Horizon scan approach to uncover current and future challenges to the genomics of wildlife diseases and identify avenues for improvement

A) Linking wildlife disease biologists with training, funding, and bioinformatics: Jill Pecon-Slattery

1) How do we improve the communication between biologists and bioinformaticians?
2) How do we improve the communication across disciplines to ensure everyone is 'speaking the same language'?
3) How can we enhance communication/understanding to bridge the gap between the computer scientists/algorithm experts and the biological scientist studying wildlife disease?
4) Can we improve the training? Or better yet, initiate training in genomics?
5) In developing countries, wildlife disease researchers had recently caught up with the genetic techniques, but now with genomics have again fallen behind due to a lack of training and financial resources. What are the strategies to mitigate this situation?
6) How do we improve training in genomics in developing countries?
7) How do we improve access to data and foster new collaborations?
8) How can we identify more funding opportunities?
9) Can web or other portals be established to link people with research, training, and funding opportunities?
10) What are the stable sources of funding that can traverse a dynamic and fluctuating political atmosphere?
11) What funding opportunities are available to support research, training, and resource development for GDW projects?
12) What publication options are most impactful for studies of GDW? I.e. what specialty journals are most relevant for publications in this realm?

B) Methodological, and technical advances: Mark Stenglein

1) What are the best approaches to optimize obtaining genomic data, both host and pathogen, from non-invasive sampling?
2) How do we maximize or improve the collection of genomic data (host and pathogen) from non-invasive sampling techniques?
3) How do we standardize methods for better comparisons across studies?
4) Will machine learning approaches be a valuable statistical tool to integrate massive datasets of genomes (host and pathogen), environmental data, pathogen data, medicine, etc?
5) Can methods to detect selection on highly recombining sequences (e.g., viruses) be improved?
6) What advantages will single-molecule sequencing provide for GDW research?
7) How much can you trust sequence quality of Genbank accessions?
8) How do we link genomic data between the host and pathogen?

9) What is the optimal strategy to balance the relationship between the number of samples vs the amount of sequence data?
10) What are the best methods of sampling in order to find potential selection occurring between hosts and pathogens?
11) How does one balance cost and coverage of the genome to find host adaptation of the disease?
12) Can whole genome studies be reduced to a core "step-by-step" framework applicable to a majority and provide consistency and comparison across studies?
13) Can a standardized or core set of requirements be developed to assess the quality of published genomes/exomes?
14) What are resources for analyzing data from raw files to figure form without a bioinformatician?
15) Where should the technical focus of GDW research lie when it comes to sequence data? Should DNA extraction and library prep be left to commercial services in order to direct attention to the biological aspects of GDW?
16) Will the field of GDW benefit from many small core sequencing facilities or several large core centers that are cheaper?

C) Taking the next step: Following-up or translating initial genomic study results into practice: Sue VandeWoude

1) What are approaches for determining what agents identified by metagenomics analysis are actually pathogenic?
2) What is the interaction between pathogens/potential pathogens and host microbiome?
3) What can we learn about coinfections/microbial interactions that lead to homeostasis or disease?
4) How do we handle co-infection data?
5) How do we foster continued research on the candidate genes or regions reported from the genomics studies?
6) How do we translate the findings from genomics directly into conservation, medical, and/or disease research?
7) How do we bridge the gap between the results of genomic studies and the application in the management of wildlife and their associated diseases?

D) Genomics and landscape ecology of pathogens and host: Daryl Trumbo

1) How do we understand pathogen transmission between wildlife?
2) How do we better integrate databases of genomic/genetic data, landscape/ecological data, disease/pathogen data, and epidemiological surveys?
3) How do we integrate phylogenetic/phylodynamic data and landscape ecology to inform cross-species transmission in a changing landscape?
4) How do anthropogenic influences (urbanization, extraction, road building, transport/movement of animals, etc) alter the landscape of wildlife diseases?
5) With increased urban greening initiatives and the return of wildlife to urban landscapes, how can we manage habitat for wildlife health and prevent infectious disease outbreaks?

6) How do we link conservation genetics and landscape ecology through spatial analysis?
7) How does wildlife microbiome vary by species and environment? Since wildlife are species least likely to encounter pharmaceuticals that artificially alter microbial populations, could studies of wildlife microbiome reflect natural microbiome/host interactions?

E) Genomics and the emergence of new questions: Bob Fitak

1) In human medicine finding genes associated with increased disease risk has been difficult. Because natural selection and evolutionary arms races can proceed more naturally in wildlife than human populations (due to modern medicine) would we expect to more readily find alleles associated with disease—can this inform these efforts in human medicine?
2) How do we leverage genomics to understand phenotypic plasticity and its relationship to host/pathogen disease dynamics?
3) What are host mechanisms for disease resistance? How does host immune response drive pathogen evolution and vice versa?
4) How do we link phylogenetic data to network modeling?
5) How do we apply phylogenomic and phylodynamic data to slowly evolving pathogens?
6) How can you recreate accurate phylogenies for rapidly evolving pathogens, such as viruses, that can determine deep evolutionary lineages?