DEB
2023

DEB-in-Practice DEB tools to Trait Based Ecology

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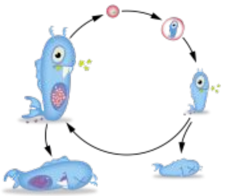
Baton Rouge, Louisiana, United States
deb2023.sciencesconf.org

Inter-species comparisons



- parameter values
- implied properties

Know your labels !!!

Careful with temperature !!!

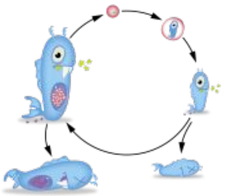
AmPtool

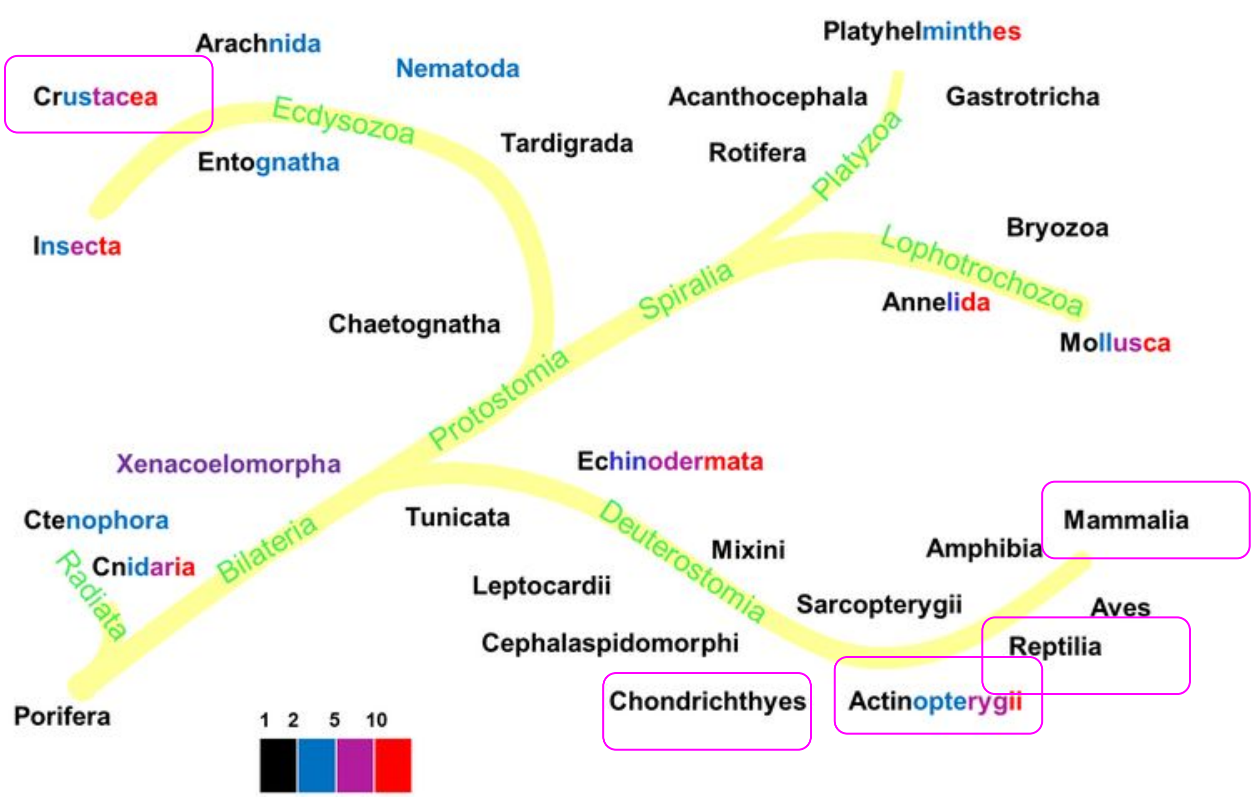
AmP data

Example to be found: GitHub [add-my-pet](add-my-pet) / **SI**

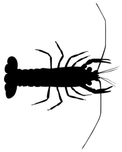
Manual: amptool.debtheory.org/docs/

Five taxonomic groups:



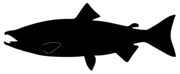


Crustacea

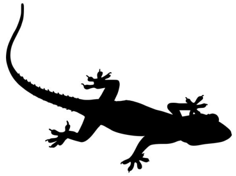


Chondrichthyes

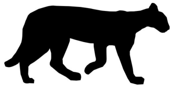
Actinopterygii



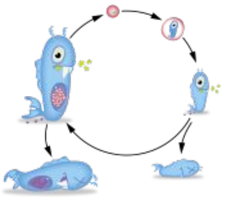
Reptilia



Mammalia

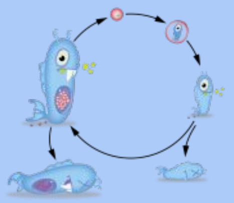


What traits co-vary?



- Primary scaling relationships
  - Covariation of primary parameters
- Secondary scaling relationships
  - Covariation of compound parameters
- Tertiary scaling relationships
  - Deal with phenomena at larger scales in time and space

Primary scaling relationship

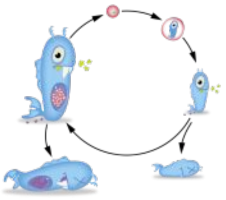


Plot maturity level at birth against maximum structural

Each of the 5 groups works with different taxa (10 min)
Then come to board and present the different graphs

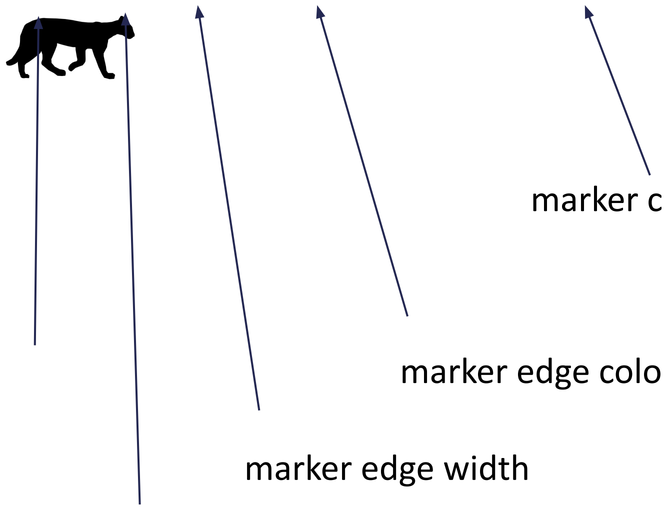
Mammalia; Crustacea; Chondrichthyes; Actinopterygii; Reptilia

Primary scaling: coding support:



1st define your legend; order matters

```
legend_mamm = { ... %
   {'o', 8, 1, [0 0 0], [0 1 1]}, 'Mammalia'
   {'o', 8, 1, [1 1 1], [0.8 0.8 0.8]}, 'Animalia'
 };
```



marker color (cyan)

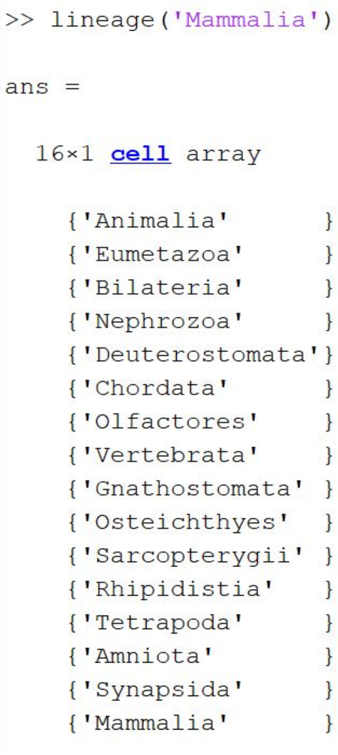
marker edge color (black)

marker

marker edge width

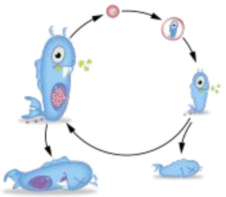
marker size

The order matters: Animalia in the back, and Mammalia in the front

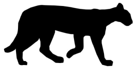


```
>> lineage('Mammalia')

ans =

  16×1 cell array

    {'Animalia'       }
    {'Eumetazoa'      }
    {'Bilateria'      }
    {'Nephrozoa'      }
    {'Deuterostomata'}
    {'Chordata'       }
    {'Olfactores'     }
    {'Vertebrata'     }
    {'Gnathostomata' }
    {'Osteichthyes'   }
    {'Sarcopterygii' }
    {'Rhipidistia'    }
    {'Tetrapoda'      }
    {'Amniota'        }
    {'Synapsida'      }
    {'Mammalia'       }
```

amptool.debtheory.org/docs/

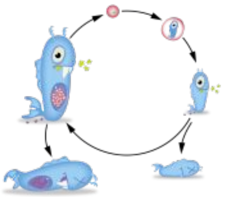


```
shstat_options('default');
LiEHb = read_allStat({'L_i', 'E_Hb'});
```



```
[Li_EHb, leg] = shstat(LiEHb, legend_mamm, 'Mammalia');
figure(Li_EHb)
xlabel('_{10}log ultimate struc length, L_i^\infty, cm')
ylabel('_{10}log E_H^b, J')
print -r300 -dpng Li_EHb_mammalia.png
figure(leg)
print -r300 -dpng leg_mammalia.png
```

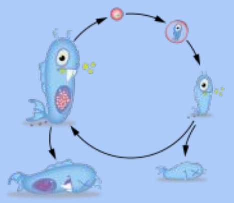
Secondary scaling relationship



$$[E_m] = \frac{\{\dot{p}_{Am}\}}{\dot{v}} = z[E_m^{\text{ref}}]$$

A large-bodied species has larger reserve capacity

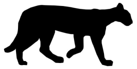
Inter-species comparison In practice:



Plot maximum reserve density again maximum length - secondary

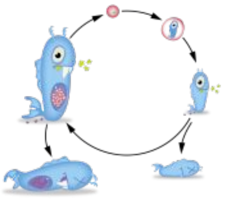
Each of the 5 groups works with different taxa (10 min)
Then come to board and present the different graphs

amptool.debtheory.org/docs/



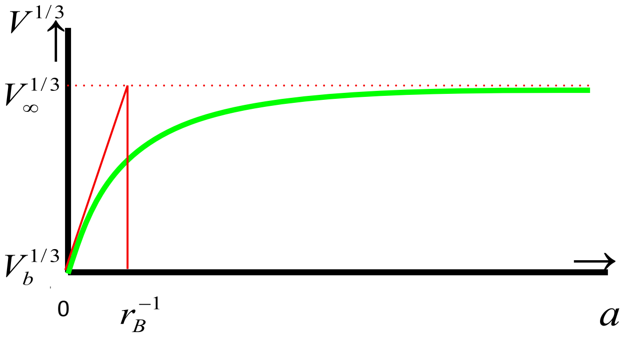
```
shstat_options('default');
LiEm = read_allStat({'L_i', 'E_m'});

[Li_Em, leg] = shstat(LiEm, legend_mamm, 'Mammalia');
figure(Li_Em)
xlabel('_{10}log ultimate struc length, L_i^\infty, cm')
ylabel('_{10}log maximum reserve density, [E_m], J/cm^3')
print -r300 -dpng Li_Em_mammalia.png
figure(leg)
print -r300 -dpng leg_mammalia.png
```

Secondary scaling relationship



von Bertalanffy growth rate:

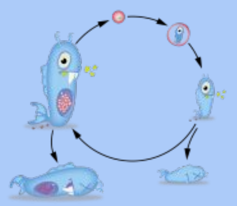
$$r_B = \frac{\dot{k}_M / 3}{1 + f / g} = \frac{\dot{k}_M^{ref} / 3}{1 + zf / g_{ref}}$$



$$V^{1/3}(a) = V_\infty^{1/3} - (V_\infty^{1/3} - V_b^{1/3}) \exp(-r_B a)$$

$\dot{r}_B$	von Bertalanffy growth rate
$\dot{k}_M$	somatic maintenance rate coeff
g	energy investment ratio
z	zoom factor

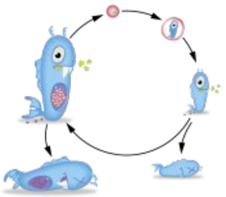
Inter-species comparison In practice:

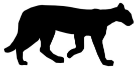


Plot von Bert as function of maximum length with and without temperature correction

10 minutes

amptool.debtheory.org/docs/

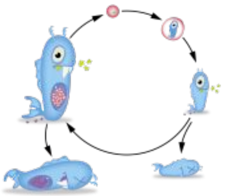




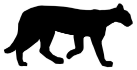
```
shstat_options('default');
 LirBcT = read_allStat({'L_i', 'r_B', 'c_T'});
     LirB = [LirBcT(:,1), LirBcT(:,2)];
 [Li_rB, leg] = shstat(LirB, legend_mamm, 'Mammalia');
 figure(Li_rB)
 xlabel('_{10}log ultimate struc length, L_i^\infty, cm')
 ylabel('_{10}log r_B, 1/d, T_typical')
 print -r300 -dpng Li_rB_mammalia.png
 figure(leg)
```

Very important: These quantities like `r_B` and `E_m` are read from AmPdata structure !!! Food dependant statistics are all given at **T_typical**

amptool.debtheory.org/docs/



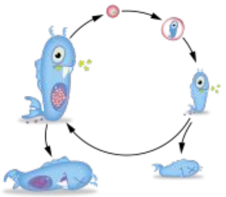
Create same plot but put the VB growth rate at reference temperature for all species:



```
shstat_options('default');
 LirBcT = read_allStat({'L_i', 'r B', 'c T'});
 LirB = [LirBcT(:,1), LirBcT(:,2)./ LirBcT(:,3)];
 [Li_rB, leg] = shstat(LirB, legend_mamm, 'Mammalia');
 figure(Li_rB)
 xlabel('_{10}log ultimate struc length, L_i^\infty, cm')
 ylabel('_{10}log r_B, 1/d, T_ref')
 print -r300 -dpng Li_rB_mammalia_Tref.png
 figure(leg)
```

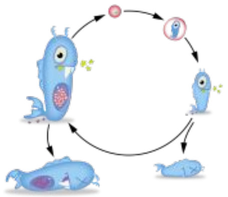
Very important: These quantities like `r_B` and `E_m` are read from AmPdata structure !!! Food dependant statistics are all given at **T_typical**

Inter-species comparison In practice:



- For example: weight at birth as function of ultimate weight.
- You can calculate quantities you do not have data for to check consistency.
- You have to think about the levels of organisation in the phylogeny to make meaningful plots
- Be careful with temperature!!!

Inter-species comparison In practice:

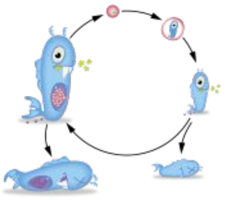


debportal.debtheory.org/docs/DEBpapers.html#Patterns

There is a link to the add-my-pet/SI GitHub repository where the matlab code that generate figures for all of the papers are provided

You can use this for inspiration

Survivor or survival function



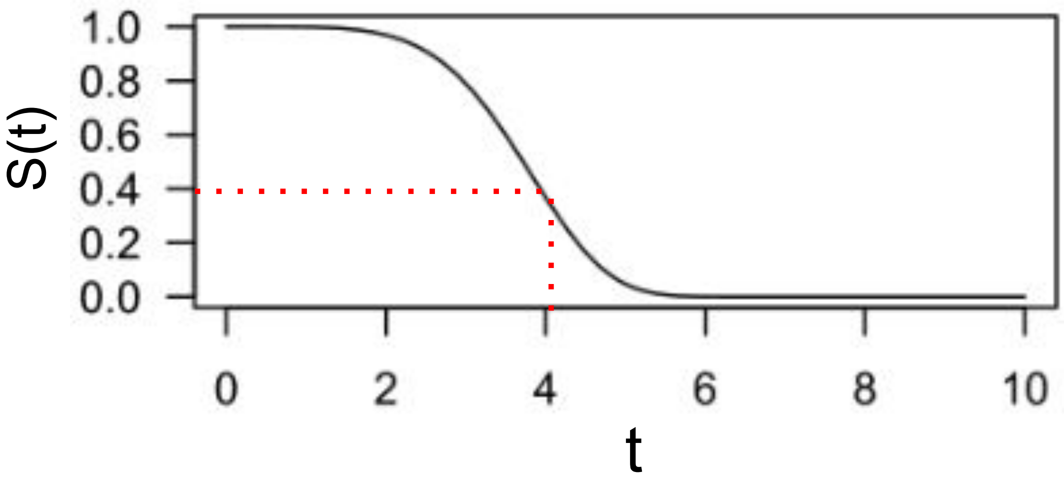
- Let *T* be a continuous random variable with probability density function *f*(*t*) and cumulative distribution function *F*(*t*) on the interval [0,∞).

The survivor function *S*(*t*) is

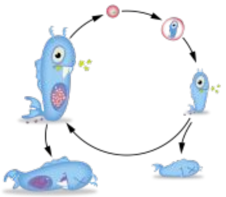
$$S(t) = P(T > t) = \int_t^{\infty} f(u)du = 1 - F(t)$$

It gives the probability that an object will survive past a certain time or the proportion of the values of *T* that are larger than t

The probability of taking values larger than 4 is 0.4; S(4) = 0.4



Empirical survivor function

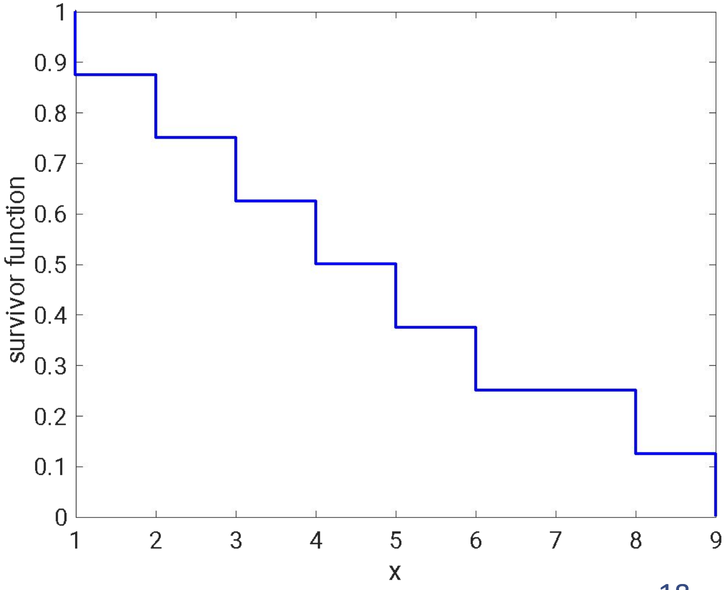


The empirical survivor function is the distribution function associated with the values of a sample. It is a step function that jumps down by $1/n$ at each of the n data points. Its value at any specified value of the measured variable is the fraction of observations of the measured variable that are greater than or equal to the specified value.

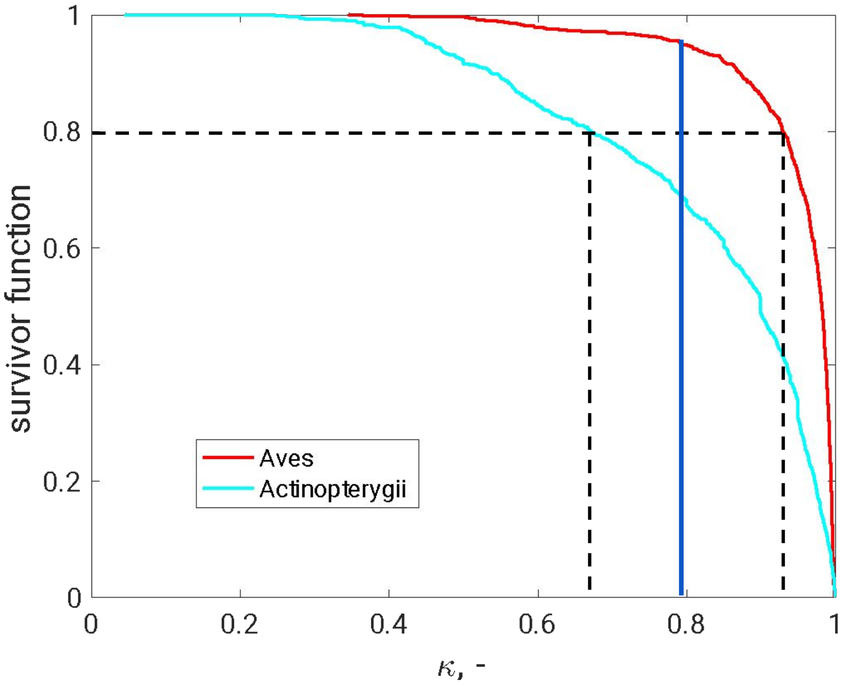
DEDtool function `surv` computes the survival function

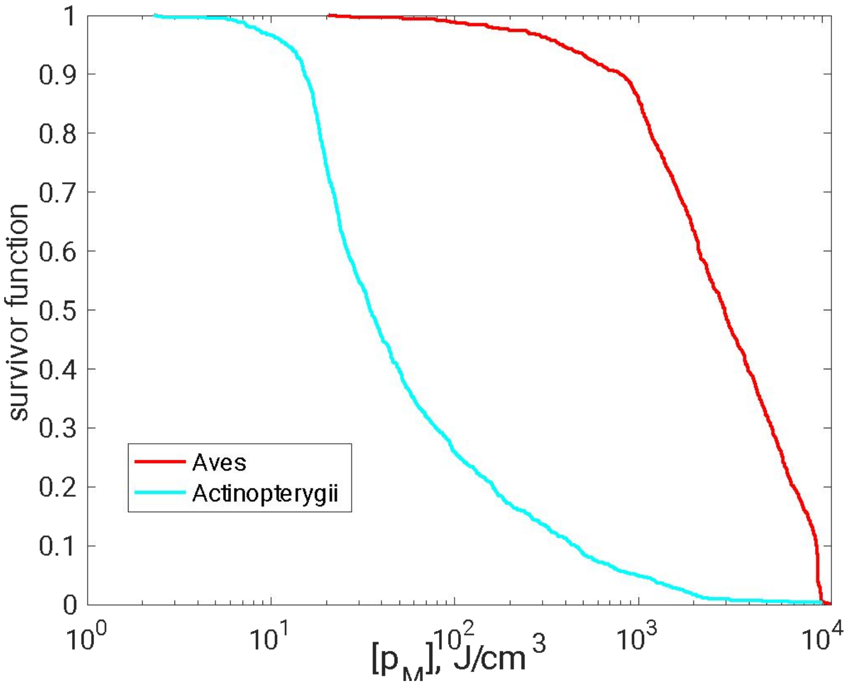
Example

```
xy = surv([3 8 2 1 4 5 6 9]);
plot(xy(:,1), xy(:,2),'b')
```



Empirical survivor function

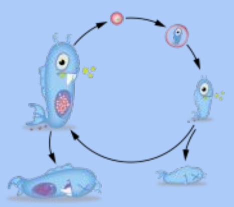




80% of Aves have κ >0.95
80% of Actinopterygii have κ >0.75

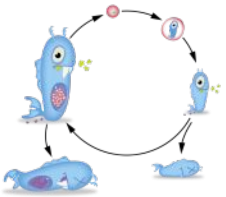
95% of Aves and 67% of Actinopterygii have
κ values larger than 0.8

Survival function of compound parameter



maximum reserve density

Survival function coding support:



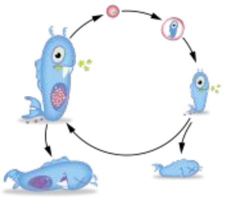
```
% line legends:

llegend_mamm = { ... %
   {'-', 2, [0 1 1]}, 'Mammalia'
   {'-', 2, [0.8 0.8 0.8]}, 'Animalia'
  };
```

line style

line width

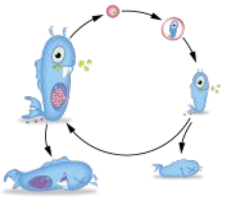
color

Survival function coding support:



```
shstat_options('x_transform', 'log10');
   hE_m = shstat({'E_m'}, llegend_mamm,'Mammalia');
   figure(hE_m)
   xlabel('_{10}log reserve capacity, [E_m], J/cm^3')
   print -r300 -dpng Em_mamm.png
```

You can also query by ecocodes:



```
select_eco('ecozone', {'MS','TS'})
```

Selection of all (terrestrial and marine) Antarctic species

```
speciesNames = select_eco('ecozone', {'MS','TS'});
```

```
LiPM_antartica = read_stat(speciesNames,{'L_i','p_M'});
plot(log10(LiPM_antartica(:,1)), log10(LiPM_antartica(:,2)), 'ro')
```

Just to show that you can make your own plots…. many plots possible but they do not always make sense. Notice that the temperature is at T reference. Taken from AmPdata !

Thank you