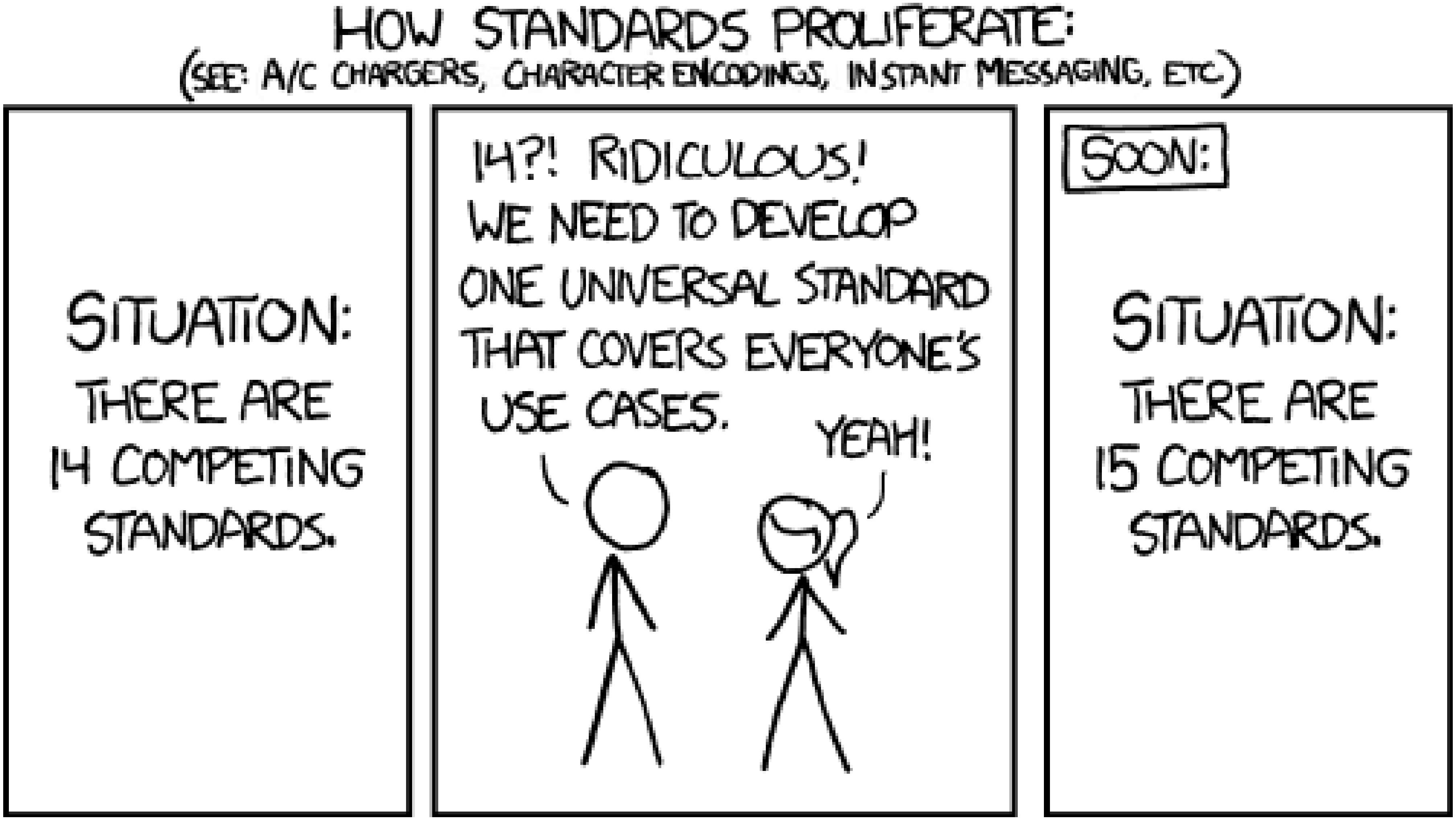
Biodiversity Working Group Report

Robert J. Robbins


HOW STANDARDS PROLIFERATE:
(SEE: A/C CHARGERS, CHARACTER ENCODINGS, INSTANT MESSAGING, ETC.)
SITUATION: THERE ARE 14 COMPETING STANDARDS.
14?! RIDICULOUS! WE NEED TO DEVELOP ONE UNIVERSAL STANDARD THAT COVERS EVERYONE'S USE CASES.
YEAH!
SOON:
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Purposes of the RCN4GSC Workshop

Develop Conceptual Framework

Characterize Benefits

Identify Opportunities

Assess Challenges

Propose Next Steps

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Efforts to discover, elucidate, and understand the planet’s biodiversity must span the macro, meio, and micro scales and must integrate traditional tools with emerging genomic and metagenomic methods. To pursue these in isolation would violate biological reality and be counter-productive to knowledge discovery.

Integration/interoperability between macro and genomic biodiversity informatics is scientifically desirable, technically feasible, and should be tackled.

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Integrative comparative analyses of genomic/macro biodiversity data sets will enable more efficient and effective research, and will support more far-reaching interdisciplinary research and discoveries.

Coherent efforts to deploy standard genomic and metagenomic methods across the multiple dimensions of biodiversity will achieve economies of scale, produce mutual benefits, generate multiplier effects, leverage support, and yield more comprehensive science.

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Opportunity to benefit multiple communities through harmonization of tools and concepts across communities.

Opportunity to advance biology through substantial extension and refinement of such fundamental concepts as individual or species.

Opportunity for consilience resulting from growth of aggregators (e.g., GBIF, EOL, Genbank, GSC, KNB, LTER, NEON, DATAONE, EMP) that are serving most of the data.

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Will need to harmonize fundamentally different sampling units in macro and genomic surveys and inventories.

Will need to deal with inconsistent implementation by INSDC of different standards, e.g., GSC and Barcode standards such as occurrence, collector data, etc.

Will need to extend data “adherence” measures from **presence** of data, to **quality** of data.

Will need to reach out to a multitude of fragmented biodiversity communities.

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➡ Propose Next Steps

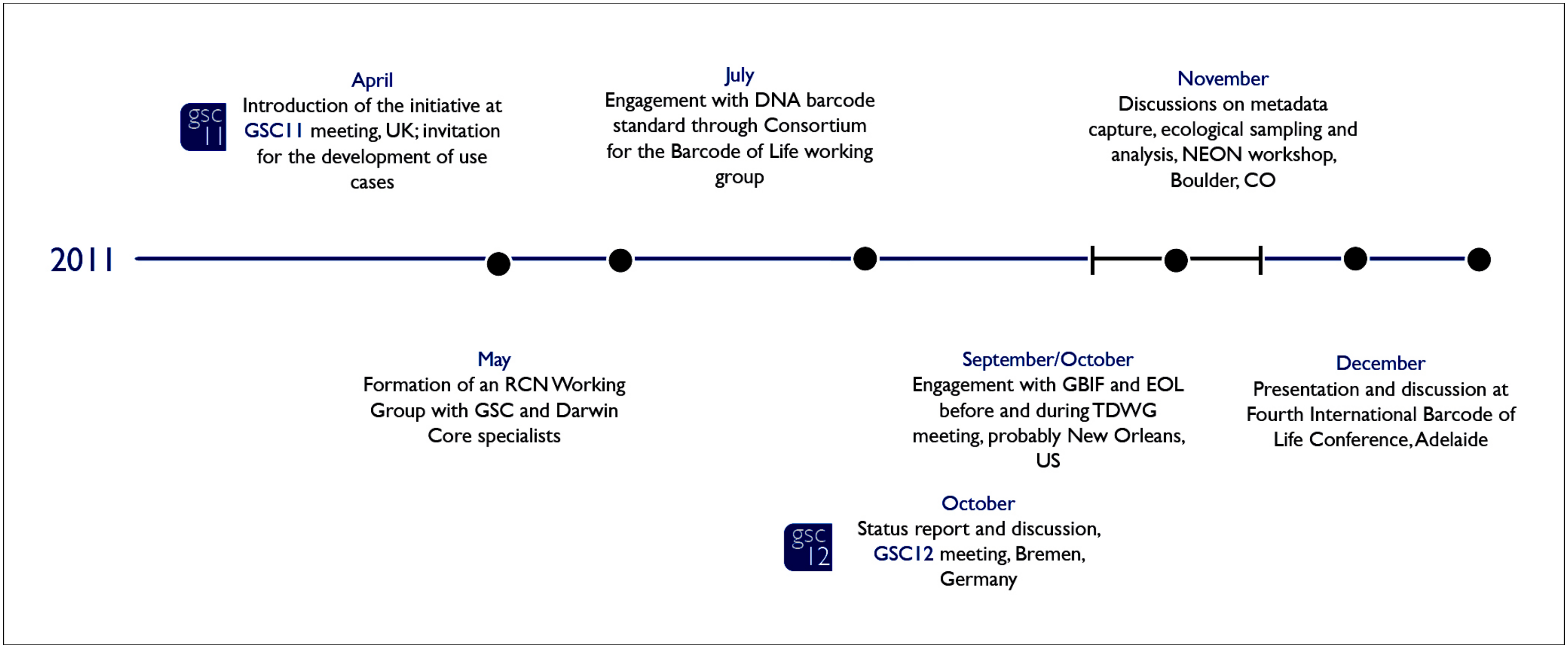
Write and publish a white paper on biodiversity, genomics, and metagenomics.

Scope and implement a focused pilot project/working group to (a) explore how to integrate genomic and macro biodiversity data and (b) explore the integration of the Darwin Core and GSC standards by mapping and reconciling the elements of the Darwin Core and GSC checklists.

Develop a set of use cases.

Examine the lessons learned from the test/pilot project and use-cases to ascertain appropriate next steps.

Time Line of Goals from March 2011



2011

April
Introduction of the initiative at GSC11 meeting, UK; invitation for the development of use cases

May
Formation of an RCN Working Group with GSC and Darwin Core specialists

July
Engagement with DNA barcode standard through Consortium for the Barcode of Life working group

September/October
Engagement with GBIF and EOL before and during TDWG meeting, probably New Orleans, US

October
Status report and discussion, GSC12 meeting, Bremen, Germany

November
Discussions on metadata capture, ecological sampling and analysis, NEON workshop, Boulder, CO

December
Presentation and discussion at Fourth International Barcode of Life Conference, Adelaide

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Actual: May Workshop in San Diego:

- Bring together relevant people
- Form Three Task Groups

	Task Group 1 **DwC MIxS Mapping**	**Task Group 2** **TDWG Interest Group (TIG)**	**Task Group 3** **Use Case Development**
Objectives	Continue to map orthogonal terms between MIxS and DwC and also review technical mechanisms for achieving the same.	Establishing TDWG / GSCBW relations; Create TDWG interest group for GSC collaboration. Create charter for Interest Group in TDWG, propose that to TDWG Executive Committee. Biodiversity Genomics	Prototype Microbial Earth Catalogue, Develop LTER Use Cases, Identify EOL use cases, Identify CBOL use cases
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Leaders	Renzo Kottmann John Wieczorek	John Deck Stan Blum	Inigo San Gil Linda Amaral-Zettler

Flash Talks

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Plus:

Todd Vision

Stephane Reviere

Jack Gilbert

END

Biodiversity Session

Robert J. Robbins

Neil Davies

FORMAT:

11:00 – 12:30	Intro / flash talks
12:30 – 13:00	General discussion
13:00 – 14:00	Lunch (keep thinking about biodiversity)
14:00 – 14:10	Create “dynamic breakout groups”
14:10 – 15:00	Hold dynamic breakout sessions
15:00 – 15:30	Report back from dynamic sessions / wrap

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Todd Vision

Stéphane Rivière

Jack Gilbert

towards a richer set of information to describe our complete genome collection

gsc genomic STANDARDS consortium

Renzo Kottmann
DwC/MIxS: technical issues + proposed solutions

John Deck
TDWG meets GBWG

John Deck
BiSciCol & Biocode use case

Inigo San Gil
LTER Use Cases

Peter Dawyndt
Microbial Earth Catalogue

David Schindel
CBOL meets GBWG

Cynthia Parr
EOL meets GBWG

Éamonn Ó Tuama
GBIF meets GBWG

Neil Davies
Minimum Information about a Genomic Observatory

Stéphane Rivière
European Nucleotide Archive (ENA) Biodiversity molecular data, ...

Todd Vision
NESCent meets GBWG

Jack Gilbert
Earth Microbiome Project meets GBWG

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END