Biological Monitoring
-Data Management-

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Data Management & Analysis Team
History...

• SWQMIS was released in 2007
• Later enhanced for biological data
• Changed from ‘paper’ packets to ‘electronic’ packets
• Now, biological data can be warehoused AND reported from SWQMIS
• Adds value to monitoring effort and data usability
Data Management Resources

• DMRG (Ch. 6, 7, and 12)
• Procedures Manual, Volume 2
• Handouts from this workshop
• Effective QAP/QAPP
• TCEQ Project Manager
• TCEQ Data Manager
• 😊 SWQMIS examples 😊
A word about data management...

Congratulations! We are all data managers.
Data Recording (in the Field)

View QAPP monitoring schedule (generic list, Table B1.1)
View QAPP Table A7 (‘expected’ list of biological parameters)
**Compare above against DMRG and forms from PM Vol. 2; KNOW BEFORE YOU GO !!!

Big difference in forms used and generic sampling categories (Nekton, for example, can require 8 pages of forms.)

1 sampling category = 1 Tag ID = 1 SWQMIS Sample Set
(refer to screen shot of SWQMIS biological Sample Event)
QAPP Monitoring Schedule

Example from QAP, Table B1.1 (generic information):

<table>
<thead>
<tr>
<th>Segment</th>
<th>TCEQ Region</th>
<th>Site Description</th>
<th>Station ID</th>
<th>Aquatic Habitat</th>
<th>Benthics</th>
<th>Nekton</th>
<th>Inst Flow</th>
<th>24-HR DO</th>
</tr>
</thead>
<tbody>
<tr>
<td>19##</td>
<td>99</td>
<td>The river at ABC located 99 units from XYZ</td>
<td>2######</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
</tbody>
</table>

Last 5 columns say: Aquatic Habitat, Benthics, Nekton, Inst Flow, and 24 HR DO.

Now look at the forms used in the field, and the sampling category names.
## Biological Monitoring Event 1336220

### Sampling Events - Sample Event

- **Sample Event ID:** 1336220
- **Station ID:** 15342
- **Segment ID:** 0304A
- **Station Description:** SWAMPoodle CREEK AT W BROAD ST
- **Start Date:** 08/22/2011
- **End Date:** 08/31/2011

### Attachments

<table>
<thead>
<tr>
<th>Description</th>
<th>File Name</th>
<th>Remove</th>
</tr>
</thead>
<tbody>
<tr>
<td>Project Activity Summ</td>
<td>Project Activity Summary Report - Swampoodle.docx</td>
<td>Remove</td>
</tr>
<tr>
<td>Elements of the Bio</td>
<td>2010&amp;2011-Swampoodle @ W Broad summary_packet_form.doc</td>
<td>Remove</td>
</tr>
<tr>
<td>Summary of Attharms</td>
<td>Summary of Attachments.docx</td>
<td>Remove</td>
</tr>
</tbody>
</table>

### View/Edit Sample Sets

<table>
<thead>
<tr>
<th>Sample Set ID</th>
<th>Station Id</th>
<th>Bio Tag Id</th>
<th>Start Date</th>
<th>Submitting Entity</th>
<th>Collecting Entity</th>
<th>Monitoring Type</th>
<th>Sampling Category</th>
<th>Data Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>13686599</td>
<td>15342</td>
<td></td>
<td>Aug 31, 2011</td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>BIO_HABITAT_TCEQ_PRTS123_PROTO</td>
<td>Habitat</td>
</tr>
<tr>
<td>13686593</td>
<td>15342</td>
<td></td>
<td>Aug 24, 2011</td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>BIO_BENTHIMACROS_RAPID_BIO_QUAL</td>
<td>Benthic Macroinvertebrate</td>
</tr>
<tr>
<td>13686592</td>
<td>15342</td>
<td></td>
<td>Aug 24, 2011</td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>BIO_NEK_SEINING</td>
<td>Nekton</td>
</tr>
<tr>
<td>13686591</td>
<td>15342</td>
<td></td>
<td>Aug 24, 2011</td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>BIO_NEK_ELECTROFISHING</td>
<td>Nekton</td>
</tr>
<tr>
<td>13686590</td>
<td>15342</td>
<td></td>
<td>Aug 24, 2011</td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>BIO_NEK_TX_REG_INDEX_SUM&amp;METAD</td>
<td>Nekton</td>
</tr>
<tr>
<td>13027436</td>
<td>15342</td>
<td></td>
<td></td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>24 HOUR FIELD MEASUREMENTS</td>
<td>Field Measurement</td>
</tr>
<tr>
<td>13023131</td>
<td>15342</td>
<td></td>
<td></td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>ROUTINE FIELD MEASUREMENTS</td>
<td>Field Measurement</td>
</tr>
<tr>
<td>13023130</td>
<td>15342</td>
<td>1278779</td>
<td></td>
<td>WC</td>
<td>FO</td>
<td>BS</td>
<td>ROUTINE CHEMICAL MEASUREMENTS</td>
<td>Analytical Result</td>
</tr>
</tbody>
</table>
SWQMIS Biological Monitoring Event

The previous slide was a screen shot showing:

• SWQMIS Sample Event with attached BLOB files for the Sample Event

• Table of 8 Sample Sets reported for this Sample Event

Sample Sets were:

• Habitat – TCEQ Parts 1, 2, and 3 Protocol

• Benthic Macroinvertebrates – Rapid Bioassessment, Qualitative

• Nekton – Seining

• Nekton – Electrofishing

• Nekton – TX Regional Index Summary & Metadata

• 24 Hour Field Measurements

• Routine Field Measurements

• Routine Chemistry
Biological Monitoring Event

• Locals use Bull Creek
• Historical – Lampasas Trail crossing with wagon ruts
• City Park – recreational use
• Small off-leash dog area
• Hiking trails for use by many
Biological Monitoring Event

Sometimes the use can be heavy... Leashed, and unleashed
Biological Monitoring Event

• After the monitoring event the data needs to be processed.

• Remember, in SWQMIS the monitoring will be represented by a Sample Event and multiple Sample Sets, plus BLOB files.

• What is a BLOB file? BLOB = binary large object and can be a .txt file containing a large amount of data, a .pdf file, an Excel spreadsheet, a document containing photos or images, etc.

• So it’s basically ‘just a file’ and will have a size limitation. In SWQMIS it’s 15 MB per attachment.

• BLOBs should be attached to the Sample Event in SWQMIS and to each Sample Set – for Biological Monitoring.
How does your data go into SWQMIS?

• If you work for the TCEQ and you manually enter data into SWQMIS – you will do the same for your biological data Sample Sets and BLOB files.

• If you are a contractor and your data is loaded into SWQMIS by Data Management, you will submit your biological data using the same process (flat files) however your BLOB files will need to be forwarded to us along with a guide.

• Refer to the DMRG, Ch. 12 – Biological Data Recording and Reporting
Parameter Code 89888

Parameter code 89888 is the key to making biological data work for data entry, and for data querying and reporting.

Parameter code 89888 is to be reported for each Sampling Category. Sampling Category examples are: Nekton electrofishing, Nekton Seining, or Benthic Macroinvertebrates Rapid Bioassessment Qualitative (DMRG Ch. 6, and 12).

* The monitoring trip = the Sample Event.

** The Sampling Categories = the various Tag IDs = Sample Sets within the Sample Event.
Sample Event Attachments/BLOBs

Project Activity Summary Report
Summary Packet - Form
Summary of Attachments
(Note the button for ‘Download Attachments >>’)
Only Data Managers can ‘Remove’ BLOBs

<table>
<thead>
<tr>
<th>Description</th>
<th>Attachments File Name</th>
<th>Remove</th>
</tr>
</thead>
<tbody>
<tr>
<td>Project Activity Summ</td>
<td>Project Activity Summary Report - Swampoodle.docx</td>
<td>Remove</td>
</tr>
<tr>
<td>Elements of the Biolo</td>
<td>2010&amp;2011-Swampoodle @ W Broad summary_packet_form_form.doc</td>
<td>Remove</td>
</tr>
<tr>
<td>Summary of Attachments</td>
<td>Summary of Attachments.docx</td>
<td>Remove</td>
</tr>
</tbody>
</table>

View/Edit Sample Sets:

| Sample Set Id | Station Id | Rfa Tag Id | Start Date | Submitting Entity | Collecting Entity | Monitor |
Sample Event Attachments/BLOBs

Click the Download Attachments button and you see this:

Note the buttons for ‘Download’

Download the file of choice and view the file contents
### Attachment/BLOB #1 – Project Activity Summary Report

#### Aquatic Life Assessment of Swampoodle Creek @ Broad Street

<table>
<thead>
<tr>
<th>Station Name</th>
<th>Station ID</th>
<th>Activity Type</th>
<th>Event Start Date</th>
<th>Sample Event #</th>
<th>Sample Set #</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>Swampoodle Cr (Project 1544)</td>
<td>15342</td>
<td>Routine</td>
<td>06/29/2010</td>
<td>1247717</td>
<td>12318632</td>
<td>---</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Field</td>
<td>06/29/2010</td>
<td></td>
<td>12318633</td>
<td>---</td>
</tr>
<tr>
<td></td>
<td></td>
<td>24 Hour DO</td>
<td>06/27/2010</td>
<td></td>
<td>12318634</td>
<td>DO avg = 5.5</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Habitat</td>
<td>06/27/2010</td>
<td></td>
<td>13612830</td>
<td>High - 22</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Nekton</td>
<td>06/28/2010</td>
<td></td>
<td>15662283</td>
<td>Intermediate - 40</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Benthic</td>
<td>06/29/2010</td>
<td></td>
<td>15612833</td>
<td>Intermediate - 40</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Field</td>
<td>08/24/2010</td>
<td>1260933</td>
<td>13612832</td>
<td>Intermediate - 22</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Routine</td>
<td>08/24/2010</td>
<td></td>
<td>12461288</td>
<td>---</td>
</tr>
<tr>
<td></td>
<td></td>
<td>24 Hour DO</td>
<td>08/24/2010</td>
<td></td>
<td>12337310</td>
<td>DO avg = 4.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Habitat</td>
<td>09/02/2010</td>
<td></td>
<td>13686533</td>
<td>High - 21</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Nekton</td>
<td>08/25/2010</td>
<td></td>
<td>15686536</td>
<td>High - 45</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Benthic</td>
<td>08/25/2010</td>
<td></td>
<td>15686537</td>
<td>Limited - 17</td>
</tr>
</tbody>
</table>

#### Project 344

<table>
<thead>
<tr>
<th>Station Name</th>
<th>Station ID</th>
<th>Activity Type</th>
<th>Event Start Date</th>
<th>Sample Event #</th>
<th>Sample Set #</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>Swampoodle Cr (Project 1544)</td>
<td>15342</td>
<td>Routine</td>
<td>06/01/2011</td>
<td>1314707</td>
<td>12889024</td>
<td>---</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Field</td>
<td>06/01/2011</td>
<td></td>
<td>12889025</td>
<td>---</td>
</tr>
</tbody>
</table>
Sample Set – Habitat TCEQ 1 2 3

Habitat Sample Set with 4 attachments

<table>
<thead>
<tr>
<th>Sample Event ID: 13X020</th>
<th>Station ID: 16342</th>
<th>Station Description: SWAMPDOLE GREEN</th>
<th>Segment ID: 0304A</th>
</tr>
</thead>
</table>

**Sample Set**

- **Sample Set ID:** 13X020
- **RPA Tag No.:**
- **Field Collector:** MWAINEBUSH
- **Quality Control Type:** FIELD MICROBIP
- **Submitting Entity:** WC
- **Collecting Entity Id:** F0
- **Monitoring Type:** BS
- **Data Type:** Habitat
- **Sampling Category:** BIO_HABITAT_TCEQ_PRTS123_PROTO
- **Medium:** Other
- **Sample Type:**
- **Replicate No.:** 0
- **Start Date:** 08/31/2011
- **Start Time:** 00:00
- **End Date:** 08/31/2011
- **End Time:** 00:00

**Sample Set Details**

- **Start Depth:**
- **End Depth:**
- **Deepest Depth:**
- **Level of Effort:**
- **Composite Category:**
- **Composite Type:**
- **Equipment Name:**
- **Equipment Type:**
- **Number Of Seconds:** (N/A)
- **Distance Covered:** (N/A)
- **Tissue Type:**
- **Species:**
- **Production Status:** PROD
- **Data Validation Level for Sample Set:** 0
- **Project Name:** Swampdole Creek ALA

**Collector Observations:**

**Comments:**

**Attachments**

- **Description:** Swampdole-Habitat Assessment Worksheet #1 (08-31-2011).doc
- **File Name:** Swampdole-Habitat Assessment Worksheet #1 (08-31-2011).doc
- **Remove:**
- **Description:** Swampdole-Habitat Assessment Worksheet #2 (08-31-2011).doc
- **File Name:** Swampdole-Habitat Assessment Worksheet #2 (08-31-2011).doc
- **Remove:**
- **Description:** Swampdole-Habitat Assessment Worksheet #3 (08-31-2011).doc
- **File Name:** Swampdole-Habitat Assessment Worksheet #3 (08-31-2011).doc
- **Remove:**
- **Description:** Swampdole Photographs 2011-08-31.png
- **File Name:** Swampdole Photographs 2011-08-31.png
- **Remove:**
Sample Set – Swampoodle Photos

Download the Swampoodle Photographs pdf
Sample Set – Swampoodle Photos

Swampoodle Photo pdf file details:

• 10 page file
• 2 photos per page
• File size = 2.5 MB
• Used Adobe’s Acrobat PDFMaker 10.1 for Word

So your photos can go into a Word document, 2 per page, with document headers / footers, and individual photo captions.

Use DMRG guidance for file naming conventions.
### Sample Event Attachments/BLOBs

#### Attachments

<table>
<thead>
<tr>
<th>Description</th>
<th>File Name</th>
<th>Remove</th>
</tr>
</thead>
<tbody>
<tr>
<td>Project Activity Summary</td>
<td>Project Activity Summary Report - Swampoodle.docx</td>
<td></td>
</tr>
<tr>
<td>Elements of the Biology</td>
<td>2010 &amp; 2011 Swampoodle @ W Broad summary_packet_form.doc</td>
<td>Remove</td>
</tr>
<tr>
<td>Summary of Attachments</td>
<td>Summary of Attachments.docx</td>
<td>Remove</td>
</tr>
</tbody>
</table>

#### View/Edit Sample Sets

<table>
<thead>
<tr>
<th>Sample Set Id</th>
<th>Station Id</th>
<th>Rfa Tag Id</th>
<th>Start Date</th>
<th>Submitting Entity</th>
<th>Collecting Entity</th>
<th>Monitoring Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>12686500</td>
<td>15242</td>
<td></td>
<td>Sep-31, 2011</td>
<td>WC</td>
<td>EQ</td>
<td>BS</td>
</tr>
</tbody>
</table>
Add an Attachment/BLOBs

Five steps:

1. Place screen in ‘Edit’ mode; go to Attachment area
2. ‘Browse’ – locate attachment file; uses Windows Explorer
3. Click ‘Add Attachment’; the File Name is added
4. Enter a ‘Description’ – (suggest StationID + EndDate + info)
5. Click ‘Save’ or ‘Save with History’ at top of screen.
Welcome Caanders

- Your password will expire on 06/14/2016.

Home

Sampling
- RFA - Search/View/Edit
- Comparison Information
- Projects
- Reports and Extracts
- Parameter Inventory Report
- Parameter Inventory Report
- Single Parameter Report
- Monitoring Station Inventory Report
- Selective Data Report
- Raw Data Report
- Full Raw Data Export
- RFA Status Report
- Sampling History Report
- Comparison Information Report
- Upload Tracking Info Report
- Biological Raw Data Report

Maps (GIS)
- Display Full Extent Map
- Assessment
- Segment - Search/View/Edit
- Administration
- Change My Password
- Forms
- System Change Request

Monitoring Stations
- Search/View/Edit
- Equipment
- Geographical Areas
- Geographic Places Search
- Constituents
- Constituents - Search/View/Edit
Querying for Biological Data

To locate Biological data in SWQMIS, do the following:

From the SWQMIS home page, locate the Reports and Extracts module and select the ‘Biological Raw Data Report’ option.

Add 1 line to the query builder and search for a geographical feature (Segment ID = 121* used in this example)

![Image of SWQMIS Biological Raw Data Report - Station Selection](image-url)
Querying for Biological Data

Click ‘Next’ on the next 2 screens, and then ‘Generate’ on the Extract Report screen.
Querying for Biological Data

The system will generate a pop-up window asking what you want to do with the data file.

Save the file to your local drive as a .txt file.

It will be pipe-delimited data that looks like this:
Querying for Biological Data

Next Step - Open Excel

Select ‘File’ -> ‘Open’ and browse to the .txt file you just saved. Excel will think you are looking for an Excel file, so tell it to look for files of all types (lower right of ‘Open’ pop-up).
Querying for Biological Data

Step 1 of 3 - Select data file type ‘Delimited’, then click ‘Next’
Querying for Biological Data

Step 2 of 3 - Check ‘Other’ for type of Delimiter, and enter a ‘pipe’ into the box by ‘Other’.
Querying for Biological Data

Step 3 of 3 - Click ‘Finish’
Querying for Biological Data

Now it appears to be in spreadsheet format. Look for the column for ‘Event Blob Indicator’ – Column E. A ‘Y’ = there’s an attachment at the Sample Event level.

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
<th>H</th>
<th>I</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Basin Id</td>
<td>Seg</td>
<td>IOn</td>
<td>Segme</td>
<td>Event Id</td>
<td>Event Blob</td>
<td>RFA/Tag II</td>
<td>Sample Sc</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>0304A</td>
<td>Y</td>
<td>1336220 Y</td>
<td>13023131 N</td>
<td></td>
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</tr>
<tr>
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<td>3</td>
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<td>Y</td>
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<td>13027436 Y</td>
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<td>1278779 N</td>
<td></td>
<td></td>
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<tr>
<td>6</td>
<td>3</td>
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<td>1336220 Y</td>
<td>13686591 Y</td>
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<td>1336220 Y</td>
<td>13686593 Y</td>
<td></td>
<td></td>
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<tr>
<td>8</td>
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<td>1336220 Y</td>
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</tr>
<tr>
<td>11</td>
<td>3</td>
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</tr>
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<td>3</td>
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<td>15</td>
<td>3</td>
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<td>Y</td>
<td>1336220 Y</td>
<td>13027436 Y</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Querying for Biological Data

Reminder:

• Query by geographical feature (station, segment, or basin) for best results

• If there is a Sample Event BLOB (‘Y’) you can go back into the Sampling module and locate the Sample Event and review the Sample Event (and BLOB files), and the Sample Sets (and BLOB files).

• Without reporting parameter code 89888 and associated values for Sampling Categories, the data usability will be low.

• Code 89888 applies to both manually entered data (TCEQ staff) and contractor deliverables/flat files.
Questions?

Cathy Anderson
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