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Introducing Primary Biological Aerosol Particles in GISS-E2.1 Earth System Model

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Introduction

- **Primary Biological Aerosol Particles (PBAP) can act as CCN or INPs**
- Biological particles form up to 25% of aerosol load that contribute to cloud formation (Despres et al 2012)

Motivation

- To what extent can Primary Biological Aerosol Particles (PBAPs), e.g. bacteria and fungal spores, impact our regional/global climate especially when they contribute to forming clouds?
- **Studies that quantify the radiative forcing of PBAP are limited**
- **Concentration of PBAPs are small to have a significant impact on climate, therefore their contribution can be ignored in comparison to dust**
- Due to the limited field measurements, the terrestrial emission flux of PBAP is highly uncertain; estimation within the range of 50-1000 Tg/yr (IPCC, AR5).
- Therefore, the emission fluxes of PBAP might be underestimated or ignored in those studies

Introducing PBAPs in GISS-E2.1

- We built an online emission routines in GISS-E2.1 that is able to calculate the emission flux of different types of PBAPs tracers, e.g. bacteria, fungal spores, pollen, and algae

- First, we introduced bacteria and use the best fit to the observations over ten types of ecosystems from Burrows et al. (2009b) as a reference.

- The total bacteria flux ($F_{bacteria}$) is the sum of bacteria fluxes (F_i) over 10 ecosystems (indicated by index i) wiegthed by the area fraction of the respective ecosystems in the gridbox (f_i).

$$F_{bacteria} = \sum_{i=1}^{10} f_i * F_i$$

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Table 2. Bacterial emission fluxes (best-fit and 95th percentiles of emission estimates by Burrows *et al* (2009a)), and ecosystem area in the CLM land model (Bonan *et al* 2002). Emissions from coastal areas are not considered with a separate emission flux in the present study, because they cannot be unambiguously attributed to a plant functional type.

Ecosystem	Area (10^6 km^2)	F_i (m^{-2} s^{-1}) in simulations PBAP and PBAP-intermediate	F_i (m^{-2} s^{-1}) in simulation PBAP-MAX
Coastal	0	900	4 996
Crops	22.7	704	1 578
Deserts	19.1	0	52
Forests	30.3	0	187
Grasslands	32.9	648	1 811
Land-ice	15.5	7.7	16
Seas	362.6	0	226
Shrubs	20.3	502	619
Tundra	7.0	0	579
Wetlands	4.2	196	14 543

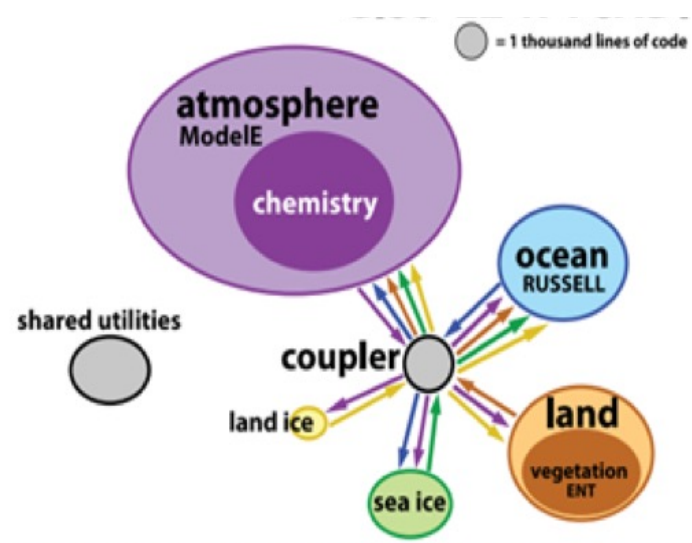
Simulations - PBAPs in GISS-E2.1

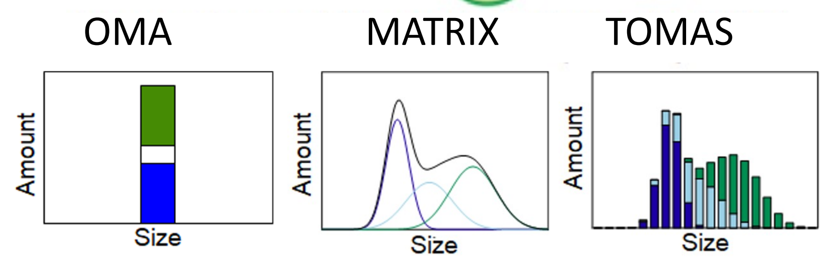
Simulation	Radiation
Flux Upper limit	off
Flux best estimate	off
Flux best estimate	on

- Bacteria size 1 μm
- Bacteria density 1000 kg/m^3
- Bacterial cell mass 5.2E-16 kg
- The model ran for 7 years
- Spinup time is five years

GISS-ModelE2.1

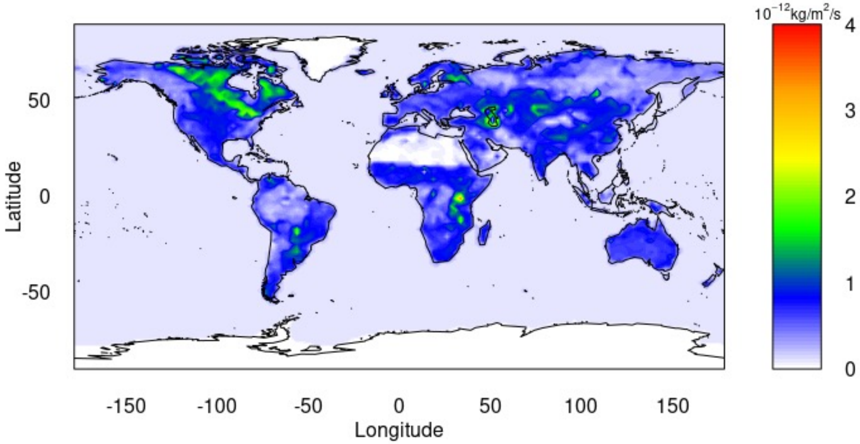
- Fully-coupled ESM
- CMIP6 version (*Kelley et al., 2020*)
- Atmosphere/Land/Ice:
    - 2°×2.5° spatial resolution, 40 vertical layers
- Ocean (GISS Ocean V1):
    - 1°×1.25° spatial resolution, 40 vertical layers
- One Moment Aerosol (OMA: *Bauer et al., 2020)*
- Direct & first indirect effect
- Time step 30 min

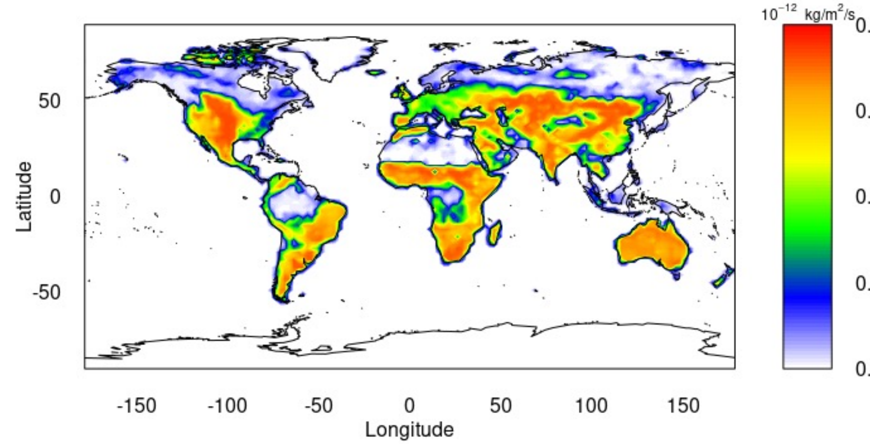


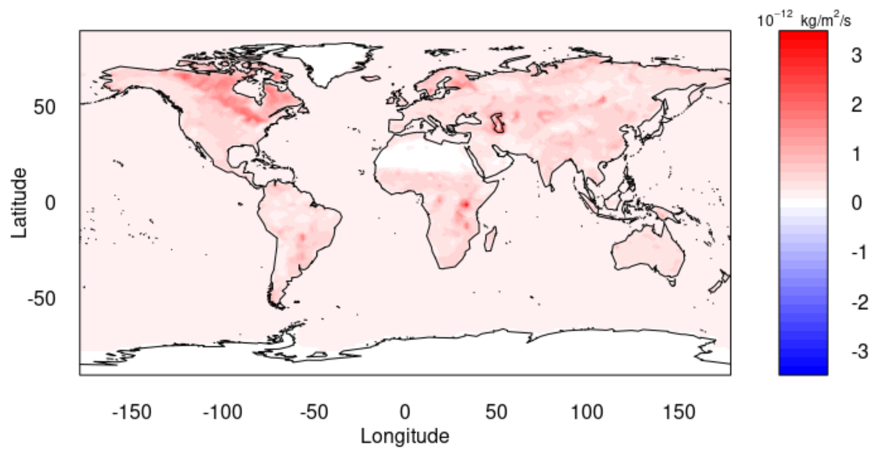


- PBAPs has not yet been introduced to GISS-E2.1

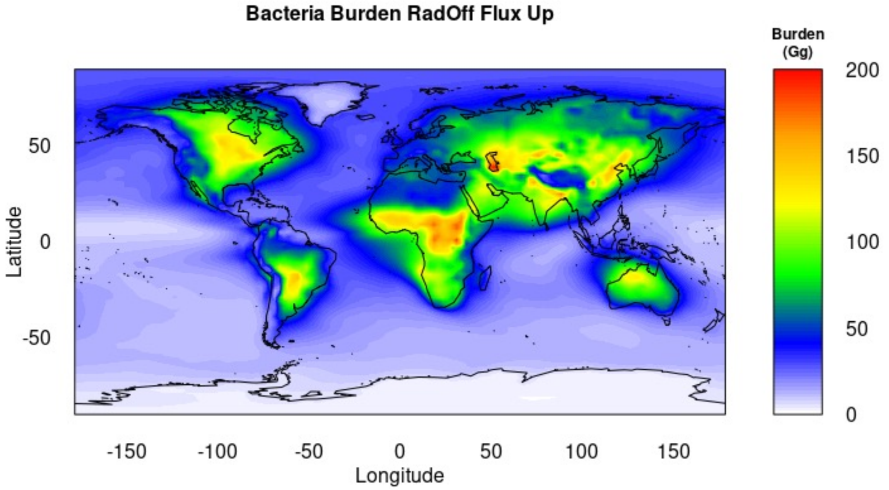
Preliminary Results of Introducing Bacteria in GISS ModelE2.1
Source/Emission

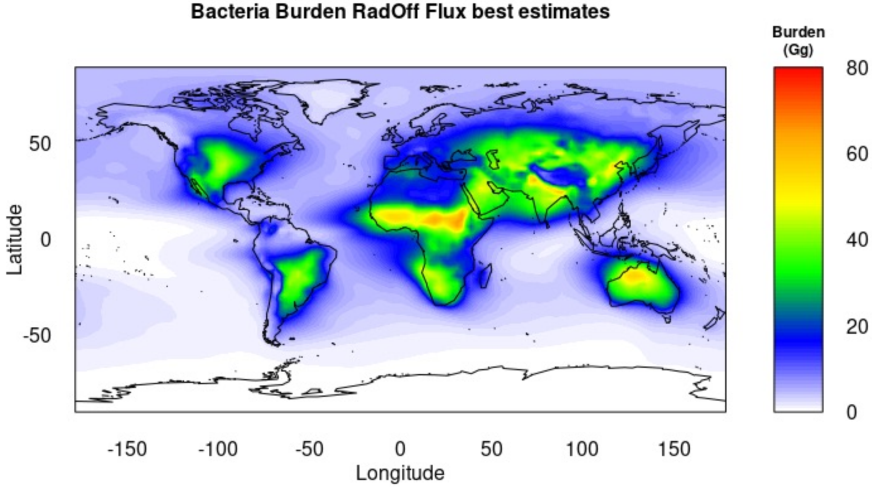


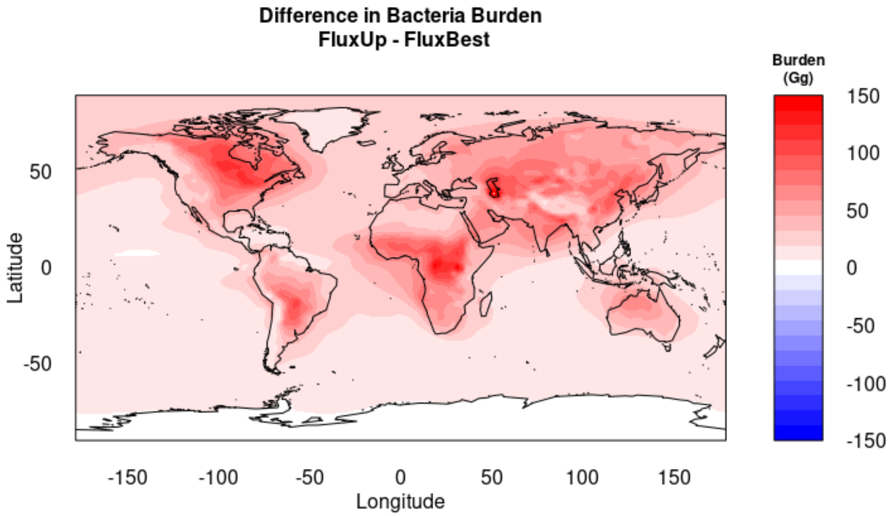




Burden


Bacteria Burden RadOff Flux Up
Burden (Gg)
200
150
100
50
0
Latitude
50
0
-50
-150
-100
-50
0
50
100
150
Longitude


Bacteria Burden RadOff Flux best estimates
Burden (Gg)
80
60
40
20
0
Latitude
50
0
-50
-150
-100
-50
0
50
100
150
Longitude


Difference in Bacteria Burden
FluxUp - FluxBest
Burden (Gg)
150
100
50
0
-50
-100
-150
Latitude
50
0
-50
-150
-100
-50
0
50
100
150
Longitude

Comparison with literature
Best estimate fluxes

Variable	Estimated global mean value from GISS ModelE2.1	Literature Value [a] Burrows et al. (2009) [b] Hoose et al. (2010) [C] Sesartic et al. (2012)
Emission rate (Tg/yr)	0.785	0.74[(a)] 0.75[(b)] 2.58[(c)]
Burden (Gg)	10.2	8.7[(a)] 4.3[(b)] 30[(c)]
Dry Depo 10^{-13} ($kg/m^2/s$)	0.15	1.7[(c)]
Wet Depo 10^{-13} ($kg/m^2/s$)	0.33	3.8[(c)]
Total Depo 10^{-13} ($kg/m^2/s$)	0.488	5.49[(c)]
Lifetime (days)	4.74	5.6[(a)] 4.2[(c)]

Size = 1 micron, density =1000 kg/m^3, mass= 0.52 pg = 5.2E-16 kg (Burrow et al ., 2009b), 50% dissolving fraction, Radiation Off

Comparison with literature
Best estimate fluxes
vs
Upper estimate fluxes from Burrows et al., 2009b

Variable	Estimated global mean value from GISS ModelE2.1	Literature Value [a] Burrows et al. (2009) [b] Hoose et al. (2010) [C] Sesartic et al. (2012)
Emission rate (Tg/yr)	0.785 3.98	0.74[a] 0.75[b] 2.58[c]
Burden (Gg)	10.2 38.7	8.7[a] 4.3[b] 30[c]
Dry Depo 10^{-13} ($kg/m^2/s$)	0.15 0.653	1.7[c]
Wet Depo 10^{-13} ($kg/m^2/s$)	0.33 1.78	3.8[c]
Total Depo 10^{-13} ($kg/m^2/s$)	0.488 2.46	5.49[c]
Lifetime (days)	4.74 3.6	5.6[a] 4.2[c]

Size = 1 micron, density =1000 kg/m^3, mass= 0.52 pg = 5.2E-16 kg (Burrow et al ., 2009b), 50% dissolving fraction, Radiation Off

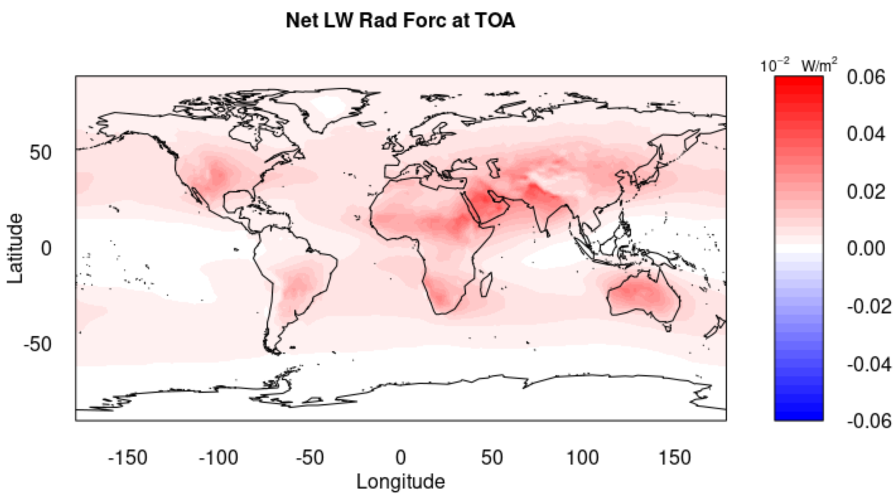
Comparison with literature

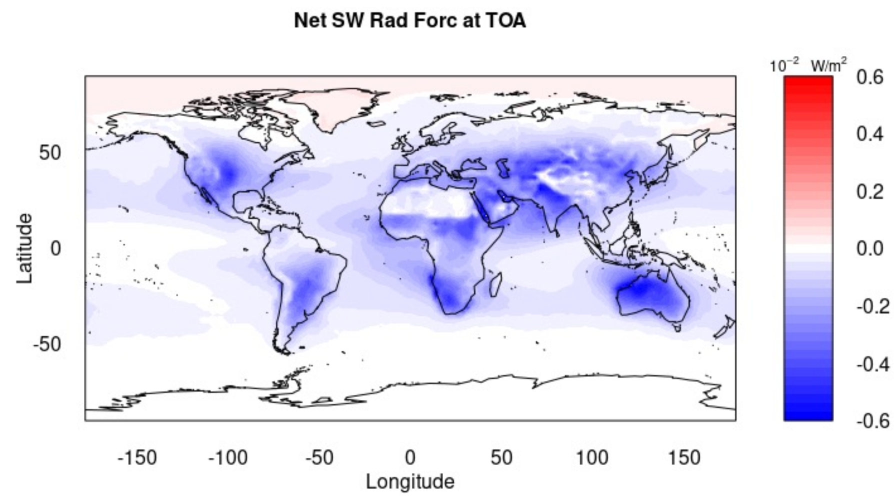
Radiation Off Vs Radiation On

Variable	Estimated global mean value from GISS ModelE2.1	Literature Value [a] Burrows et al. (2009) [b] Hoose et al. (2010) [C] Sesartic et al. (2012)
Emission rate (Tg/yr)	0.785 0.785	0.74[(a)] 0.75[(b)] 2.58[(c)]
Burden (Gg)	10.2 10.1	8.7[(a)] 4.3[(b)] 30[(c)]
Dry Depo 10^{-13} ($kg/m^2/s$)	0.15 0.148	1.7[(c)]
Wet Depo 10^{-13} ($kg/m^2/s$)	0.33 0.33	3.8[(c)]
Total Depo 10^{-13} ($kg/m^2/s$)	0.488 0.488	5.49[(c)]
Lifetime (days)	4.74 4.69	5.6[(a)] 4.2[(c)]

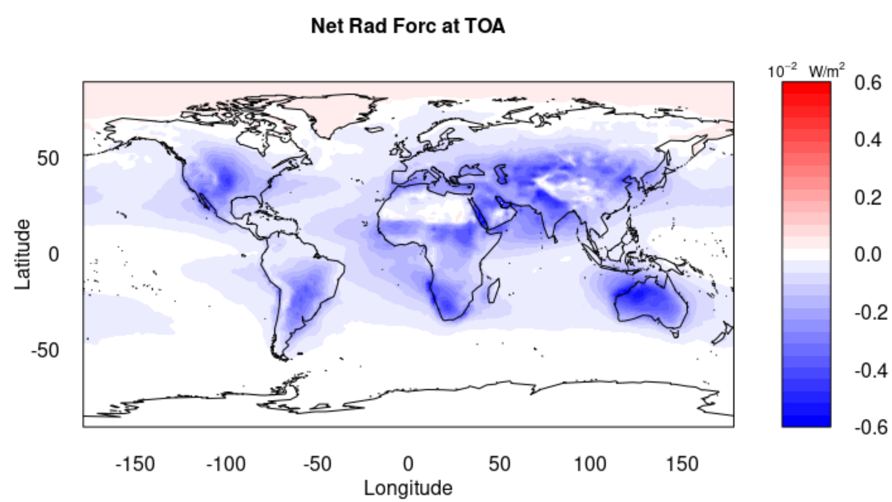
Size = 1 micron, density =1000 kg/m^3, mass= 0.52 pg = 5.2E-16 kg (Burrow et al ., 2009b), 50% dissolving fraction
Best estimate fluxes from Burrows et al., 2009b

Preliminary Results of Introducing Bacteria in GISS ModelE2.1
Radiation at TOA

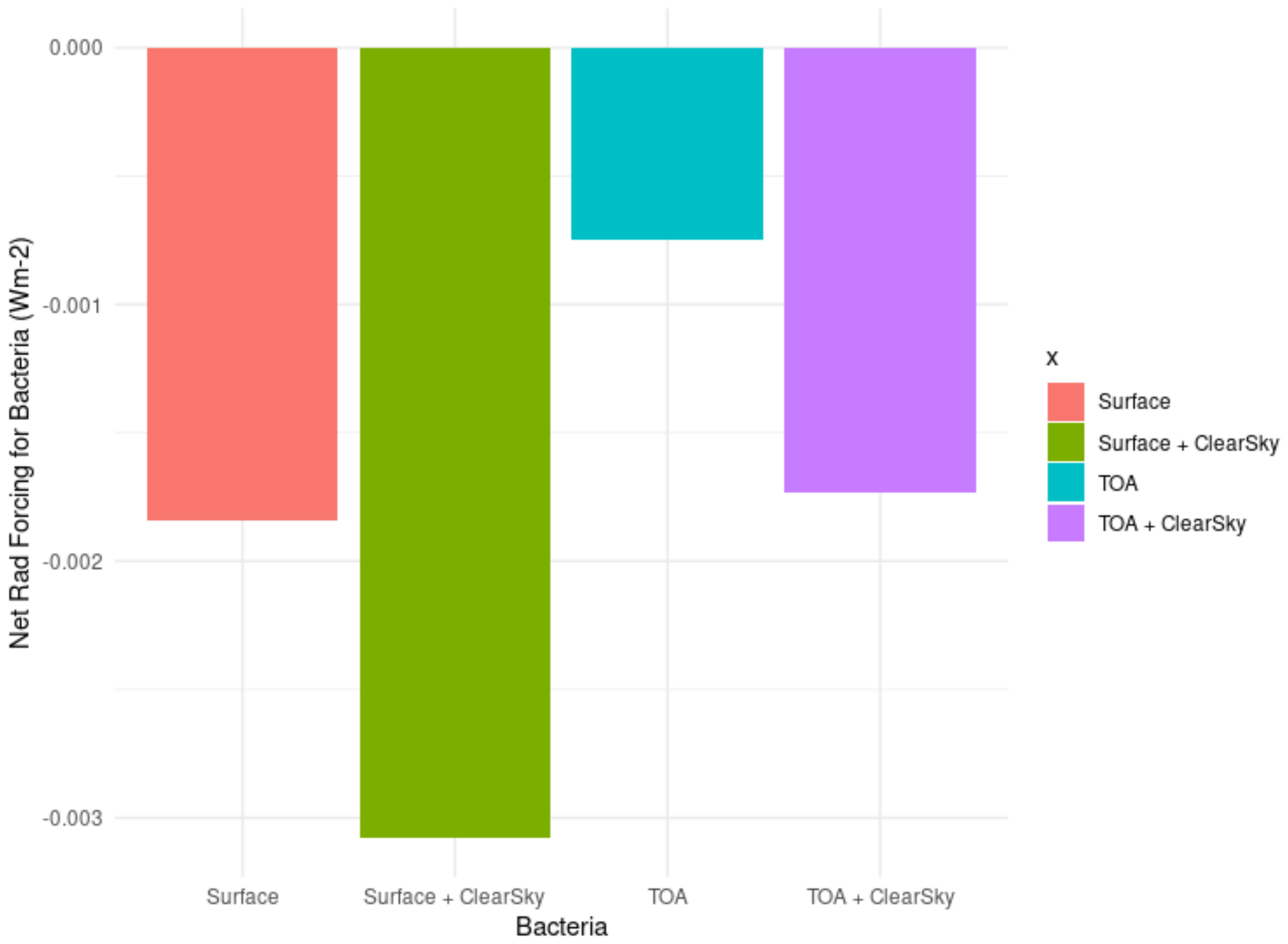




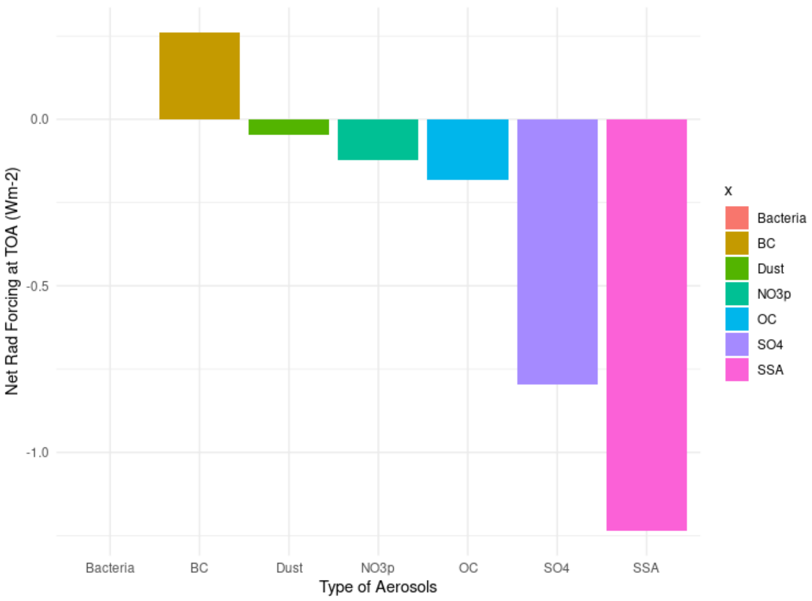
In this simulation, we did a double call to the radiation

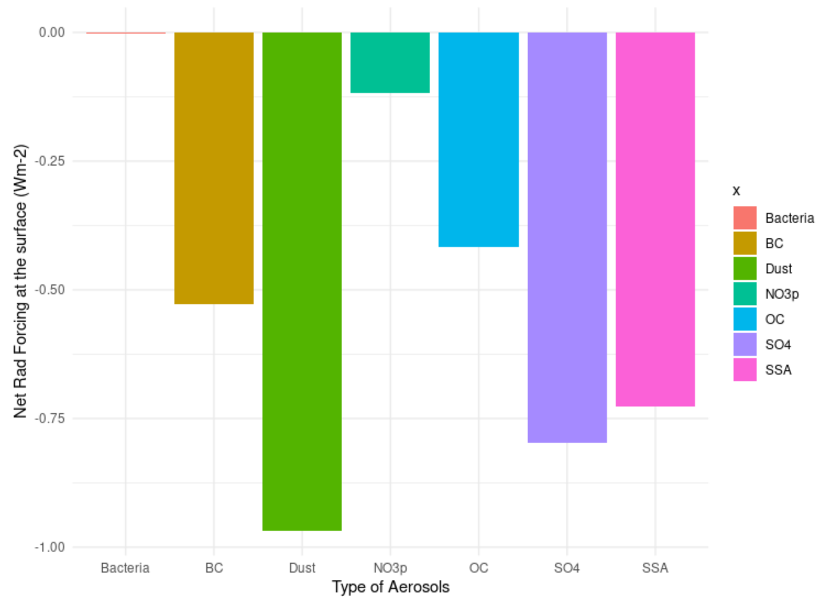


Global Annual Mean of Net direct Radiative Forcing of Bacteria



Net direct Radiative Forcing
Bacteria vs Aerosols





Summary

Achieved:

- An emission routine/model of PBAPs is developed (still on progress) and implemented into GISS ModelE2.1

Take home message:

- **Bacteria have a cooling net direct radiative forcing**
- **But,** direct cooling effect is **negligible** in comparison with other types of aerosol

However,

- **Regionally**, bacteria might have an impact where fluxes of bacteria are high
- **Bacteria – cloud** interaction is **not** yet included
- **More importantly**, this resulted impact is from using the best estimates of bacteria emission fluxes, where ocean and forest fluxes were 0

Thanks for listning