from Harning et al. (2023) and Kolling et al. (2020)), as sedimentation rates across the Arctic and sub-Arctic oceans span a wide range, the samples would have accumulated over different periods, ranging from a few years to several millennia (Stein, 2008; Wegner et al., 2015).

As a result, most of the core tops represent coarse time composites that cannot be paired with SIC data over the same period. Considering the accelerated sea ice loss over the last couple of decades (Stroeve & Notz, 2018), we avoid using SIC data from this period in our calibration to prevent the potential overrepresentation of anthropogenic signals. The period 1979-2000 is hence chosen to maximise the limited satellite observations available. This means that samples recently collected from regions with high sedimentation rates (>0.1 cm/year) may be mismatched with SIC from an earlier period; however, such rapid sediment deposition is rare in the Arctic (Stein, 2008; Wegner et al., 2015). In our database, only Belt et al. (2015) reported accumulation rates of this order, for sites in the Barents Sea. In general, all matched SIC values remain estimates of the real conditions recorded by the core tops, with the largest discrepancies expected in areas that experienced dramatic SIC changes over recent decades to centuries (e.g. the MIZ). The full satellite SIC record (1979-2022) and datasets derived from historical sources (1950-2000 and 1950-2017) are also used to evaluate model sensitivity to the calibration period.

Pairing core-top biomarker measurements with SIC observations from the nearest satellite grid assumes minimal lateral transport. This assumption is valid in ice-covered regions, such as the Eurasian Basin, where vertical transport has been shown to account for the majority of the carbon fluxes to the sediments (Belt & Müller, 2013; Legendre et al., 1992; Nöthig et al., 2020). In other locations, however, lateral advection and resuspension have been found to affect biomarker fluxes, for example, on the Lomonosov Ridge (Fahl & Nöthig, 2007; Fahl & Stein, 2012) and in the eastern Fram Strait (Lalande et al., 2016; Salter et al., 2023). By modelling particle trajectories, Salter et al. (2023) showed that a source area could have a radius of approximately 100 km. This particularly complicates the interpretation of samples near the MIZ, where such a large integration area may span the full gradient of SIC values, resulting in a mixed proxy signal. In reality, due to variable lateral transport rates across the Arctic, each core top likely integrates biomarker fluxes over a different area, which may also have changed through time. As this source of uncertainty is poorly constrained, we do not explicitly include it in our model; nonetheless, it mainly affects core tops near the ice edge, which are already down-weighted in the regression based on their IQR values.

3.3 Spatiotemporal Variation in Proxy Seasonality

Given that biomarker production and IP₂₅ release primarily occur during algal blooms and ice melt, respectively (Belt et al., 2008, 2013; Brown et al., 2011, 2016), the proxies are biased towards seasonal sea ice conditions (figure 4a-b). As sympagic algal blooms, sea ice thawing, and pelagic algal blooms do not occur simultaneously, the seasonal signal recorded by ln(PIP₂₅) is a mixture of these timings and is not straightforward to characterise. Previous calibrations assumed a stationary proxy seasonality, usually towards spring (March-April-May or April-May-June, e.g. Müller et al., 2011; Navarro-Rodriguez et al., 2013; Smik et al., 2016). However, some studies also found good correlations between the PIP₂₅ index and sea ice in summer (July-August-September, e.g. Su et al., 2022; Xiao et al., 2015) or autumn (October-November-December, e.g. Kolling et al., 2020). In another study, a longer calibration interval spanning the full sea ice retreat period (March-September) similarly produced statistically significant results (Stoyanova et al., 2013). The proxy seasonality therefore remains poorly diagnosed.

In reality, the seasonal bias in the ln(PIP₂₅) index is expected to vary with location as the timing of algal blooms is determined by numerous factors, most notably light intensity and nutrient availability (e.g. Leu et al., 2015; Oziel et al., 2019), and thus is asynchronous across the Arctic (e.g. Ji et al., 2013; Leu et al., 2011). The onset of ice melt, dictated by temperature and regional atmosphere-ocean dynamics (e.g. Horvath et al., 2021; Mortin et al., 2016), also differs significantly across latitudes (e.g. Bliss & Anderson, 2018; Markus et al., 2009) (figure 2). The significant delay of these events from one region to another means that the ln(PIP₂₅) indices obtained from different cores likely reflect sea ice conditions for different months of the year.

In order to constrain this spatially varying seasonality, we analyse published IP₂₅ fluxes measured in sediment traps across the Arctic by compositing fitted PDFs and the corresponding SIC

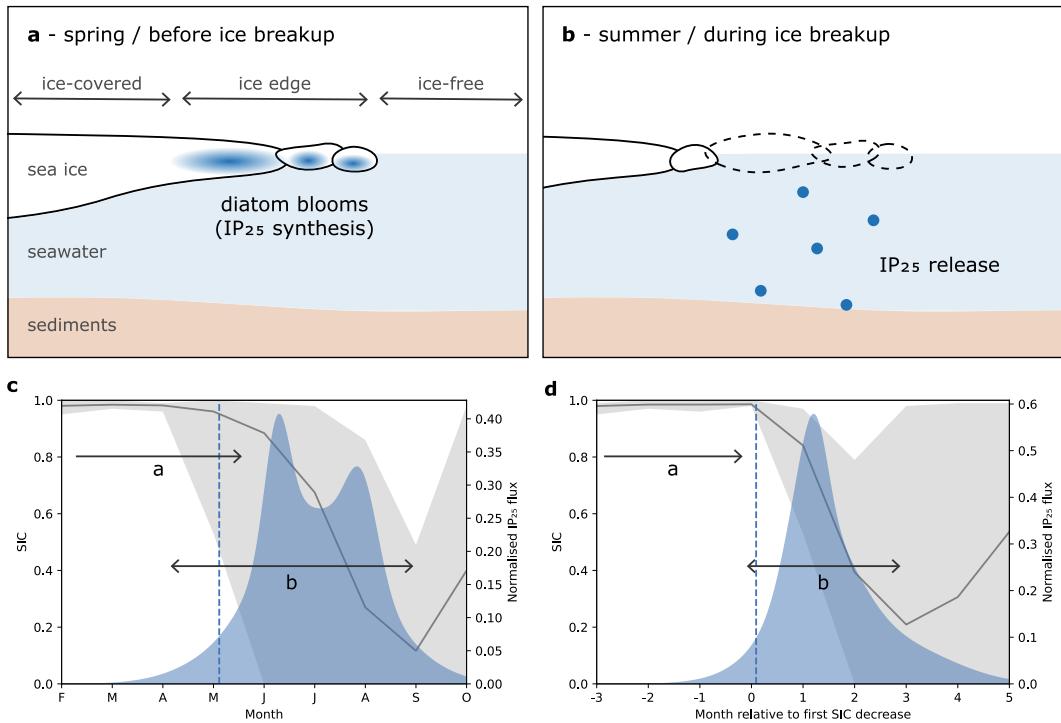


Figure 4. Schematic diagrams of the IP₂₅ proxy system (a) in spring / before sea ice breakup, and (b) in summer / during sea ice breakup, as well as composite probability density functions (PDFs) of IP₂₅ fluxes aligned to (c) calendar months and (d) months relative to the first month of sea ice concentration (SIC) decrease. Dashed line denotes the 5th percentile of the PDF. Shaded area shows the range of SIC observed across all sediment traps, and the trend line represents the error-weighted mean, calculated based on the range of SIC found within a 100 km radius of each trap during the collection period. Arrows indicate the approximate periods corresponding to those illustrated in (a-b).

records (figure 4c). The resultant PDF shows that, on average, IP₂₅ release begins in May (>95% confidence), coincident with the average initial sea ice breakup. The highest fluxes occur between June and August, concurrent with the main ice melt period, corroborating a close link between IP₂₅ deposition and sea ice thawing. For an Arctic-wide static calibration, the conventional calibration interval of March-April-May (supported by our model; see section 4.2 for details) then corresponds to the three-month interval before IP₂₅ release, reflecting IP₂₅ production in ice-edge diatom blooms prior to sea ice breakup. This suggests that IP₂₅ in the sediments records the maximum SIC before sea ice disintegration, i.e., the ln(PIP₂₅) index is biased towards the time interval immediately prior to local ice melt.

However, the timing of sea ice breakup differs significantly across the trap locations, with an offset of up to three months, and the bimodal distribution of the PDF indicates that fluxes happen in two distinct periods, both supporting a spatially varying seasonal bias. To account for local differences in the timing of ice melt, we align each time series to the month of the first SIC decrease leading to the minimum SIC of the year (figure 4d). The aligned PDF shows that IP₂₅ release begins in the same month as initial sea ice breakup (>95% confidence), with the flux peaks synchronised to the following one to two months. The tightened distribution indicates a more precise calibration interval for each sample, which can be determined quantitatively as the three-month interval before the first SIC decrease.

By identifying the proxy seasonality for every individual core, in place of an ambiguously defined "seasonal" bias for the whole Arctic, the spatially varying calibration allows for more accurate and consistent SIC reconstructions across different regions, especially on geologic timescales. While the timing of sea ice breakup at each individual site may have remained largely constant over the accumulation period of the core tops and the sediment traps, it likely differed significantly further back in time under the influence of changing orbital configurations and gateway geometries (e.g. Karami et al., 2021; Timm et al., 2008). It is then unreasonable to assume that a bias to March-April-May SIC persists throughout the reconstruction period.

For illustration of the non-stationarity in proxy seasonality through time, SIC simulations are obtained from the TraCE-21ka dataset, which employs the National Center for Atmospheric Research Community Climate System Model version 3 (NCAR CCSM3) to reconstruct the transient climate evolution over the last 21 ka (Liu et al., 2009). The monthly average ICEFRAC (equivalent to SIC) for the pre-industrial, Mid Holocene, and Last Glacial Maximum experiments are used to derive climatologies, from which the month of the first SIC decrease is calculated. As shown in figure 5, the calendar month in which SIC loss is first observed at any given location shifts with time. Thus, the intimately linked proxy seasonal bias is also expected to change, and the necessity of a varying calibration becomes evident.

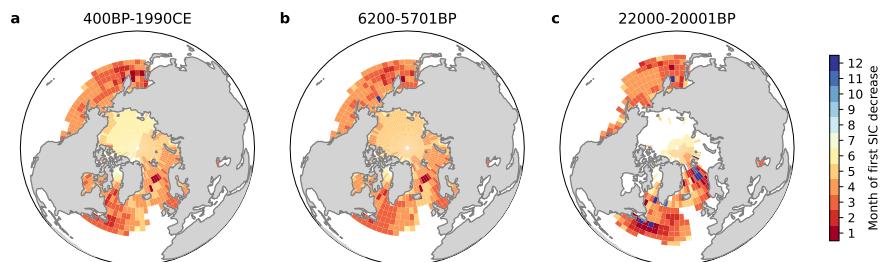


Figure 5. Spatial variations in the timing of the first sea ice concentration (SIC) decrease, derived from the TraCE-21ka experiments for the (a) pre-industrial, (b) Mid Holocene, and (c) Last Glacial Maximum.

368 **3.4 Other Environmental Drivers of $\ln(\text{PIP}_{25})$**

369 While sea ice conditions evidently control the timing and spatial distribution of IP_{25} and
 370 sterol production, other potential environmental drivers should not be neglected. For example,
 371 salinity is known to affect the productivity of sea ice algae (e.g. Glud et al., 2007; Gosselin et al.,
 372 1986; Ralph et al., 2007), with laboratory culture experiments showing that sea ice diatom growth
 373 decreases with reduced salinity (Grant & Horner, 1976; Søgaard et al., 2011; Zhang et al., 1999).
 374 Hyposaline conditions caused by freshwater discharge from large rivers have been implicated in
 375 progressively lower IP_{25} concentrations measured near estuaries in the Kara and Laptev Seas (Xiao
 376 et al., 2013) and a fjord in Northeast Greenland (Belt, 2018; Ribeiro et al., 2017). Based on ra-
 377 tios between IP_{25} and C_{25} -HBI diene, Xiao et al. (2013) suggested that saturation in HBIs may
 378 decrease with lower sea surface salinity (SSS), but research on IP_{25} sensitivity to salinity remains
 379 limited. A subsequent study by Limoges et al. (2018) found an increase in the abundance of IP_{25}
 380 producers with a slight decrease in bottom sea ice salinity, but did not preclude negative impacts
 381 of low salinity on IP_{25} synthesis.

382 In our dataset, a number of outlying samples with low $\ln(\text{PIP}_{25})$ values and high correspond-
 383 ing SIC originate from locations with low SSS values of $< 7 \text{ g kg}^{-1}$ (figure 3b). When analysing
 384 $\ln(\text{PIP}_{25})$ with SSS, we find suggestions of a logarithmic relationship between the two under ice-
 385 covered conditions, with $\ln(\text{PIP}_{25})$ decreasing exponentially as SSS lowers (figure 6a). In such
 386 cases, SSS appears to overtake SIC as the limiting factor for IP_{25} production, hindering direct in-
 387 terpretation of sea ice conditions from $\ln(\text{PIP}_{25})$ values. As SSS rises to normal levels, this trend
 388 disappears and is replaced by a strong negative correlation between $\ln(\text{PIP}_{25})$ and SSS, likely an
 389 expression of the co-variation between SSS and SIC. As relatively sparse data exist for hypos-
 390 aline settings, further research is needed to establish a robust relationship between SSS and $\ln(\text{PIP}_{25})$.
 391

392 To disentangle the influence of low SSS on $\ln(\text{PIP}_{25})$ from that of SIC in our calibration,
 393 we conduct change point analyses on the dataset sorted by SSS using the *ruptures* package (Truong
 394 et al., 2020) (see figure S4 for details). The change point is interpreted as a threshold below which
 395 SSS overshadows SIC as the dominant predictor of $\ln(\text{PIP}_{25})$. For an Arctic-wide calibration to
 396 March-April-May, the change point occurs at SSS $\sim 21.74 \text{ g kg}^{-1}$ for both P_DIP_{25} and P_BIP_{25} .
 397 For a spatially varying calibration to the three-month interval before the first SIC decrease, the
 threshold is detected at SSS $\sim 21.26 \text{ g kg}^{-1}$.

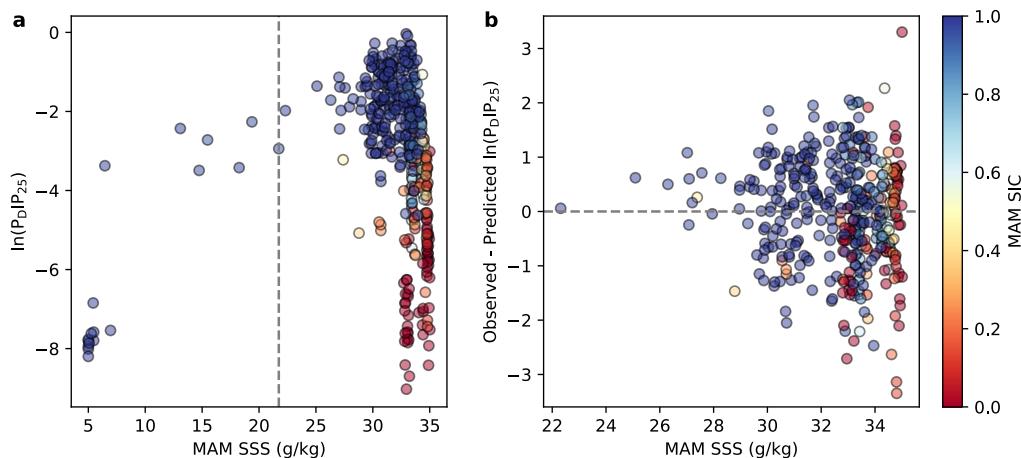


Figure 6. (a) Mar-Apr-May sea surface salinity (SSS) vs. $\ln(\text{P}_D\text{IP}_{25})$, with dashed line indicating change point (SSS ~ 21.74). (b) SSS vs. model residuals. Colours denote sea ice concentration (SIC).

More generally, as summarised by Belt and Müller (2013), sympagic algal blooms are influenced by a range of factors, including nutrient supply in the water column (e.g. Arrigo et al., 2010; Gradinger, 2009; Leu et al., 2015; Oziel et al., 2019; Rózańska et al., 2009), light availability (which is in turn regulated by the thicknesses of the ice and snow cover; e.g. Arrigo et al., 2010; Leu et al., 2015; Mundy et al., 2005; Oziel et al., 2019), and bottom ice melt rate (Castellani et al., 2017; Lavoie et al., 2005). Their effects on the production of IP₂₅ specifically, however, have not been studied in detail. Furthermore, as normalisation by phytoplankton-derived sterols in the ln(PIP₂₅) index negates, to a certain extent, the effects of nutrient levels and light intensity on biomarker synthesis (Müller et al., 2011; Stoyanova et al., 2013), and considering that sea surface temperature co-varies with SIC, the sensitivity of ln(PIP₂₅) to these variables is likely low. We therefore leave the identification of additional environmental predictors and their incorporation into the ln(PIP₂₅) calibration for future work.

4 Bayesian Calibration Model

4.1 Model Design

A Bayesian proxy system model (*BaySIC*) is developed to relate ln(PIP₂₅) to SIC based on core-top observations. Since the calibration is based on the spatial relationship between ln(PIP₂₅) and its environmental drivers, and is applied to predict temporal changes in these values, the model assumes ergodicity (Tierney & Tingley, 2014), i.e., the response of the proxy to different environments across space is taken to represent its response to environmental changes over time.

To account for the nonlinear relationship between ln(PIP₂₅) and SIC, as well as to respect the inherent limit of SIC between 0 and 1, the core-top data may be described with a logistic function:

$$\text{SIC} = \frac{1}{1 + \exp -(\beta_0 + \beta_1 \ln(\text{PIP}_{25}))}, \quad (3)$$

where SIC and ln(PIP₂₅) are vectors representing the core-top data, β_0 is the intercept, and β_1 is the slope. However, a regression model in this form considers SIC as a function of ln(PIP₂₅), which contradicts the natural causal relationship between the proxy and its environmental predictors. In nature, SIC serves as the predictor variable for ln(PIP₂₅). Assuming that the prediction errors are normally distributed, the relationship can be expressed as follows:

$$\ln(\text{PIP}_{25i}) \mid \beta_0, \beta_1, \phi \sim \mathcal{N}(g(\text{SIC}_i), \phi), \quad (4)$$

where PIP_{25i} denotes the core-top sample, SIC_i denotes the corresponding SIC data, $g(x) = \frac{-\ln(\frac{1}{x} - 1) - \beta_0}{\beta_1}$ is the inverse of equation 3, and ϕ is the variance, which is introduced by uncertainties in the SIC observations. Thus, we obtain the forward model in the following form:

$$\ln(\text{PIP}_{25i}) = \frac{-\ln(\frac{1}{\text{SIC}_i} - 1) - \beta_0}{\beta_1} + \epsilon_i, \quad (5)$$

$$\epsilon_i \sim \mathcal{N}(0, \phi), \quad (6)$$

where ϵ_i represents the residual error associated with each sample. The inverse logistic function (equation 5) has a domain of (0, 1), which allows the transformation of SIC data within the same range. As SIC approaches 0, ln(PIP₂₅) decreases exponentially; as SIC approaches 1, ln(PIP₂₅) increases exponentially.

The model parameters (β_0 , β_1 , and ϕ) are inferred using a Bayesian framework. Instead of a single estimate for each parameter, Bayesian analyses yield probability distributions (posteriors), which serve to quantify the uncertainties of model predictions. The posteriors are derived from (i) the priors, which are assigned to reflect the current scientific understanding of the parameters, and (ii) the likelihood, which is computed from the data given the parameters. Therefore, the posteriors represent updated beliefs of the parameters that are informed by the data, which, in our case, consist of the core-top ln(PIP₂₅) values and their corresponding satellite SIC observations. Accordingly, their spread reflects uncertainties in both the data and the calibration.

To the best of our knowledge, there exists no published nonlinear calibration for $\ln(\text{PIP}_{25})$ that can provide a basis for prior expectations for the regression coefficients. Hence, uninformative priors are used such that the posteriors are predominantly influenced by the data. The normal distribution is chosen for its real-valued, unbounded domain (i.e., $\beta \in \mathbb{R}$), and is centred around 0 so as not to favour positive or negative values a priori. For variance, a prior constrained to positive real numbers is required (i.e., $\phi \in \mathbb{R}^+$); the inverse gamma distribution is conventionally employed in Bayesian models for this purpose. The distributions are defined as follows:

$$\beta_0 \sim \mathcal{N}(0, 3), \quad (7)$$

$$\beta_1 \sim \mathcal{N}(0, 3), \quad (8)$$

$$\phi \sim \mathcal{IG}(2, 0.5); \quad (9)$$

Using larger prior standard deviations in sensitivity tests does not result in significant changes in the posteriors, indicating that the model is robust to the choice of priors.

Since our 22-year SIC dataset constitutes only a fraction of the time represented in most samples, and its grids do not perfectly match the areas integrated by the core tops, we further treat the SIC corresponding to each $\ln(\text{PIP})$ as an unknown. [Under the Bayesian framework](#), the distribution associated with each SIC parameter thus simulates the year-to-year sea ice variability over the (unknown) time and area integrated by the core top.

The prior for each SIC parameter is defined by a beta distribution, chosen for its flexibility to accommodate vastly different distributions within the fixed limits of 0 and 1, as follows:

$$\text{SIC}_i \sim \mathcal{Beta}(\alpha_i, \beta_i), \quad (10)$$

$$\alpha_i = \frac{\mu_i}{\text{IQR}_i}, \quad (11)$$

$$\beta_i = \frac{1}{\text{IQR}_i} - \alpha_i, \quad (12)$$

where μ and IQR are the mean and interquartile range of the 1979-2000 SIC dataset, respectively. This centres the prior distribution on the mean with a variance proportional to the IQR, effectively assigning smaller regression weights to samples with higher SIC variability. The Kullback–Leibler divergence, a measure of the difference between probability distributions (Kullback & Leibler, 1951), is small across all SIC parameters, indicating that the simulated distributions provide good approximations of the empirical distributions (figures S5 and S6). SIC values of zero are assumed to be under the satellite detection limit and are replaced by the minimum non-zero SIC value in the dataset.

In the forward model, the spatially varying seasonal bias in $\ln(\text{PIP}_{25})$ is addressed by matching each core-top sample with the climatological mean SIC of the calibration interval deduced from sediment trap studies, i.e., the three months before the first SIC decrease (figure 4d). This means that model-estimated SIC values for different months will be used to infer $\ln(\text{PIP}_{25})$ values at different locations. For example, in high latitude regions where sea ice breakup does not begin until July, the calibration interval will be May–June–July. As the timing of sea ice retreat changes through time, the model also accommodates temporal changes in proxy seasonality, facilitating its application in geologic time. The month of the first SIC decrease at a given location is determined by rounding the monthly climatologies to the nearest 0.05 and finding the month of the maximum SIC leading to the minimum. This requires seasonally varying SIC and fails where SIC remains constant throughout the year, such as locations that are always ice-free or ice-covered. For these cases, the month of the first SIC decrease is taken from the nearest grid with variable SIC, assuming that any IP_{25} deposition occurs either by lateral transport or during sea ice thinning which would be concurrent with nearby SIC decrease.

The likelihood is then calculated by:

$$\mathcal{L}(\ln(\text{PIP}_{25}) \mid \beta_0, \beta_1, \phi, \text{SIC}) = \prod_{i=1}^n P(\ln(\text{PIP}_{25i}) \mid \beta_0, \beta_1, \phi, \text{SIC}_i), \quad (13)$$

484 [Modified from $\mathcal{L}(\beta_0, \beta_1, \phi, \text{SIC} | \ln(\text{PIP}_{25})) = \prod_{i=1}^n f(\ln(\text{PIP}_{25i}) | \beta_0, \beta_1, \phi, \text{SIC}_i)$,] where n is the total
485 number of core tops, and $P(\cdot)$ is used to denote PDFs.

486 By Bayes' Theorem, the following proportionality may be obtained:

$$P(\beta_0, \beta_1, \phi, \text{SIC} | \ln(\text{PIP}_{25})) \propto \mathcal{L}(\ln(\text{PIP}_{25}) | \beta_0, \beta_1, \phi, \text{SIC}) P(\beta_0, \beta_1, \phi, \text{SIC}), \quad (14)$$

487 [Modified from $f(\beta_0, \beta_1, \phi, \text{SIC} | \ln(\text{PIP}_{25})) \propto \mathcal{L}(\beta_0, \beta_1, \phi, \text{SIC} | \ln(\text{PIP}_{25})) f(\beta_0, \beta_1, \phi, \text{SIC})$,] where
488 $f(\beta_0, \beta_1, \phi, \text{SIC})$ is the product of all the prior distributions, with the assumption that the pa-
489 rameters are independent of one another. Given the large number ($>400n + 3$) of parameters, we
490 use the *t-walk* (Christen & Fox, 2010), a Markov chain Monte Carlo sampler to infer the poste-
491 riors for all parameters. The ensemble of parameters obtained, representing possible calibra-
492 tion curves given the data, can then be used to calculate the predictive distribution, which in-
493 tegrates over model uncertainties and provides a probabilistic estimate of $\ln(\text{PIP}_{25})$ given any SIC
494 value.

495 Based on change point analyses (Truong et al., 2020), we exclude samples with low SSS
496 in our calibration to focus on the relationship between SIC and $\ln(\text{PIP}_{25})$. Therefore, the model
497 can only predict $\ln(\text{PIP}_{25})$ from SIC when and where SSS meets the determined threshold, which
498 differs slightly depending on the calibration interval. Should the proposed logarithmic relation-
499 ship between SSS and $\ln(\text{PIP}_{25})$ be independently verified in the future, we suggest a pre-treatment
500 of samples from hyposaline settings to correct for the additional influence.

501 Since the logit function describes a one-to-one relationship between SIC and $\ln(\text{PIP}_{25})$, the
502 forward model can be inverted to estimate past SIC directly from downcore $\ln(\text{PIP}_{25})$ values (equa-
503 tion 3). Through Bayesian inference, the same ensemble of parameters is used to propagate cal-
504 ibration uncertainties into the predictions. However, as the timing of the first SIC decrease is un-
505 known in the inverse case, a spatiotemporally stationary proxy seasonality must be assumed. We
506 experiment with different calibration intervals to determine the optimum interval for such an Arctic-
507 wide static calibration. Results from the inverse model should also be analysed with salinity data
508 wherever possible; if SSS is below the detected threshold for the calibration, the model may be
509 prone to underestimate SIC.

510 4.2 Model Results

511 The *BaySIC* model and its residuals are shown in figure 7, and its metrics in table 1. The
512 relationship between SIC and $\ln(\text{PIP}_{25})$ is well described by the inverse logistic function. The spa-
513 tially varying calibration explains 74% of the variance in the $\ln(\text{PIP}_{25})$ index calculated with
514 our core-top biomarker database, showing a marked improvement from the previous pan-Arctic
515 calibration (Xiao et al., 2015). The model has a root mean square error of prediction of 0.96, which
516 is reasonable given the spread of the core-top data, particularly in locations with more variable
517 SIC. As these samples are down-weighted in the regression, the calibration curve is largely de-
518 termined by data points with SIC close to 0 or 1. In general, there exists no strong spatial pat-
519 tern in the residuals, supporting model application across the Arctic. This is not the case in sen-
520 sitivity tests that include samples from Stoynova et al. (2013) and Su et al. (2022) (figure S7), fur-
521 ther justifying their exclusion from our calibration database.

522 The posteriors for the regression coefficients have significantly smaller spreads than the pri-
523 ors (figure S8), indicating the dominance of the likelihood function, i.e., the intercept and slope
524 of the model are mostly informed by the core-top data. Similar results are obtained using the full
525 satellite SIC record (1979-2022) or historical datasets (1950-2000 and 1950-2017) to inform the
526 priors (see table S2 for details), further supporting the model's robustness to different temporal
527 frameworks. The posterior for variance shows an increase from the prior, reflecting data constraints
528 on the precision of the model.

529 The 95% highest density interval (HDI) spans approximately 3 $\ln(\text{PIP}_{25})$ units, which represent quantified
530 uncertainties in both the observations and the calibration. Uncertainties in both the observations and the
531 calibration can be quantified using the 95% highest density interval (HDI), which is the smallest

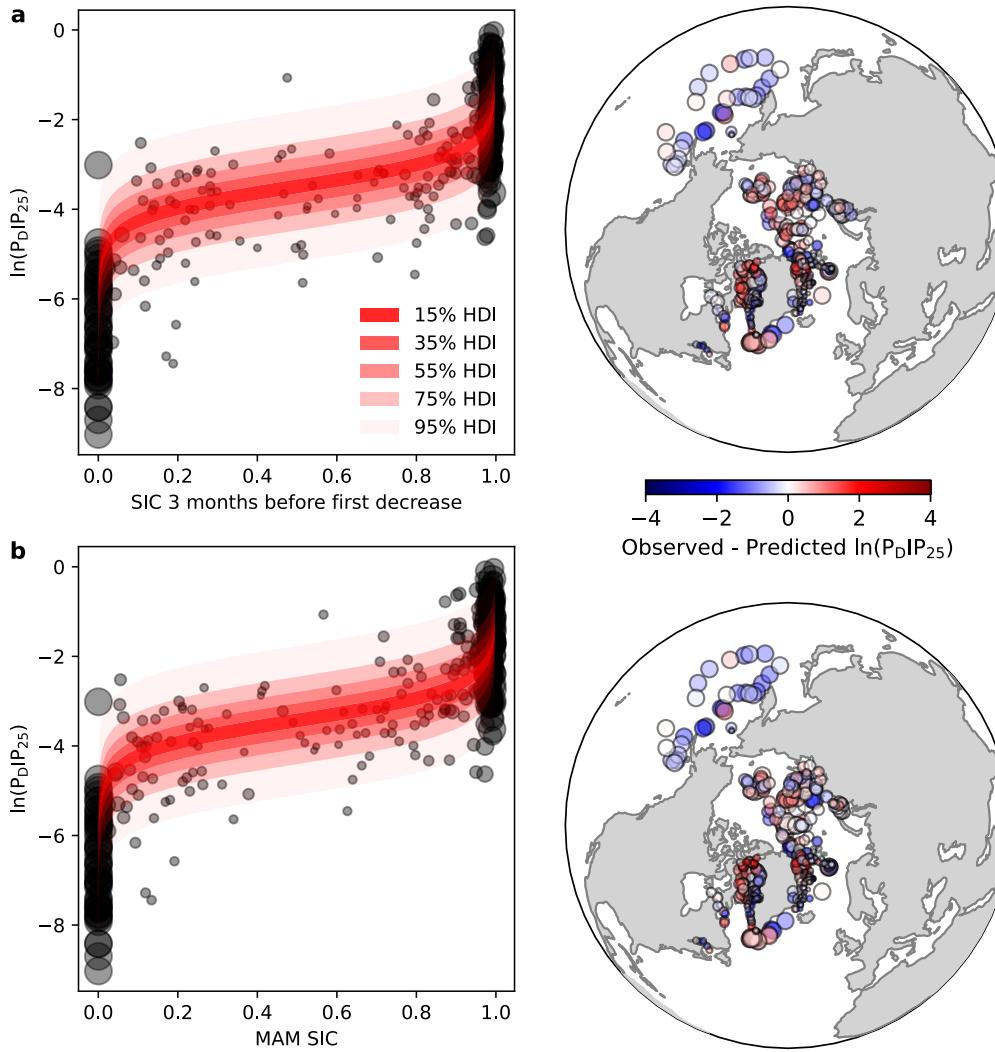


Figure 7. Calibrations (left) for $\ln(P_{D\text{IP}}_{25})$ using the sea ice concentrations (SIC) of (a) the average of the three months before the first SIC decrease and (b) Mar-Apr-May, and the corresponding spatial distributions of residuals (right). Bubble size is inversely proportional to the interquartile range of the SIC over the 22-year calibration period. HDI = highest density interval.

Table 1. Calibration results of different $\ln(\text{PIP}_{25})$ indices to the sea ice concentration (SIC) of different months (e.g. MAM = Mar-Apr-May). RMSEP = root mean squared error of prediction.

	3 months before first SIC decrease	MAM	AMJ	Apr	May
$\ln(P_{D\text{IP}}_{25})$					
R^2	0.74	0.74	0.72	0.73	0.70
RMSEP	0.96	0.96	1.01	0.99	1.04
$\ln(P_{B\text{IP}}_{25})$					
R^2	0.63	0.63	0.59	0.63	0.57
RMSEP	1.47	1.48	1.54	1.47	1.58
SSS threshold	21.26	21.74	21.45	23.05	21.61

532 region that contains 95% of the posterior distribution, representing the most credible values. In
 533 this calibration, the 95% HDI spans approximately 3 $\ln(\text{PIP}_{25})$ units. Since the inverse logistic
 534 function is characterised by a gently-sloped body between steeply-sloped tails, the *BaySIC* model
 535 is more sensitive to extreme than intermediate SIC values. This means that in the inverse fram-
 536 ing, where downcore $\ln(\text{PIP}_{25})$ are used to reconstruct SIC, the uncertainties associated with ex-
 537 treme $\ln(\text{PIP}_{25})$ values will be smaller than those associated with intermediate $\ln(\text{PIP}_{25})$ values
 538 (see section 5 for illustrated examples). As the core-top data show that $\ln(\text{PIP}_{25}) \sim -4$ can result
 539 from the full range of SIC, SIC reconstructions from these values are highly uncertain and should
 540 be interpreted with caution. Away from this step-like transition, the model can distinguish be-
 541 tween ice-free and ice-covered conditions with relatively high certainty. Moreover, within the ex-
 542 isting core-top database, there is a $\sim 1:4$ imbalance of paired IP_{25} -sterol data collected from sea-
 543 sonally ice-free ($\text{SIC} \sim 0$) versus seasonally ice-covered ($\text{SIC} \sim 1$) locations (figure 7). Increas-
 544 ing data coverage near the seasonally ice-free transition would provide more constraints on the
 545 lower end of the slope.

546 Following the removal of core tops matched with low SSS, no significant trend is observed
 547 between SSS and the residuals among the remaining samples (figure 6b). Since the influence of
 548 salinity on $\ln(\text{PIP}_{25})$ is only apparent at anomalously low SSS levels, the filtering procedure is
 549 deemed more suitable than the addition of a second predictor in the calibration model. Analy-
 550 ses with SST and nutrient data similarly show no correlation between the residuals and these en-
 551 vironmental variables (figure S9), suggesting that they are not major drivers of $\ln(\text{PIP}_{25})$. Future
 552 work is needed to identify the source(s) of the variance left unexplained by *BaySIC*.

553 Similar calibration curves are obtained for $\ln(\text{P}_B \text{IP}_{25})$, but some structures in the spatial
 554 distribution of residuals are discernible (see Appendix A). In particular, strong negative resid-
 555 uals exist to the northeast of Svalbard, where low $\ln(\text{P}_B \text{IP}_{25})$ values are associated with ice-covered
 556 conditions (and normal SSS levels). As Belt et al. (2015) pointed out in their original study, ad-
 557 dditional brassicasterol may be contributed by non-pelagic sources, which would explain the lower-
 558 than-expected IP_{25} -brassicasterol ratios. However, as these core tops lack corresponding dinos-
 559 terol measurements, it is possible that their $\ln(\text{P}_D \text{IP}_{25})$ values are equally low, which would point
 560 to other causes of discrepancy. *BaySIC* incorporates this unknown source of uncertainty by tak-
 561 ing into account these anomalous samples and converging to a higher variance. Thus, the $\ln(\text{P}_B \text{IP}_{25})$
 562 calibration has a greater uncertainty range that reflects potential additional influences on the proxy
 563 (see examples below).

564 For an Arctic-wide static calibration, March-April-May appears to be the optimum cali-
 565 bration interval, with an alternative calibration to April-May-June yielding similar results. This
 566 is consistent with previous calibrations and corroborates the interpretation that $\ln(\text{PIP}_{25})$ reflects
 567 SIC shortly before sea ice breakup (discussed in section 3.3). Although this model performs simi-
 568 larly to the spatially varying model in replicating core-top samples, we argue that the consider-
 569 ation of a variable proxy seasonality remains important for accurate predictions. By identifying
 570 $\ln(\text{PIP}_{25})$ as recording the maximum SIC before sea ice disintegration, the model outputs for the
 571 corresponding months may be used to reconstruct the maximum sea ice extent, rather than the
 572 average sea ice conditions over a loosely defined Arctic spring.

573 To test this hypothesis and to evaluate model performance, we apply *BaySIC* to out-of-sample
 574 SIC observations from locations with paired IP_{25} -sterol sediment trap data. The average SIC of
 575 the three months before the first SIC decrease during the sampling period are supplied to the model
 576 to generate probabilistic $\ln(\text{PIP}_{25})$ estimates. For the traps at $\sim 75^\circ$ latitude (Gal et al., 2022),
 577 this interval is March-April-May. For those at $\sim 83^\circ$ latitude (Nöthig et al., 2020), it is April-
 578 May-June. The results are compared against the observed $\ln(\text{PIP}_{25})$ values, which are calculated
 579 using the total biomarker fluxes measured over the sampling period. Overall, there is good agree-
 580 ment between the *BaySIC* predictions and sediment trap data, with the observations always falling
 581 within the 95% HDI (figure 8). The maximum a posteriori (MAP) estimation, representing the
 582 mode of the predictive distribution, converges closely with the observation.

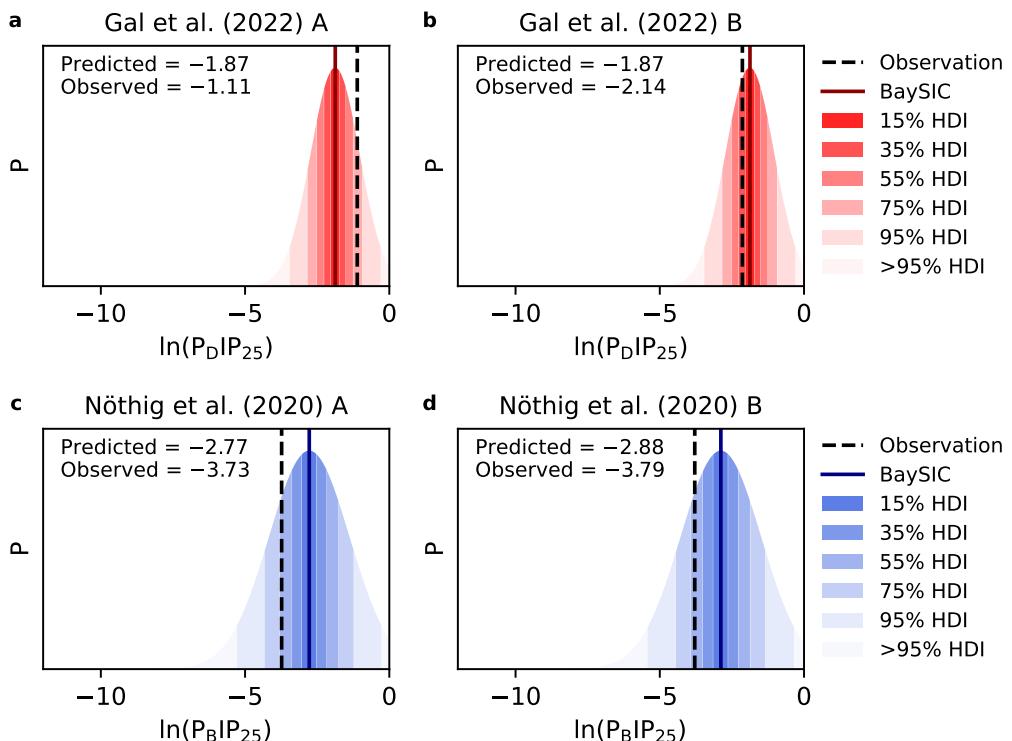


Figure 8. Predictions of the spatially varying forward model vs. observations from sediment traps of (a-b) $\ln(P_{DIP25})$ and (c-d) $\ln(P_{BIP25})$. Trap locations are shown in figure 2. HDI = highest density interval.

We repeat the exercise using the Arctic-wide static March-April-May calibration to assess the potential impacts of assuming stationary proxy seasonality. For the two traps located at a higher latitude, this results in a one-month offset from the seasonal bias diagnosed by the spatially varying model. In both cases, the prediction deviates further from the observation than that obtained above by $\sim 0.11 \ln(\text{PIP}_{25})$ units (not shown). This supports our hypothesis that the consideration of a dynamic proxy seasonality yields more accurate forward modelling results and, despite relatively small differences derived here from modern observations, is consequential in deep-time applications (discussed in section 3.3).

5 Palaeoclimate Applications

5.1 Quantitative SIC Reconstruction from Downcore Biomarker Measurements

By establishing a fully quantitative relationship between SIC and the new $\ln(\text{PIP}_{25})$ index, *BaySIC* overcomes the longstanding limitation to semi-quantitative SIC reconstruction of the original PIP_{25} index. To exemplify its palaeoclimate applications, we apply *BaySIC* to a sediment core in northeastern Fram Strait (MSM5/5-712-2; $78^\circ 54.94'N$, $6^\circ 46.04'E$; 1487 m; Budéus, 2007) that has been analysed for both biomarkers and dinoflagellate cyst (dinocyst) assemblages. The published IP_{25} and sterol measurements (Cabedo-Sanz & Belt, 2016; Müller & Stein, 2014; Müller et al., 2012) are placed on the same chronology as the palynological data (Falardeau et al., 2019) to permit comparisons between the records, which extend into the Last Glacial Maximum (LGM; 23 ka).

Paired IP_{25} -dinosterol and IP_{25} -brassicasterol measurements are supplied to the inverse model to estimate past SIC from $\ln(\text{P}_D\text{IP}_{25})$ and $\ln(\text{P}_B\text{IP}_{25})$, respectively. Within *BaySIC*, all biomarker measurements are treated with the best estimate of the detection limit prior to calculating the $\ln(\text{PIP}_{25})$ index (discussed in section 3.1). Based on reconstructions presented by Falardeau et al. (2018), SSS at the core site fluctuated between 24 and 36 psu in the last 23 ka, remaining well above the determined threshold (table 1). Thus, salinity is assumed to have negligible influence on the biomarker records presented here.

Overall, the SIC reconstructions using either index show good agreement with each other (figure 9a-b). For the LGM, both indices reconstruct near-complete ice cover, with amplified SIC fluctuations in the $\ln(\text{P}_D\text{IP}_{25})$ reconstruction. Partial ice cover persisted during Heinrich event 1 and the Bølling-Allerød, but higher SICs are reconstructed from $\ln(\text{P}_B\text{IP}_{25})$ in several intervals. These discrepancies are due to differences in the IP_{25} -sterol ratios and are also found in reconstructions using the original PIP_{25} index (see section 5.2). Near-identical trends are obtained for the Younger Dryas (YD) and throughout most of the Holocene, only diverging in the last 2 ka. The inconsistencies here are due to the integration of the Cabedo-Sanz and Belt (2016) dataset, which reports lower IP_{25} concentrations than (and similar brassicasterol concentrations as) measurements at the same depths provided by Müller et al. (2012), and does not include data for dinosterol. Near the top of the core, rapid sea ice loss is inferred from both indices and the reconstructions converge towards the modern March-April-May SIC observed at the core site.

The 95% HDI for both reconstructions are large (given site MSM5/5-712-2's location near the MIZ), but realistic considering the various sources of uncertainty incorporated. As explained in the previous section, the uncertainty ranges associated with extreme $\ln(\text{PIP}_{25})$ values are smaller, for example, during the YD when the proxy strongly indicates ice-covered conditions. In addition, reconstructions based on $\ln(\text{P}_D\text{IP}_{25})$ feature less uncertainty than those derived from $\ln(\text{P}_B\text{IP}_{25})$, which reflects higher confidence in its correlation with SIC in the core-top calibration.

5.2 Comparison with Prior SIC Reconstruction Approaches

To illustrate the differences in SIC reconstruction via $\ln(\text{PIP}_{25})$ and the original PIP_{25} index, we apply previous linear calibrations for the region of East Greenland and West Spitsbergen (Müller et al., 2011) to the same biomarker data. As the core was divided into sections and

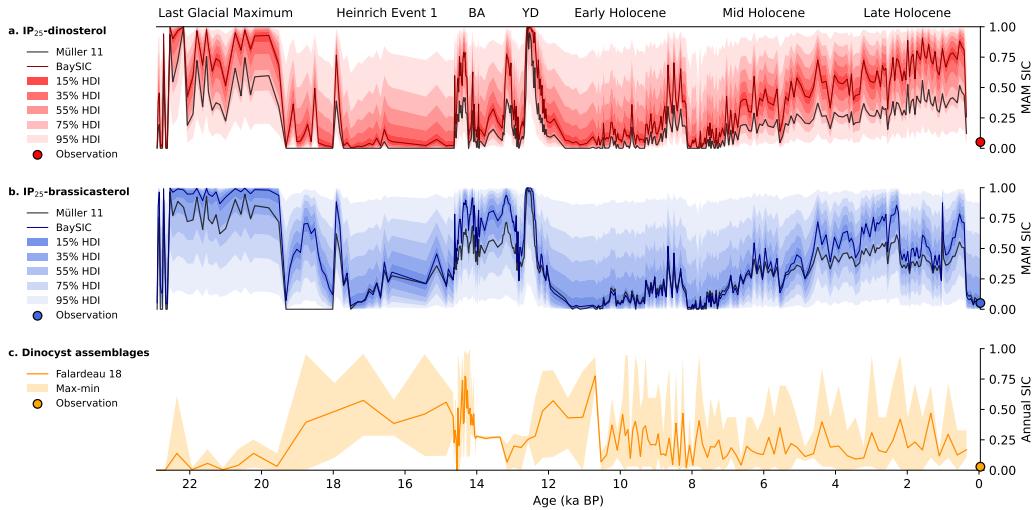


Figure 9. Reconstructions of Mar-Apr-May sea ice concentration (SIC) at site MSM5/5-712-2 based on paired (a) IP₂₅-dinosterol and (b) IP₂₅-brassicasterol measurements (Cabedo-Sanz & Belt, 2016; Müller & Stein, 2014; Müller et al., 2012), using the *BaySIC* inverse model and the regional linear calibrations presented by Müller et al. (2011). HDI = highest density interval. (c) Reconstruction of annual SIC at the same site via dinocyst assemblages from Falardeau et al. (2018). Circles denote modern (1979-2000) SIC observed at the core site. Grey shading indicates cold intervals. YD = Younger Dryas; BA = Bølling-Allerød.

analysed separately, different c factors were employed in the calculation of PIP₂₅ by each study (Cabedo-Sanz & Belt, 2016; Müller & Stein, 2014; Müller et al., 2012). In order to use the published calibrations, we recalculate the P_DIP₂₅ and P_BIP₂₅ values based on the c factors derived by Müller et al. (2011). The highly variable and somewhat arbitrarily defined c factor is an inherent limitation of the original PIP₂₅ index approach; by eliminating it from ln(PIP₂₅), *BaySIC* enables consistent proxy interpretation over space and time. Its applicability across the Arctic further removes the need for a regional calibration, allowing quantitative proxy interpretation in locations where it was previously not possible.

Unlike *BaySIC*, the linear regression model takes SIC beyond 0 and 1 at extreme PIP₂₅ values; we place additional limits on the reconstructions to restrict them to the natural range of the parameter. In general, *BaySIC* predictions are consistent with the results of the adapted PIP₂₅ index approach (figure 9a-b), which reflects the common biomarker data used for both indices. *BaySIC* tends to estimate greater magnitude SIC changes than the linear regression model, for instance, the rapid decrease from full ice cover at the end of the LGM. Similarly, the reconstructions diverge from Mid Holocene onwards, with *BaySIC* suggesting near-complete ice cover in contrast to the partial ice cover indicated by the linear calibration model. This is an expression of the demonstrated nonlinearity of the proxy: at the transition between ice-covered and ice-free conditions, *BaySIC* captures small shifts in ln(PIP₂₅) and deduces relatively large SIC changes.

Between 18 and 19 ka, completely ice-free conditions are reconstructed from the original PIP₂₅ indices, whereas *BaySIC* estimates partial ice cover. These inconsistencies arise from the zero IP₂₅ concentrations measured for the sediment samples, leading to zero PIP₂₅ values indicative of open ocean conditions. However, based on the low corresponding sterol concentrations, Müller and Stein (2014) concluded that the biomarkers record permanent ice cover instead. This has conventionally been handled by designating a PIP₂₅ value of 1 to samples with IP₂₅ and sterol concentrations under or near their limit of detection (Belt, 2018). *BaySIC* results show that once the biomarker measurements are treated with the detection limit, they can be readily related to

657 the full range of SIC via the $\ln(\text{PIP}_{25})$ index (section 4.2), suggesting that the relative biomarker
 658 abundances remain informative even when absolute abundances are low. As reported IP_{25} and
 659 sterol concentrations both tend to 0, $\ln(\text{PIP}_{25})$ approaches -2.35 to -3.06 , depending on the sterol
 660 and the unit of measurement used. According to the calibrations, these values would indicate mostly
 661 ice-covered conditions, in agreement with previous interpretations of the proxy system. As biomarker
 662 concentrations increase, their ratio becomes less sensitive to the added minimum concentrations.
 663 The *BaySIC* approach maintains the separation between observation and interpretation to avoid
 664 introducing additional bias into SIC reconstructions.

665 Despite similarities in the reconstructions, the major breakthrough made by *BaySIC* lies
 666 in its fully quantitative proxy interpretation. Owing to challenges in quantifying the original PIP_{25}
 667 index, it has traditionally been used to reconstruct sea ice only semi-quantitatively by categoris-
 668 ing sea ice conditions and matching each to a range of index values. In their original [studyrecon-
 669 struction](#), Müller et al. (2012) distinguish between extended, marginal, and variable/less ice cover,
 670 as well as ice-free conditions, instead of deriving SIC from the PIP_{25} index as attempted here.
 671 With *BaySIC*, $\ln(\text{PIP}_{25})$ is mapped to the full, continuous range of SIC, clarifying the proxy in-
 672 terpretation and facilitating direct comparison with model outputs. Its Bayesian framework fur-
 673 ther quantifies the uncertainties, which have been lacking in previous linear calibrations for PIP_{25} .
 674 The resultant probabilistic estimates may help reconcile different proxy records and achieve more
 675 robust palaeoclimate reconstructions.

676 As an example, we compare *BaySIC* results against an independent sea ice reconstruction
 677 using dinocyst assemblages (Falardeau et al., 2018). The reconstruction is converted from ice-
 678 covered months per year, where ice cover is defined as $\text{SIC} > 0.5$, to annual SIC (figure 9c); a
 679 good correlation has previously been shown between the two variables (de Vernal, Rochon, et
 680 al., 2013). The average SIC reconstructions are therefore expected to be lower and less variable
 681 than those from $\ln(\text{PIP}_{25})$ and PIP_{25} , which are seasonally biased. A detailed analysis of the record
 682 is presented in the original study; here, we highlight several key differences between the proxy
 683 reconstructions.

684 During the LGM, persistent ice cover is reconstructed from $\ln(\text{PIP}_{25})$, followed by a rapid
 685 transition to mostly ice-free conditions at 19 ka. An opposite trend is shown by dinocyst assem-
 686 blages, which suggest little to no ice cover throughout the LGM, succeeded by partial ice cover.
 687 The contradiction is likely due to limitations of the modern analogue technique employed in quan-
 688 titative sea ice reconstruction from dinocyst assemblages: as Falardeau et al. (2018) pointed out,
 689 the best matches found for their LGM samples were from a location that experienced distinct hy-
 690 drographical conditions to those expected for the core site. Without suitable modern equivalents,
 691 the resultant SIC reconstructions may be inaccurate. In contrast, the diverse settings in which IP_{25}
 692 and the sterols have been detected and the clear relationship between the $\ln(\text{PIP}_{25})$ index and SIC
 693 renders the proxy applicable in different palaeo-environments.

694 Both proxies record a relatively short-lived SIC increase at 14 ka, followed by partial ice
 695 cover during the Bølling-Allerød. Evidence of the YD cooling is similarly clear in all reconstruc-
 696 tions, with the $\ln(\text{PIP}_{25})$ indices indicating a sharper SIC rise to completely ice-covered condi-
 697 tions, compared to a slower and more modest increase shown by dinocyst assemblages. The el-
 698 evated SIC persisting into Early Holocene registered by the dinocyst assemblages is not discernible
 699 in $\ln(\text{PIP}_{25})$ reconstructions. From Mid to Late Holocene, the reconstructions further diverge:
 700 a steady SIC increase is reconstructed via $\ln(\text{PIP}_{25})$, following the decline in the orbital forcing
 701 in the Northern Hemisphere, while the dinocyst assemblages suggest relatively stable, low an-
 702 nual SIC. As $\ln(\text{PIP}_{25})$ tracks the maximum SIC, sea ice changes in seasonally ice-covered lo-
 703 cations are more readily observable, providing more precise insights into past sea ice conditions.

704 5.3 Sea Ice in Past Warm Periods

705 The new calibrations offer opportunities to reevaluate available proxy records for proba-
 706 bilistic insights into Arctic sea ice responses to past warming. For additional examples, we ap-
 707 ply *BaySIC* to sites with paired IP_{25} -sterol measurements dated to the Last Interglacial (LIG, \sim

130 – 118 ka) and the mid-Pliocene Warm Period (mPWP, ~ 3.3 – 3.0 Ma). These data have previously been interpreted either qualitatively or semi-quantitatively (summarised in table 2). In the absence of reliable salinity data for each site and period, we ignore, for illustrative purposes, the possibility of drastic SSS changes. The published biomarker concentrations (Clotten et al., 2017; Knies et al., 2014; Kremer et al., 2018; Stein et al., 2017, 2018; Steinsland et al., 2023) are averaged over the target interval as inputs for the inverse model, yielding a non-Gaussian PDF for each SIC reconstruction (figure 10). This means that the HDIs are not centred at the MAP estimation, i.e., there is a higher probability for SIC to fall closer to one end of the spectrum (also seen in figure 9), and reflects that most of the ocean is either ice-covered or ice-free, such that the chances of the core site being within the MIZ is relatively low.

Table 2. Previous interpretation of sea ice conditions during the mid-Pliocene Warm Period (mPWP) or the Last Interglacial (LIG) at each site. Core locations are shown in figure 10.

Core	Previous sea ice interpretation	Study
mPWP		
ODP910C	Similar to the modern summer minimum	Knies et al. (2014)
ODP151-907A	Ice-covered in spring, ice-free in summer	Clotten et al. (2018)
LIG		
PS2200-5	Perennial ice cover	Stein et al. (2017)
PS2138-2	Spring/summer SIC of $\sim 20\%$ or less	Stein et al. (2017)
PS92/039-2	Perennial ice cover	Kremer, Stein, Fahl, Ji, et al. (2018)
PS93/006-1	Partially ice-covered in summer	Kremer, Stein, Fahl, Bauch, et al. (2018)
GS16-204-22CC-B	Marginal ice zone	Steinsland et al. (2023)

For the LIG, *BaySIC* predicts relatively high (~ 0.7 or more) March-April-May SIC for PS2200-5, PS93/006-1, and GS16-204-22CC-B, supporting the presence of sea ice in spring as formerly inferred for these sites (Kremer, Stein, Fahl, Bauch, et al., 2018; Stein et al., 2017; Steinsland et al., 2023). The tight PDF obtained for PS2200-5 in particular indicates high confidence in the interpreted ice-covered conditions, which is broadly consistent with this site's northerly location. Slightly more sea ice coverage is estimated for GS16-204-22CC-B than in the original study, which considered the biomarkers individually rather than combined in an index. Compared with the traditional approach of classifying sea ice conditions, with categories like the MIZ spanning a wide range of SIC, the redefined $\ln(\text{PIP}_{25})$ index and its calibration to SIC allow more specific reconstructions.

BaySIC estimates very low (~ 0.1 or less) March-April-May SIC for PS92/039-2, contradicting the previously inferred perennial ice cover (Kremer, Stein, Fahl, Ji, et al., 2018). This disagreement stems from the setting of PIP_{25} to 1 for samples with low IP_{25} and brassicasterol concentrations in the original study, as opposed to the detection limit treatment implemented within *BaySIC* (discussed in section 5.2). By considering the ratios of the biomarkers via $\ln(\text{PIP}_{25})$, our model suggests that this site had more likely experienced ice-free conditions during the LIG. For PS2138, the *BaySIC* prediction via $\ln(\text{P}_B\text{IP}_{25})$ corroborates sea ice conditions deduced from P_BIP_{25} by Stein et al. (2017), but diverges from the much higher SIC predicted via $\ln(\text{P}_D\text{IP}_{25})$. Further investigation is needed to explain this discrepancy. One potential cause is additional brassicasterol sources (discussed in section 2.1), in which case the local SIC over the LIG would have been previously underestimated. As *BaySIC* provides the full probability distributions for each reconstruction, it is also possible to determine the most probable SIC as indicated by all biomarkers by considering the results obtained via both sterols.

Turning to the mPWP, a similar divergence is observed in predictions for ODP151-907A: the $\ln(\text{P}_D\text{IP}_{25})$ record strongly indicates SIC to be close to 1, whereas the $\ln(\text{P}_B\text{IP}_{25})$ record pro-

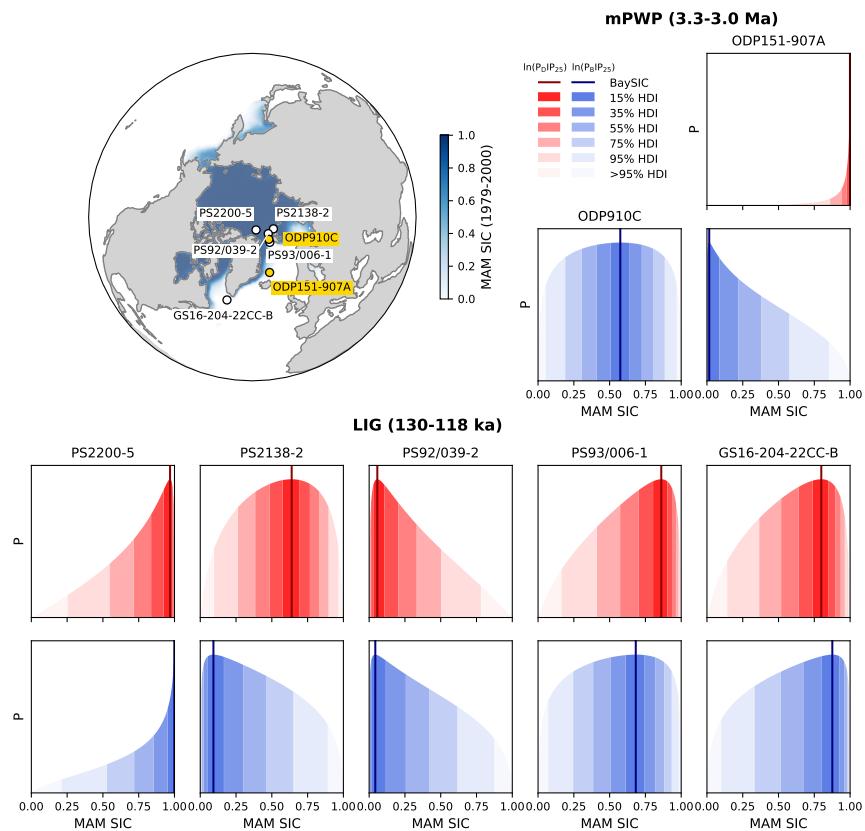


Figure 10. *BaySIC* reconstructions of Mar-Apr-May sea ice concentration (SIC) for seven sites with mid-Pliocene Warm Period (mPWP, yellow) or Last Interglacial (LIG, white) paired IP_{25} -sterol measurements. The map shows their locations and modern (1979-2000) SIC. MAP = maximum a posteriori (estimation); HDI = highest density interval.

743 vides only weak constraints on SIC. Clotten et al. (2018) attributed the decoupling of the two sterols
 744 during this period to non-marine sources of brassicasterol, which would lend more credibility
 745 to the fully ice-covered scenario suggested by $\ln(P_{DIP25})$. The ODP910C site is estimated to be
 746 ice-free based on $\ln(P_{BIP25})$, consistent with the former interpretation (Knies et al., 2014). How-
 747 ever, dinosterol data is not available for this core. Given the occasional but significant conflicts
 748 between SIC reconstructions employing different sterols, interpretations based on only one of the
 749 two should be treated with extra caution.

750 Direct comparisons of SIC across distant localities and distinct ages, as shown above, have
 751 previously proven difficult due to issues pertaining to the c factor and regional correlations; *BaySIC*
 752 facilitates spatially and temporally consistent sea ice interpretations, bringing a new perspective
 753 to ongoing debates about Arctic sea ice extent during past warm periods. While recent studies
 754 have inferred seasonally ice-free conditions in the LIG indirectly through summer surface air tem-
 755 perature proxies (Sime et al., 2023), or qualitatively through the presence of an open water proxy
 756 (Vermassen et al., 2023), more proxy-based investigations are required to confirm such propo-
 757 sition and to better define sea ice sensitivity to warming. In this regard, *BaySIC* provides a crit-
 758 ical step toward achieving direct and quantitative solutions.

759 6 Conclusions

760 A new $\ln(P_{IP25})$ index is proposed as a robust Arctic sea ice proxy that enables fully quan-
 761 titative proxy reconstructions of palaeo-sea ice concentration (SIC). It improves on the established
 762 P_{IP25} index by eliminating the use of a problematic balance factor, thus allowing direct compa-
 763 rison across different Arctic regions and consistent interpretations on longer (geologic) timescales.
 764 The $\ln(P_{IP25})$ index is found to correlate nonlinearly with SIC, with an apparent additional in-
 765 fluence of low sea surface salinity warranting further investigation. Observations from published
 766 sediment trap studies indicate a proxy seasonal bias towards the interval preceding local sea ice
 767 breakup, which varies over both space and time.

768 Using a pan-Arctic core-top biomarker database, we develop a set of Bayesian models, called
 769 *BaySIC*, to calibrate the $\ln(P_{IP25})$ index to seasonal SIC. Calibration uncertainties are quantified
 770 and propagated to model predictions, providing better constraints on model uncertainties. The
 771 spatially varying forward model considers differences in the timing of ice melt, yielding more
 772 accurate proxy predictions while facilitating proxy-model comparisons and palaeoclimate data
 773 assimilation. An inverse model is also devised, by assuming an Arctic-wide stationary bias to
 774 March-April-May, to support direct SIC reconstructions from downcore $\ln(P_{IP25})$ measurements.
 775 Finally, we provide a number of examples that demonstrate the applicability of *BaySIC* to palaeo-
 776 climate investigations, which highlight the advances made in sea ice reconstruction using IP_{25}
 777 and open-water sterols.

778 As the first model of its kind, *BaySIC* represents an important step in translating the now
 779 well-established sea ice proxy into a quantified climate variable, opening up new possibilities for
 780 its use in constraining the long-term variability of Arctic sea ice, thereby improving our under-
 781 standing of past and future climate changes. Future research may provide more insights into the
 782 proxy system, including the identification of other environmental factors affecting $\ln(P_{IP25})$, which
 783 may help explain the remaining variance in the index. Additional core-top biomarker datasets,
 784 especially from currently under-sampled Arctic and sub-Arctic regions, may further strengthen
 785 the constraints on the calibration curves and their associated uncertainty ranges, enabling more
 786 robust sea ice, and thus global climate, reconstructions.

787 Appendix A Model results for $\ln(P_{BIP25})$ calibrations

788 Open Research

789 The core-top biomarker database investigated for the development of *BaySIC* is available as Sup-
 790 porting Information. The *BaySIC* software package (Python) is publicly available on GitHub via

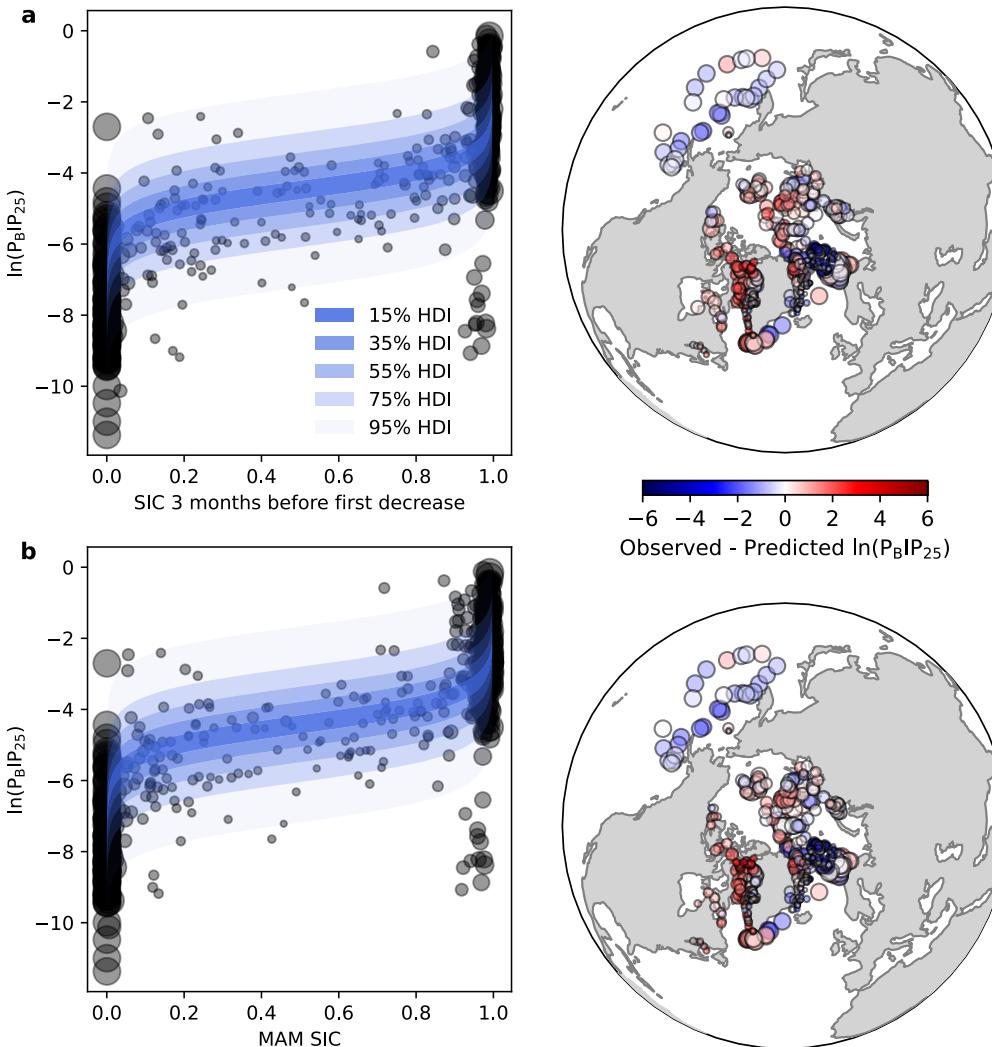


Figure A1. Calibrations (left) for $\ln(P_B|P_{25})$ using the sea ice concentrations (SIC) of (a) the average of the three months before the first SIC decrease and (b) Mar-Apr-May, and the corresponding spatial distributions of residuals (right). Bubble size is inversely proportional to the interquartile range of the SIC over the 22-year calibration period. HDI = highest density interval.

791 <https://github.com/CrystalCYFu/PyBaySIC> with the Creative Commons Attribution-NonCommercial
 792 4.0 International License. Both the software and the data are also archived in Zenodo (Fu et al.,
 793 2025a, 2025b).

794 **Acknowledgments**

795 We thank Simon Belt for many useful discussions and for help in steering early versions of this
 796 manuscript, and Henriette Kolling for graciously sharing IP₂₅ and sterol core-top data. We are
 797 deeply grateful to the numerous scientists who collected core-top samples from across the Arctic
 798 seafloor, measured them in laboratories, and generously made their hard-earned data publicly
 799 available. C.Y.F. acknowledges financial support from Girton College (University of Cambridge),
 800 Quacquarelli Symonds, and the Cambridge Commonwealth, European & International Trust. Fund-
 801 ing for this work was provided by a U.S. NSF Office of Polar Programs grant (OPP-2202667) to
 802 M.B.O.

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