

Report on the Second SCAR Retrospective Analysis of Antarctic Tracking Data Workshop

Hanse-Wissenschaftskolleg (HWK)
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<http://www.h-w-k.de/>

4 - 8 April 2016

Attendees: Mark Hindell (Co-convenor and workshop chair), Yan Ropert-Coudert (co-convenor), Phil Trathan, Mary-Anne Lea, Horst Bornemann (co-convenor), Antonie Haas, Kerstin Jerosch, Dominik Nachtsheim, Luis Huckstadt, Ian Jonsen, Ryan Reisinger, Anton Van de Putte, Simon Wotherspoon

Video attendees: Ben Raymond

Apology: Bruno Danis



SCAR EG-BAMM and EG-ABI sponsored a second five-day workshop on the Retrospective Analysis of Antarctic Tracking Data (RAATD). The overarching goals of the RAATD project are to undertake a multi-species assessment of habitat use of Antarctic top predators in the Southern Ocean based on existing animal tracking data to identify *Areas of Ecological Significance* (AES), which are regions that are important for foraging to a range of predators and which have high diversity and abundance of lower trophic levels. The project will provide (i) a greater understanding of fundamental ecosystem processes in the Southern Ocean (ii) facilitate future projections of predator distributions under varying climate regimes and (iii) provide input into spatial management planning decisions for management authorities such as CCAMLR. The synopsis of multi-predator tracking data will also expose potential gaps of data coverage in regions or seasons that are important but under-represented, either as a result of a low regional research presence or a low ecological significance. This will provide an important input for directing future studies.

The first workshop in Brussels established a database (with associated metadata) of over 2000 individual tracks from the Southern Ocean, drawing on contributions from more than 30 data owners. The workshop also established an analytical frame work for analyses of these data to identify AES in the Southern Ocean based on existing animal tracking data.

The second meeting was hosted by the Hanse-Wissenschaftskolleg (institute for Advanced Studies) in Delmenhorst, Germany, with financial support from HWK, the Alfred Wegner Institute, Deutsche Forschungsgemeinschaft (DFG), SCAR, and Macquarie University. The participants included database specialists, spatial ecologists and statisticians with the objective to consolidate the database and to develop the habitat utilisation models (HUMs) that underpin the RAATD goals.

The meeting opened with a short overview of the project and a summary of the last RAATD meeting in Brussels by MH. There were then reports from YR-C about progress regarding the

database since the last meeting, IJ on recent developments of his state space animal movement model, SW on progress on statistical model development since the last meeting and RR describing his multi-species tracking analysis for Marion Island.

There was then a detailed discussion about the modelling approach to be adopted in light of the decisions made in Brussels and the progress made by the modelling group (BR, IJ, SW and MH) since that time. The general framework of (i) developing a habitat utilization model (HUM) for each species, (ii) using that HUM to make global predictions of important habitat based on colony locations (where appropriate) and then (iii) combining these species specific global predictions to indicate Areas of Ecological Significance was agreed.

For development of HUMs it was agreed to continue exploring at least three approaches:

1. Track-based comparison of where animals went (the actual track) with areas that were available them (a set of random tracks with similar movement characteristics to the actual track). A set of environmental variables is derived for each location (actual or random) and these are compared in a statistical model to establish those variables that best distinguish the particular areas used by the species. This is the approach used by BR and RR in their prior analyses, and can be regarded as “selectivity” model. This will be called the “track selectivity” approach.
2. The gridded comparison of actual tracks and random tracks. This is a modification of the track-based approach and combines the information for each individual and each deployment location onto spatial grids. It produces two sets of grids; an “availability” grid consisting of the number of times a track, real or random, used a grid cell, and a “usage” grid consisting of the number of times only a real track used a grid cell. Each grid is then modelled against a set of environmental variables to provide an “availability” and a “usage” model. The product of these two model outputs provides a measure of preference for each cell. This is another form of selectivity model and will be called the “gridded selectivity” approach
3. A “usage” model that only uses information from observed tracks. In this case, a region is gridded and the mean time that each track spent in each cell is calculated. These are then modelled against a set of environmental variables to determine which variables are associated with areas of high and low usage. This is termed the “gridded usage” model, and is similar to kernel density analyses commonly used with tracking data.

MH outlined the scope and objectives for this meeting before a discussion on the best way to achieve these objectives. We then divided into two working groups – the data management group and the modelling group.

The agreed objectives of the meeting were:

(i) Database Management group

1. Compile metadata records
2. Compile list of species for each of the temporal groupings (*e.g.* breeding non-breeding)

3. Identify and source missing datasets
4. Obtain a list of colony locations for all species
5. Initial quality control of datasets (pre-filtering and post-filtering data clean-up)
6. Prepare manuscript for a data paper

(ii) Data modelling group

1. Run State Space Animal Movement Models (SSAMMs) for each species
2. Generate random tracks, using parameters from the SSAMMs, to define available areas
3. Extract environmental datasets
4. Develop statistical habitat use models for each species
5. Generate spatial predictions for each species
6. Combine predictions to identify Areas of Ecological significance

Achievements of the workshop

(i) Database Management group

1. Compile metadata records

Metadata records were compiled over the week. Many inconsistencies were detected and the addition of a few new datasets meant that a near final set of homogenous and corresponding metadata and data files was not obtained before the end of the workshop. This work will continue out of session with a view to completion by the end of May. **Action Item 1**

2. Compile list of species

At the end of the workshop, the RAATD dataset contained **3447** individual tracking data files from 15 species; ten species of seabirds and five species of marine mammals. The majority of the individuals (53% of the seabirds and 95% of the marine mammals) were tracked by satellite telemetry (PTT). Five species (one marine mammal species) were tracked by GLS, while 8 out of 10 seabird species were tracked with GPS; no marine mammals were tracked using GPS technology.

Table 1: A summary of the data included in the RAATD dataset at the end of the 2016 WHK meeting. Data are summarised by the number of individuals tracked in each species, and by the tracking methodology: PTT (Argos Satellite Tracking), GPS (Geographic positioning system) and GLS (light-based geo-location).

Species	GLS	GPS	PTT	Total
<i>Aptenodytes forsteri</i>			143	143
<i>Aptenodytes patagonicus</i>		9	101	110
<i>Diomedea exulans</i>	134	104	28	266

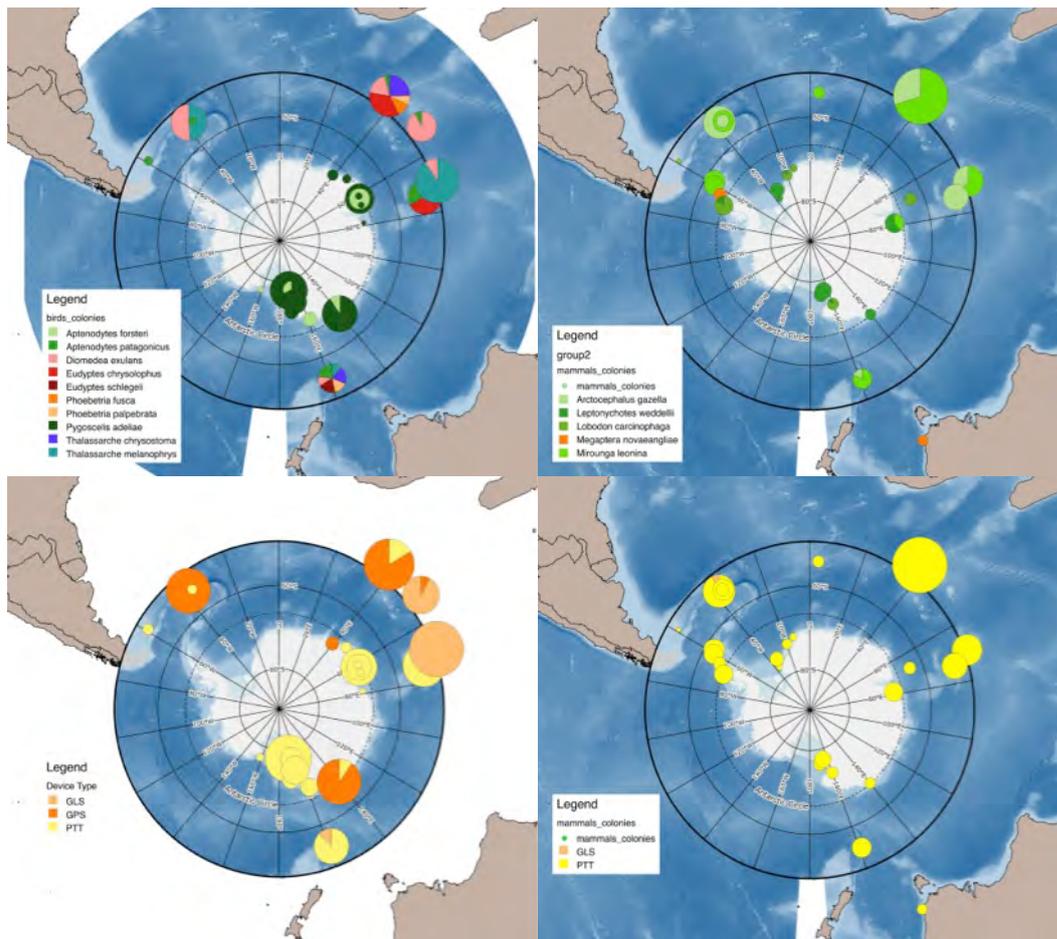
<i>Eudyptes chrysolophus</i>		75	87	162
<i>Eudyptes schlegeli</i>			20	20
<i>Phoebetria fusca</i>		23		23
<i>Phoebetria palpebrata</i>	3	10	25	38
<i>Pygoscelis adeliae</i>		166	574	740
<i>Thalassarche chrysostoma</i>	3	53	17	73
<i>Thalassarche melanophrys</i>	229	81	18	328
Total	369	521	1013	1903

Species	GLS	PTT	Total
<i>Arctocephalus gazella</i>	71	438	509
<i>Leptonychotes weddellii</i>		169	169
<i>Lobodon carcinophaga/us?</i>		105	105
<i>Megaptera novaeangliae</i>		46	46
<i>Mirounga leonina</i>		715	715
Total	71	1473	1544

RAATD has so far accumulated a grand total of **2,426,456** location fixes. 55.5% of all locations belong to the marine mammal dataset, with elephant seals locations accounting for 33.3% of the total. In the seabird group, nearly 20% of the locations are shared between Adelie penguins and wandering albatrosses.

Importantly, these data come from 37 separate data owners (Table 2), who have agreed to share their hard won data with the RAATD project.

Figure 1. Summary maps of (a) the number of bird species per deployment location, (b) the number of mammal species per deployment location, (c) the tracking methods used for birds per deployment location and (d) the tracking methods used for mammals per deployment location. The size of the circle indicates the number of individuals tracked. Please note that these are figures drawn using raw data, and will be refined as the metadata task is completed and additional tracking data added.



3. Identify and source missing datasets

Four species coordinating teams have been responsible for approaching data owners and then collating data. These were:

Phil Trathan and Yan Ropert-Courdert: Penguins

Luis Huckstadt: Weddell and Crabeater seals

Mark Hindell and Jose Xavier: elephant seals and albatross

Mary-Anne Lea: Antarctic fur seals

Several additional datasets were identified, and data owner permission obtained during and just after the workshop. Some of these were through the new Birdlife International Seabird Tracking Database (<http://www.seabirdtracking.org/>), which is proving to be an invaluable resource for RAATD. There were:

(i) Adélie Penguin data from the US AMLR Program (Jefferson Hinke and Wayne Trivelpiece), Argentina (Mecha Santos) and Japan (Akinori Takahashi) from the Antarctic Peninsula, filling an important gap in our coverage for this species.

(ii) Macaroni Penguin data from South Georgia (BAS) and from Kerguelen (France, Charly Bost), also filling important gaps for this species.

In addition, tracking data on Humpback whales were obtained with the permission to use from Luciano Dalla Rosa from the Universidade Federal do Rio Grande.

It was decided that from the end of the workshop onwards any incoming new datasets would be stored into a separate folder (RAATD_additional_datasets after April 2016) on both the Google Drive and the Dropbox folder. This would minimise confusion with existing datasets that are being pre-processed at the moment. It was also decided that the group would stop looking for new datasets from the end of May 2016. Until that date, potential new datasets to be included are:

1. White-chinned petrels - MH to contact David Thompson, Richard Phillips, Henri Weimerskirch
2. Antarctic fur seals - M-AL to contact Christophe Guinet, Andy Lowther and Akinori Takahashi for additional datasets.

Action Item 2.

Table 2: List of all 37 data owners who have contributed to RAATD so far. They come from 23 different institutions from 11 different countries

Data Owner	Organisation	Country
Akinori Takahashi	National Institute for Polar Research	Japan
Ari Friedlander	Oregon State University	USA
Barbara Wienecke	Australian Antarctic Division	Australia
Ben Raymond (on behalf of various AADC contributors)	Australian Antarctic Data Centre	Australia
Charly Bost	CEBC	France
Christophe Guinet	CEBC	France
Colin Southwell	Australian Antarctic Division	Australia
Dan Costa	University of California, Santa Cruz	USA
David Ainley	H.T. Harvey & Associates	USA
Erling S. Norday	University of Tromso	Norway
Graham Robertson	Australian Antarctic Data Centre	Australia
Henri Weimerskirch	CEBC	France
Horst Bornemann	Alfred Wegner Institute	Germany
Iain Staniland	British Antarctic Survey	United Kingdom
Jean-Benoit Charrassin	L'Ocean	France
Jefferson Hinke	NOAA	USA
Jerry Kooyman	Scripps	USA
Karine Delord	CEBC	France
Kit Kovacs	Norwegian Polar Institute	Norway
Klemens Pütz	Antarctic Research Trust	Germany

Luciano Dalla Rosa	Federal University of Rio Grande	Brazil
Mark Hindell	University of Tasmania	Australia
Marthan Bester	University of Pretoria	South Africa
Mary-Anne Lea	University of Tasmania	Australia
Mecha Santos	Instituto Antartico Argentino	Argentina
Mike Fedak	Sea Mammal Research Unit	United Kingdom
Mike Goebel	NOAA	USA
Monica Muelbert	Federal University of Rio Grande	Brazil
Newi Makhado	Department of Environmental Affairs	South Africa
Nico De Bruyn	University of Pretoria	South Africa
Norman Ratcliffe	British Antarctic Survey	United Kingdom
Peter Boveng	NOAA	USA
Peter Ryan	Percy Fitzpatrick Institute	South Africa
Phil Trathan	British Antarctic Survey	United Kingdom
Pierre Pistorius	Nelson Mandela Metropolitan University	South Africa
Rachael Alderman	DPIPWE	Australia
Richard Phillips	British Antarctic Survey	United Kingdom
Rob Crawford	Department of Environmental Affairs	South Africa
Silvia Olmastroni	University of Sienna	Italy
Wayne Trivelpiece	NOAA	USA
Yan Ropert-Coudert	CEBC	France

4. Obtain list of colony locations for all species

A list of colony locations was obtained from the Australian Antarctic Data Centre. Although not a complete list of all locations, this will be good starting point; a complete list for each species still need to be finalised. These will be used in the predictive phase of the modelling to predict species distributions from all known breeding locations for all species.

5. Initial quality control of datasets (*pre-filtering and post-filtering data clean-up*)

This was the largest job for the database management group. There are two phases; pre-filtering and post-filtering quality control.

Pre-filtering requires visual inspection of all individual tracks to:

1. Determine if there are sufficient locations in a track to warrant its inclusion in the analysis. This is very species specific. For some species which make short foraging trips of one or two days very short tracks might be included, but this is not appropriate for far ranging migratory species such as whales.

2. Establish if the location file needs to be “trimmed”. Tags are sometimes turned on before deployment, resulting in spurious locations which need to be removed. Also, tag performance can deteriorate after some time, with fewer and fewer locations received towards the end of a record. If these become too sparse the resulting time gaps will cause problems for the SSAMM and so these need to be identified and removed. Deciding whether a tag has been

moulted and is tracking seaice, rather than the target species is also necessary for some tracks.

3. Establish if the track is a breeding season or non-breeding season track.

4. Location files that span more than one type of breeding status need to be split to form a file for each status. In some very long albatross deployments that go for multiple years this will result in several new files – one for each season. For example, BBAL 123 might have been tracked for 2 years, covering 2 breeding seasons and two non-breeding seasons. The track would then need to be split into 4 files (breeding season1, non-breeding1, breeding2, non-breeding2) and the initial single meta data record (BBAL 123) changed to 4 records (BBAL 123_BS1, BBAL 123_NB1, BBAL 123_BS2, BBAL 123_NB2).

5. Establish the appropriate track interpolation time step for each species.

After the pre-filter quality control, the tracks are run through the SSAMMs with species appropriate time steps to provide (i) a filtered set of locations, with uncertainly estimates for each location and (ii) movement parameter estimates which will be used to generate tracks for the habitat utilisation modelling (HUM) phase described in detail below. Before the HUM modelling can begin there needs to be a final visual inspection of each filtered track to ensure proper movement model fit and convergence. These final checks are to be made by the species coordinators after IJ has run the movement models. He has supplied the coordinators with working versions of code to produce pre-filter maps of all the tracks and to run the movement models.

This work was well advanced by the end of the meeting, but not completed. LH, RR and MH undertook to complete the pre-filtering work within two weeks to ensure the work of the modelling group could continue as soon as possible. **Action Item 3.**

6. Prepare manuscript for a data paper

It was decided that the data paper would be written after the workshop but that it would not be submitted as a stand-alone paper. We will rather make it a companion paper to the first main analysis paper. MH, YR-C and AVdP will write to all data owners to make sure they agree with their data being used for this paper, as it requires that all data are stored in a publicly accessible database. **Action Item 4.**

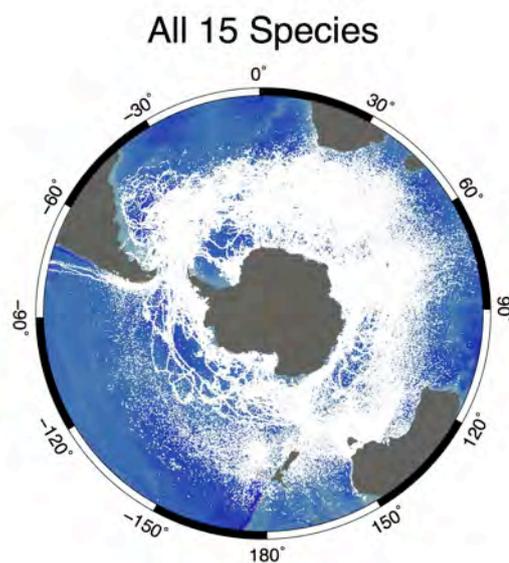
AVdP agreed to be charge of drafting the data paper with YR-C, LH and MH. Co-authorship of RAATD papers was discussed and it was proposed that all the Principal Investigators (data owners) of datasets will be primary authors and will be asked to suggest (and justify) others who might be co-authors. Further discussion of the first analytical paper is reported below.

(ii) Data modelling group

1. Run Movement models for each species.

IJ has made a number of very significant changes and improvements to his State Space Animal Movement Model (SSAMM). Significantly, it now runs much faster and can process all the RAATD locations in about a day. He has also now made it interface directly with files and metafiles in the RAATD format. He described the changes in detail as well as giving all of the data coordinators a tutorial on how to run the pre-filter visualisation step and the final filtering step. It was agreed that each of the data coordinators would take responsibility for the post-filter check of model fits, but that IJ would do the final set of model runs after feedback from the data coordinators, and after the pre-filter changes have been made. This will be by the end of April to give the species coordinators the data sets they need to begin running statistical models as soon as possible. **Action Item 5.**

Figure 2: Map of all 3386 individual deployments available to RAATD in early April 2016. Note that these have been through a preliminary filtering process, but the data in this figure have not been through the full quality control process.

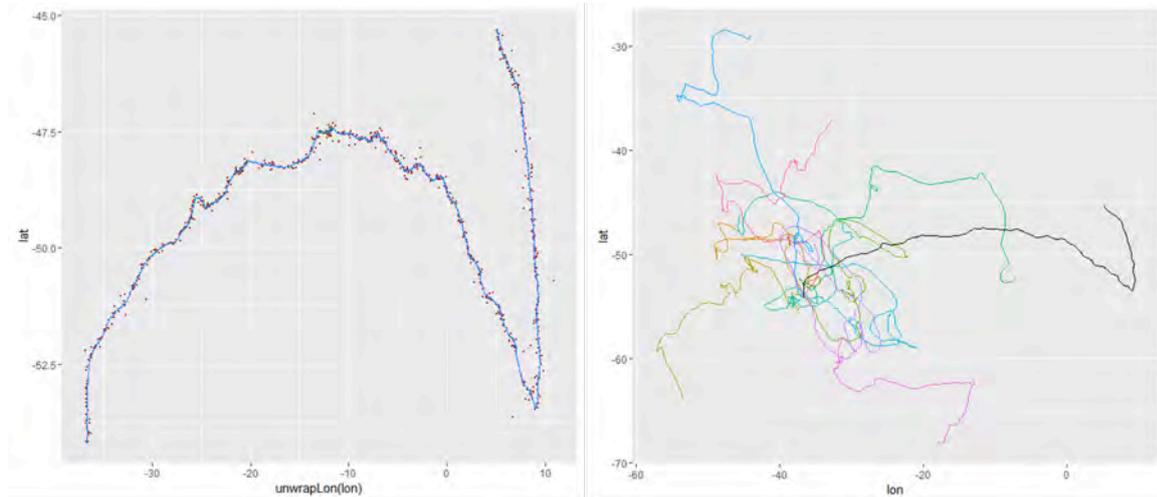


2. Generate Random tracks to define available areas

The strategy for generating realistic random tracks for the selectivity approaches was developed prior to the meeting by BR and SW. Their method takes the movement parameters estimated by the SSAMM and uses them to generate random (or pseudo) tracks which have the same characteristics as the actual track. There are two important features of these random tracks. The first is that they will perform looping tracks that return to the starting place (or other pre-designated haul-out spots) for those species that have colony-based trips. The other is that the tracks do not need to be split into individual trips. They use fixed points with the deployment site, or other resting site, to define the beginning and end of a random track. When a random track gets within a user defined distance of the set points it is deemed to have returned. The R code for doing this was prepared by SW and BR and made available to the

data coordinators in the *Bremerhaven R* package. All coordinators were given instructions for doing running this code for their particular group of species.

Figure 3. Illustration of (a) the SSAMM model where the red dots are original unfiltered data and the blue are the filtered locations on a regular 6 hourly time step, and (b) 10 random (or pseudo) tracks generated by the *Bremerhaven* package, with the actual track in black.



a. State Space movement model of one southern elephant seal track

b. 10 "pseudo-tracks" generated from the movement model to quantify habitat availability

3. Extract environmental datasets

Code for extracting the environmental data sets was also prepared before the workshop by SW and BR and provided in the *Bremerhaven* package. Climatologies for a large suite of environmental data sets were provided to the workshop from the Australian Antarctic Data Centre. These included a range of satellite products such as SST, SSH, ice concentration, wind strength etc., as well as numerous derived variables, such as distance to ice edge, distance to polynya's etc. A list of variables is provided in Appendix 2. This will not be the final list of variables used in the analyses, but was intended to enable the data coordinators to start running models and to consider what variables might be most biologically meaningful for their particular species. The intention is to enlarge the available environmental datasets after the data coordinators have thought about what variables are likely to be most relevant.

The gridded selectivity and the usage approaches both require climatologies of environmental data as they inevitably aggregate tracking data over large time periods, and there is no date associated with any particular grid. Further, importance of habitat is in many cases determined by long-term or time-invariant ecological properties (such as average front positions or locations of bathymetric features). Some temporal information may be advantageous to include, such as time of year (summer vs winter or breeding vs non-breeding) but it was decided that for first model runs we would focus on the coarsest level of temporal aggregation. The individual track selectivity approach retains its time component and so each location can be linked to a specific set of environmental variables collected on the same day as the location.

4. *Develop statistical habitat use models for each species*

This was the biggest and most challenging task for the modelling group. Several steps and decisions were required before preliminary models could be run. We needed to develop R code to produce the response variable data for each of the three approaches (individual track “selectivity”, gridded “selectivity” and gridded “usage”). SW had done this for the gridded “selectivity” approach and included it in the *Bremerhaven* package, and then developed code for the other approaches during the workshop, and then integrated all three approaches into one set of code. He will continue fine-tuning this code and deliver it to the data coordinators as soon as possible. **Action Item 6.**

We also had to decide on the best type of statistical model to use to develop the HUM. The most likely candidates are generalised additive models (GAMs), boosted regression trees (BRT) and boosted GAMs. For the purposes of the workshop we began with GAMs, and preliminary HUMs were derived for each species using the gridded selectivity approach. However, as these were based on datasets that have not been through the quality control steps, or include all the data now available it would not be appropriate to present them in this report. It can be reported that even these preliminary models showed promisingly good fits to the data, at least in terms of % deviance explained, ranging from 30-70%.

The best way to determine what statistical modelling framework to use is to try all three on a range of different species. It was agreed that RR and MH would compare GAMs, BRT and boosted GAMs on a subset of seals, penguins, whales and albatross. They would complete this work within 4 weeks of the end of the workshop **Action Item 7.**

Once the best framework is established the data coordinators can develop models for each species, using their specialist knowledge to ensure the most sensible combination of variables is used. The species were allocated as follows:

LH; Weddell seals, Crabeater seals and Humpback whales

M-AL; Antarctic fur seals & Southern elephant seals

MH; Black-browed, wandering, grey-headed and light-mantle albatross

PT; (with help from MH); Adelie, emperor, king and macaroni (including royal) penguins.

The species-specific models will be developed in conjunction with the modelling team (BR, SW, IJ, Sophie Bestley, RR, and others) and with discussion with data contributors, where appropriate. This model development phase will also identify more biologically-relevant predictor variables for each species, which will be developed (where possible) and added to the available predictors (BR, SB). **Action Item 8**

An important consideration is that we are most interested in using the models for prediction of spatial use rather than interpreting the biological significance of the relationships underpinning the models. While the underlying biology of the HUM models needs to be realistic (and more biologically-relevant models will tend to give better predictions),

describing this is not the initial focus of the RAATD analysis. Rather we need to be confident that spatial predictions that we make for unstudied colonies are the best possible. So once a statistical framework has been decided we will then run a series of cross validations to estimate the uncertainty associated with these predictions. The nature of the cross-validation process has yet to be determined.

5. *Generate spatial predictions for each species*

Preliminary spatial predications were run for some species using the GAMs for the gridded selectivity data. Again it would be premature to present these preliminary results here as they were only intended to test the basic code for preparing and using the response variables. One challenge for this step is how to predict for colonies with no tracking data. SW developed code during the workshop to do this in a simple way and has include this into his latest version of the *Bremerhaven* package, so that we can quickly generate these predictions once the final datasets are prepared and the modelling framework decided on. Some questions still remain to be determined out of session, in particular should the size of each colony be including as weighting factor for the predictions. If so, larger colonies would be more influential than smaller colonies. The alternative approach is to simply identify important species specific habitats for each irrespective of its size.

6. *Combine predictions to identify Areas of Ecological Significance*

This final step was discussed among the modelling group, but no final decisions made on how best to do it. Further development of possible approaches was allocated to SW, BR, IJ and MH to work on out of session.

The workshop concluded with discussion on (i) the first set of RAATD outputs (ii) future work and responsibilities and (iii) the need for a third RAATD workshop.

Regarding RAATD outputs, it was decided that there would be two initial papers, one detailing the Areas of Ecological Significance in the Southern Ocean and relating these to the intensity of human activity in those areas (perhaps based on the recent Halpern et al. (2015) global analysis of human maritime activity) and also the hotspots of Southern Ocean climate change in terms of changes in ice and SST. This would be submitted to a high impact journal and at the same time the data paper would be submitted as a companion piece. It was recognised that an overview paper would not be able to contain all of the detail regarding analytical approaches, and that there would need to be several methodological papers and possibly an R package to be developed. It was agreed that the first two papers would be submitted later this year with MH and others leading the writing of the analysis paper and AVdP leading the data paper.

In terms of future work, most of the identified tasks have been highlighted as action items throughout this report.

There was unanimous agreement that a RAATD III (and possibly more) workshop is required to continue to progress the data analysis and production of outputs. Shortly after the workshop we were notified of the successful application for a CESAB grant (from the French Foundation for the Research on Biodiversity) by YR-C, MH and others that will provide support for ongoing RAATD work. As this was successful, all the data providers will need to be contacted to ask for inclusion of their data in this on-going work. **Action Item 9**

Conclusion

The RAATD II workshop was a great success and achieved almost all of its stated aims. At the conclusion of the workshop we have:

- Consolidated the available datasets into a collection of over 3000 individual deployments and over 2 million locations from more than 30 international data providers.
- Finalised the metadata associated with these data, locating and fixing numerous errors.
- Established and initiated a process for data quality control.
- Have working R code for running SSAMM.
- Have working R code for calculating 3 different response variables for our HUMs and tested it on a subset of preliminary data.
- Have a mechanism for establishing the best statistical modelling framework for the SMDs.
- Have a process to implement the best statistical modelling framework to provide the species specific HUMs
- Have preliminary R code for making spatial prediction across the entire Southern Ocean based on the HUMs and the location of all colonies.
- Have allocated tasks to members of the group to ensure timely progression of the RAATD objectives

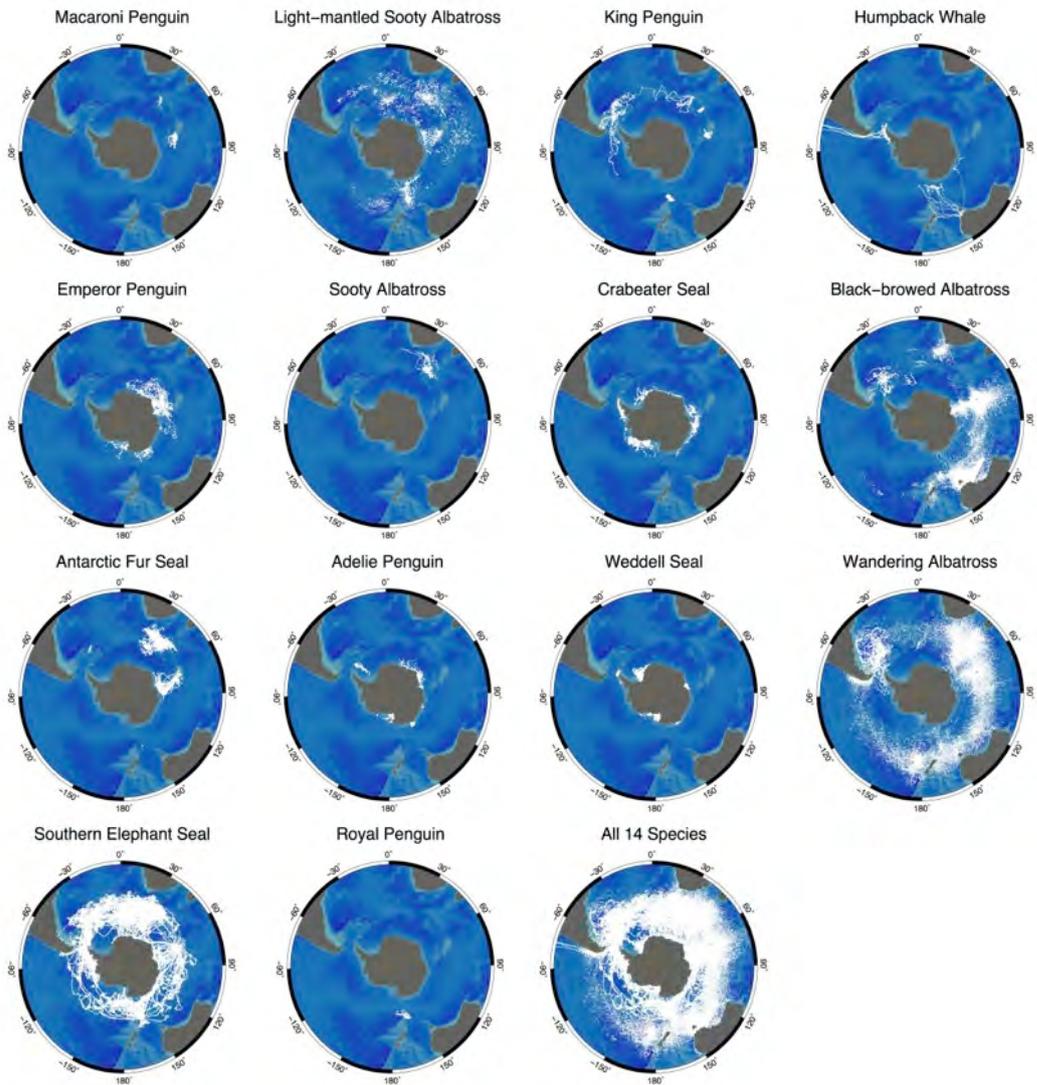
Acknowledgements:

The RAATD team would like to thank the Hanse-Wissenschaftskolleg for its considerable financial and logistic support, and also for providing the first rate meeting facilities. In particular Doris Meyerdierks for her on-the-ground help and kindness. Additional financial support was provided by SCAR Life Science group, the Alfred Wegner Institute, the Deutsche Forschungsgemeinschaft, and Macquarie University. Horst Bornemann was the local organiser and his efforts were largely responsible for the success of the workshop. Appendix One: List of environmental covariates available for use in the workshop (provided by B. Raymond, AADC).

bathymetry	nox_50_interpolated_summer_climatology	si_200_interpolated_summer_climatology
bathymetry_slope	nox_50_interpolated_winter_climatology	si_200_interpolated_winter_climatology
benthic_regionalisation	nox_50_summer_climatology	si_200_summer_climatology

caisom_floor_current_speed	nox_50_winter_climatology	si_200_winter_climatology
caisom_floor_salinity	oxygen_0_interpolated_summer_climatology	si_500_interpolated_summer_climatology
caisom_floor_temperature	oxygen_0_interpolated_winter_climatology	si_500_interpolated_winter_climatology
caisom_floor_vertical_velocity	oxygen_0_summer_climatology	si_500_summer_climatology
caisom_surface_current_speed	oxygen_0_winter_climatology	si_500_winter_climatology
chl_summer_climatology	oxygen_200_interpolated_summer_climatology	si_50_interpolated_summer_climatology
distance_antarctica	oxygen_200_interpolated_winter_climatology	si_50_interpolated_winter_climatology
distance_colony	oxygen_200_summer_climatology	si_50_summer_climatology
distance_max_ice_edge	oxygen_200_winter_climatology	si_50_winter_climatology
distance_shelf	oxygen_500_interpolated_summer_climatology	ssh
distance_subantarctic_islands	oxygen_500_interpolated_winter_climatology	ssha_variability
distance_to_canyon	oxygen_500_summer_climatology	ssh_spatial_gradient
distance_to_fast_ice	oxygen_500_winter_climatology	sst_spatial_gradient
distance_to_polynya	oxygen_50_interpolated_summer_climatology	sst_summer_climatology
distance_upper_slope	oxygen_50_interpolated_winter_climatology	surface_meridional_wind_annual
fast_ice	oxygen_50_summer_climatology	surface_meridional_wind_summer
floor_nitrate_cars2009a_mean	oxygen_50_winter_climatology	surface_meridional_wind_winter
floor_oxygen_cars2009a_mean	pelagic_regionalisation	surface_wind_annual
floor_phosphate_cars2009a_mean	salinity_0_interpolated_summer_climatology	surface_zonal_wind_annual
floor_salinity_cars2009a_mean	salinity_0_interpolated_winter_climatology	surface_zonal_wind_summer
floor_silicate_cars2009a_mean	salinity_0_summer_climatology	surface_zonal_wind_winter
floor_temperature	salinity_0_winter_climatology	t_0_interpolated_summer_climatology
floor_temperature_cars2009a_mean	salinity_200_interpolated_summer_climatology	t_0_interpolated_winter_climatology
floor_temperature_interpolated	salinity_200_interpolated_winter_climatology	t_0_summer_climatology
geomorphology	salinity_200_summer_climatology	t_0_winter_climatology
light_budget	salinity_200_winter_climatology	t_200_interpolated_summer_climatology
mixed_layer_depth_summer_climatology	salinity_500_interpolated_summer_climatology	t_200_interpolated_winter_climatology
mixed_layer_depth_summer_climatology_interpolated	salinity_500_interpolated_winter_climatology	t_200_summer_climatology
nox_0_interpolated_summer_climatology	salinity_500_summer_climatology	t_200_winter_climatology
nox_0_interpolated_winter_climatology	salinity_500_winter_climatology	t_500_interpolated_summer_climatology
nox_0_summer_climatology	salinity_50_interpolated_summer_climatology	t_500_interpolated_winter_climatology
nox_0_winter_climatology	salinity_50_interpolated_winter_climatology	t_500_summer_climatology
nox_200_interpolated_summer_climatology	salinity_50_summer_climatology	t_500_winter_climatology
nox_200_interpolated_winter_climatology	salinity_50_winter_climatology	t_50_interpolated_summer_climatology
nox_200_summer_climatology	seaice_gt85	t_50_interpolated_winter_climatology
nox_200_winter_climatology	seaice_summer_variability	t_50_summer_climatology
nox_500_interpolated_summer_climatology	si_0_interpolated_summer_climatology	t_50_winter_climatology
nox_500_interpolated_winter_climatology	si_0_interpolated_winter_climatology	vertical_velocity_250
nox_500_summer_climatology	si_0_summer_climatology	vertical_velocity_500
nox_500_winter_climatology	si_0_winter_climatology	

Appendix Two. Maps for each species of all data available to RAATD in early April 2016.



AGENDA

<p>Monday April 4, 09:00-10:30.</p> <p>Welcome: M. Hindell</p> <p>Recap of the first workshop: M. Hindell</p> <p>Update on modelling work since the first workshop: I. Jonsen, S. Wotherspoon</p> <p>Update on database collation and management since first workshop: Y. Ropert-Coudert</p> <p>Discussion on structure and anticipated outputs from the second workshop: M. Hindell</p>	<p>10:30 Coffee</p>
<p>Monday, April 4, 10:45-12:45.</p> <p>Break into two working groups:</p> <p>(i) Database Management group – tasks for this group</p> <ul style="list-style-type: none"> • Compile metadata records • Identify and source missing datasets • Initial quality control of data sets. See (http://web.science.mq.edu.au/~ijonsen/raatd/) for Ian’s first cut at filtering • Prepare manuscript for a data paper <p>(ii) Data modelling group – tasks for this group</p> <ul style="list-style-type: none"> • Run movement models for each species • Generate random tracks to define available areas • Extract environmental data sets • Develop statistical habitat use models for each species • Generate spatial predictions for each species • Combine predictions to identify Areas of Ecological significance 	<p>12:45 Lunch</p>
<p>Monday, April 4, 13:30-17:30.</p> <p>Working groups continue</p>	<p>15:30 Coffee</p> <p>18:00 Buffett</p>
<p>Tuesday, April 5, 9:00-10:00. Update on progress of working groups</p>	<p>10:00 Coffee</p>
<p>Tuesday, April 5, 10:30-17:30. Working groups continue</p>	<p>12:30 Lunch</p> <p>15:30 Coffee</p> <p>18:00 Dinner</p>
<p>Wednesday, April 6, 9:00-10:30.</p> <p>Update on progress of working groups</p> <p>Discussion on publishing strategy – how many papers and what journals</p>	<p>10:30 Coffee</p>
<p>Wednesday, April 6, 11:00-12:30. Working groups continue</p>	<p>12:30 Lunch</p>
<p>Wednesday, April 6, 13:30-17:30. Working groups continue</p>	<p>15:30 Coffee</p> <p>19:00 Dinner</p>
<p>Thursday April 7, 09:00-12:30.</p> <p>Update on progress of working groups</p> <p>Working groups continue</p>	<p>10:30 Coffee</p> <p>12:30 Lunch</p>
<p>Thursday, April 7, 13:30-17:30. Working groups continue</p>	<p>15:30 Coffee</p> <p>18:00 Dinner</p>
<p>Friday April 8, 09:00-12:00.</p> <p>Update on progress of working groups</p> <p>Discussion on outputs and future work</p> <p>Work on workshop report</p> <p>Workshop closing comments</p>	<p>10:30 Coffee</p> <p>12:00 Lunch</p>