

Appendix A

Detailed Description of NSI Data

Sources of the NSI Data

The scope of the data compilation component of the NSI was to collect, review, and compile readily available data that could be used to evaluate the incidence of sediment contamination throughout the United States. As a result, emphasis was placed on gathering data sets with sediment chemistry data since those were the most prevalent data available on a national basis. The minimum data elements for inclusion in the NSI were date of sample collection, latitude/longitude, reliable units (e.g., mg/kg), and source of data. The electronic data sources used for the NSI are listed below.

- EPA's Storage and Retrieval System (STORET)
- EPA's Ocean Data Evaluation System (ODES)
- NOAA's Coastal Sediment Inventory (COSED)
- EPA Region 4's Sediment Quality Inventory
- EPA Gulf of Mexico Program's Contaminated Sediment Inventory
- EPA Region 10/COE Seattle District Sediment Inventory
- EPA's Great Lakes Data Base
- EPA's Environmental Monitoring and Assessment Program (EMAP)
- EPA Region 9 Dredged Material Tracking System (DMATS)
- USGS Massachusetts Bay Data (metals only)
- National Source Inventory (PCS and TRI)

In several cases, the readily available data sources for the NSI were compilations of existing data. For example, the EPA Gulf of Mexico Program's Contaminated Sediment Inventory included data from ODES, STORET, and EMAP. Since those data sources had been reviewed independently, they were deleted from the Gulf of Mexico Inventory before that data set was added to the NSI. A similar screening of data was conducted for the other data sets included in the NSI. Below is a summary of the remaining contributors to the individual data sets:

STORET	Numerous federal and state agencies	
ODES	Boston Harbor	Tennessee
	Massachusetts Bay	Kentucky
	Cape Arundel	Florida
	City of Gloucester	GLNPO/ARCS
	Mile 106	Galveston Bay
	South Carolina	San Diego Pre-301(h)
	Alabama	Orange County 301(h)
	Mississippi	Oxnard 301(h)
	Georgia	Los Angeles 301(h)
	North Carolina	Thums Ocean Dumping
	Encina 301(h)	Puget Sound
	Morro Bay 301(h)	Anchorage
	Hyperion 301(h)	Endicott 403(c)

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	Goleta 301(h) San Francisco NEP LA2 Ocean Dumping LA5 Ocean Dumping	Kuparuk STP 403(c) Prudhoe Bay 403(c) Port Valdez 403(c)
COSED	NOAA NS&T	Ed Long
Region 4	City of Tampa Dept of Navy EPA Region 4 Florida DER South Florida Water Mgmt Dist. USACE	USACE, Jacksonville USACE, Mobile USACE, Savannah USACE, Wilmington USFWS
Gulf of Mexico	ADEM (Mobile) Army Corps Eng. EPA-Houston ERL-N GCRL, Mississippi	TVA USACE (Mobile) USEPA Region 6 USGS
Seattle COE	Department of Social and Health Services Department of Ecology U.S. Fish and Wildlife Service Puget Sound Water Quality Authority Tetra Tech, Inc. Department of Fisheries Department of Natural Resources Department of Wildlife EPA Region 10 Batelle Northwest Sequim Laboratory Environmental Systems Corporation Department of Health College of Ocean and Fisheries Science PTI Environmental Services National Oceanic and Atmospheric Admin. Fish and Wildlife Health Consultants City of Bellingham U.S. Army Corps of Engineers, Seattle Columbia Northwest, Inc. Hulbert Mill King County Municipality of Metropolitan Seattle Wildlife Health Consultants U.S. Navy City of Olympia, LOTT treatment plant Port of Bellingham Port of Everett Port of Olympia Port of Port Townsend Thurston County Dept of Public Health U.S. Coast Guard	Department of Parks and Recreation Environmental Information Consultants South. CA Coastal Water Research Proj., Army Corps of Engineers, San Francisco Environmental Science Associates, Inc. E.V.S. Consultants, Sausalito, CA Marine Bioassay Labs, Watsonville, CA MEC Analytical Systems, Watsonville, CA San Francisco Port Commission ToxScan, Inc., Watsonville, CA Tetra Tech, Inc., Lafayette, CA Port of Grays Harbor Port of Tacoma Tristar Marine Morton Marine Port of Seattle South Park Marina U.S. Oil and Refining Company Weyerhaeuser Day Island Yacht Club Shell Oil Capital Regional District, Victoria, BC Environment Canada Greater Vancouver Regional District E.V.S. Consultants, Seattle, WA E.V.S. Consultants, Vancouver, BC British Petroleum Oil Company American Petroleum Institute
Great Lakes	Heidelberg College, Tiffin, Ohio Illinois EPA Michigan Tech. Univ., Houghton, MI	US Army COE, Buffalo District Beak Consultants, Inc Ontario Ministry of the Environment

	Univ. of Wisconsin-Superior, WI Michigan Dept. Natural Resources Ohio EPA Illinois Geological Survey USEPA-GLNPO USEPA-ERL-Duluth	Aqua Tech, Melmore, OH Bionomics/Aqua Tech Environ. Cnslt. Applied Biology, Inc., Decatur, GA Recra Research, Inc., Tonawanda, NY USFWS, Columbia, MO - ARCS Michigan State University
EMAP	Louisianian Province	Virginian Province
DMATS	USEPA Region 9	
USGS Massachusetts Bay	A.D. Little, 1990 ACE_NED permit file #29-91-00473E ACE_NED permit file 199102068 ACE_NED permit file 09-89-2777 ACE_NED permit file 09-89-530 ACE_NED permit file 1989-2911 ACE_NED permit file 199101096 ACE_NED permit file 20-87-2002 ACE_NED permit file 20-89-2206 ACE_NED permit file 22-87-927 ACE_NED permit file 23-198902070 ACE_NED permit file 24-87-912 ACE_NED permit file 24-89-1180 ACE_NED permit file 25-81-374 ACE_NED permit file 25-86-1007 ACE_NED permit file 25-86-290E ACE_NED permit file 25-86-641 ACE_NED permit file Boston Harbor ACE_NED permit file Bridge marine- Salisbury, MA ACE_NED permit file CENED-OR (1145-2-303b) ACE_NED permit file HULL-72-CHA30 ACE_NED permit file Long Wharf Boston	ACE_NED permit file Navigation Improvement Study Feasibility Report and Environmental Assessment; Mystic RI ACE_NED permit file Navigation Improvement Study Dredge Material Disposal Plan Supplement to Feasibility Rep Boehm, 1983 Bajek, 1983 Battelle, 1984; 1987 a, b Boehm & Farrington, 1984 Boehm et al., 1984 CDM, 1980 Cudmore, 1988 Enseco, 1987a Enseco, 1987b GCA Corp., 1982 Gardner et al., 1986 Gardner et al., 1988 Hubbard, 1987 Jason M. Cortell & Assoc., 1982
USGS Massachusetts Bay	ACE_NED permit file MA DPW Beverly-Salem Bridge and By-Pass Project ACE_NED permit file MA-HULL-81-180 ACE_NED permit file MA-HULL-84-210 ACE_NED permit file MWRA- Stoney Brook Conduit ACE_NED permit file Massport Bird Island Flats - Harborwalk phase III ACE_NED permit file Navigation Improvement Study Dredge Material Disposal Plan Supplement to Feasibility Rep USACOE, 1981 Wong, 1983 USEPA MBDS, 1989 USACOE, 1990b (DAMOS)	Jason Cortell, 1990 MA DEQE, 1985 MA DEQE, 1986 MA DPW, 1991 MA DEQE, 1982 MacDonald, 1991 NET Atlantic, 1990 Nolan et al., 1981 Penney et al., 1981 Phillips, 1985 Pruell et al., 1989 Ryan et al., 1982 Robinson et al., 1990 Shea et al., 1991 Shiaris et al., 1986

Types of Data Included in the NSI

In addition to sediment chemistry data, tissue residue, benthic abundance, toxicity (solid-phase and elutriate), histopathology, and fish abundance data have been gathered and included in the NSI, although only the sediment chemistry, tissue residue, and toxicity data have been evaluated for this report to Congress. The NSI also includes

loadings data from the Permit Compliance System (PCS) and the Toxic Release Inventory (TRI). A summary of the types of data available in the NSI is provided below.

Sediment chemistry. Sediment chemistry data include detailed analytical results, analyte sampled, remark codes, sampling methods, analytical methods, sample weight, core depths, and grain size information. Percent organic carbon and acid-volatile sulfide content of sediments are also included when available.

Tissue residue. Tissue residue data include detailed analytical results, analyte sampled, remark codes, sampling methods, clean-up procedures, analytical methods, species, sex, anatomy sampled, life stage, and wet/dry reporting basis.

Toxicity. Toxicity data include test conditions (DO, pH, flushing hardness, feeding, salinity, etc.), test species, dilution, endpoints (e.g., mortality), and test duration. Solid-phase and elutriate data are provided when available.

Benthic abundance. Benthic abundance data include enumeration of species collected and numerous community-level summaries/indices.

Histopathology. Histopathology data include the number of fish with body, branchial, and buccal pathologies; number of species; and abundance.

Fish abundance. Fish abundance data include mean and standard deviation of fish length and abundance of species.

For each data set included in the NSI, Table A-1 identifies the number of sampling stations at which the following parameters were measured:

- Sediment chemistry
- Tissue residue
- Benthic abundance
- Toxicity
- Histopathology
- Matched data
 - sediment chemistry and tissue residue
 - sediment chemistry and benthic abundance
 - sediment chemistry and toxicity
 - sediment chemistry and histopathology
 - sediment chemistry, tissue residue, and toxicity
 - sediment chemistry, benthic abundance, and toxicity

Table A-2 presents the total number of sampling stations at which each of these parameters was measured and the number of sampling stations for which coordinates (i.e., latitude/longitude) were available. Only data from sampling stations with coordinates could be used to classify sampling stations into Tier 1, Tier 2, or Tier 3.

How the Data Are Organized

The NSI data are contained in a series of tables that correspond to the different types of data described above. In some cases multiple tables were created for one type of data. The primary table in the NSI is the station table. Each record in the table corresponds to a unique sampling station. The records in the station table can be related to tables for each type of data, such as sediment chemistry data, tissue residue data, etc. These tables can then be related to additional look-up tables that include ancillary information such as chemical or species names. Figure A-1 illustrates the relationship between the station, sediment chemistry, tissue residue, toxicity, and related look-up tables.

Table A-3 summarizes the tables available in version 1.1 of the NSI (the current version). Some of these tables have not required updating since version 1.0 of the NSI (the version used to prepare the preliminary

Table A-1. Number of Sampling Stations at Which Various Types of Data Were Collected

Data Set	Number of Stations Where Measured										
	Sediment Chemistry	Tissue Residue	Benthic Abundance	Toxicity	Histopathology	Sediment Chemistry and Tissue Residue	Sediment Chemistry and Benthic Abundance	Sediment Chemistry and Toxicity	Sediment Chemistry and Histopathology	Sediment Chemistry, Tissue Residue, and Toxicity	Sediment Chemistry, Benthic Abundance, and Toxicity
STORET	12,907	6,057				1,533					
Region 4	1,024										
ODES	1,317	1,722	2,592	296		37	664	70		2	49
COSED	1,104										
Gulf of Mexico	210			82				6			
Great Lakes	761	26	476	373		26	449	369		26	68
DMATS	213	202		245		169		188		163	
Mass. Bay	979										
EMAP LA Prov. VA Prov.	260 200	199	259 212	259 212	259	198	259 202	259 202	259	198	259 202
Seattle USCOE	2,116		365	876			365	707			270
Total	21,093	8,206	3,904	2,343	259	1,963	1,939	1,801	259	389	848

Table A-2. Number of Sampling Stations With Data Included in the NSI

Measurement Parameters	Total Number of Stations	Stations with Coordinates	
		Number	% of Total Number of Stations w/Coordinates ^a
Sediment Chemistry	21,093	19,546	76
TOC	6,170	5,335	21
AVS	425	371	1
Tissue Residue	8,206	7,208	28
Toxicity	2,343	1,523	6
Elutriate Phase	630	—	—
Solid Phase	1,865	—	—
Benthic Abundance	3,904	1,844	7
Histopathology	259	259	1
Sediment Chemistry & Tissue	1,963	1,930	8
Sediment Chemistry & Toxicity	1,801	1,263	5
Sediment Chemistry & Abundance	1,939	1,340	5
Sediment Chemistry & Histopathology	259	259	1
Sediment Chemistry, Tissue, & Toxicity	389	359	1
Sediment Chemistry, Toxicity, & Abundance	848	733	3

^aTotal number of stations with coordinates = 25,555.

evaluation of sediment chemistry data described in Chapter 2). Key changes to the data set from version 1.0 include the following:

- Inclusion of Regional/state review codes. (See data element NSIREVCD in tables ALLSEDI and ALLTISS.)
- Resolution of species codes for tissue residue data.
- Inclusion of biotoxicity control data for EMAP programs.
- Revised loadings data from Permit Compliance System (PCS) and Toxic Release Inventory (TRI). Facilities with no loadings data are included as a separate table.
- Inclusion of species information and toxicity phase for purposes of the NSI evaluation methodology.

The remainder of this section contains a listing of the field names and descriptions associated with each table in the NSI.

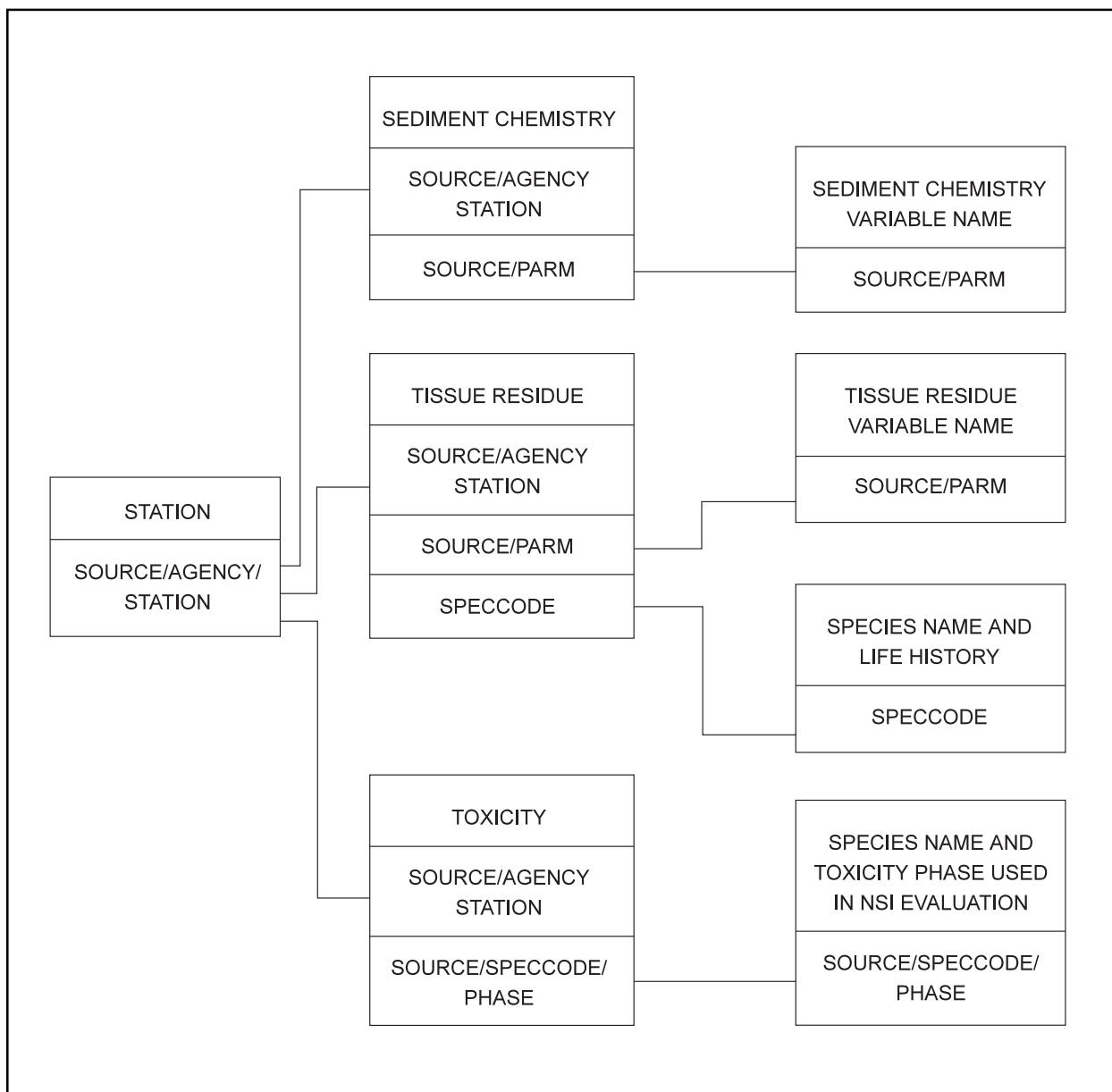


Figure A-1. Organization of NSI Data.

Table A-3. Data Tables Available in the NSI

Table Name	Table Description
ALLSTAT.DBF	Station
ALLSEDI.DBF	Sediment chemistry
ALLTISS.DBF	Tissue residue
ALLBIOT.DBF	Biotoxicity
ALLSEDM.DBF	Sediment grain size and miscellaneous sediment chemistry
ALLTISM.DBF	Miscellaneous tissue residue
ALLELUT.DBF	Elutriate
LOADD.DBF	PCS/TRI loadings
LOADS.DBF	PCS/TRI facilities (have loadings data)
LOADO.DBF	Other PCS/TRI facilities (no associated loadings data)
BIOTCODE.DBF	Toxicity phase for biotoxicity table (ALLBIOT)
ELUTPARM.DBF	List of analytes for elutriate table (ALLELUT)
SED_PARM.DBF	List of analytes for sediment tables (ALLSEDI, ALLSEDM)
TIS_CODE.DBF	List of species for tissue tables (ALLTISS, ALLTISM)
TIS_PARM.DBF	List of analytes for tissue tables (ALLTISS, ALLTISM)
SEACOE.DBF	EPA Region 10/COE Seattle District's Sediment Inventory Code file (important for interpreting a large number of codes unique to this data source)
REMARK.WP	Text file on remark codes (important for remark codes other than "K" or "U")
ALLSUPR.DBF	Superfund facilities
ALLBENA.DBF	Benthic species abundance
ALLBENC.DBF	Benthic community
ALLHIST.DBF	Histopathology
ALLFISA.DBF	Fish abundance
SPEC-CD.DBF	Species codes for benthic data
FISH-CD.DBF	Species codes for fish abundance data

ALLSTAT.DBF	Station
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
COUNTY	County
DEPTH	Water depth (m)
DEPT_MAX	Maximum water depth (m)
DEPT_MIN	Minimum water depth (m)
DREDGESI	Dredged site
DRWATERB	Dredged water body
GEOCODE	Geologic code
INSTIT	Institution
LAT	Latitude (decimal degrees)
LAT_2	Latitude #2 forming a rectangle (decimal degrees)
LNG	Longitude (decimal degrees)
LNG_2	Longitude #2 forming a rectangle (decimal degrees)
LOCATION	Location
LOC_CODE	Location code
NSIREACH	Reach File 1 reach
ORIGIN	Origin
ORG_NAME	Organization name
REFER	Reference, literature citation
SR_SCI	Senior scientist
STATE	State
WATERBOD	Waterbody
EPA_REG	EPA Region
FIPS	FIPS code
FIPS_DIS	Distance to nearest FIPS (mile)
HUC_DIS	Distance to nearest catologic unit (mile)
RF1_DIS	Distance to RF1 reach (mile)

ALLSEDL.DBF	Sediment chemistry
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
SUBSAMPL	Unique subsample identifier code
REPLICAT	Unique replicate identifier code
SEQ	Computer-generated sequence number when multiple samples were taken; SOURCE, AGENCY, STATION, and DATE were identical; and no SAMPLE, SUBSAMPL, or REPLICAT codes were provided
CAS	CAS number for analyte
CLEANUP	Sample cleanup code to indicate an additional step taken to further purify the sample extracts or digestates
COMMENTS	Comments
DRY_WGT	Percent of total sample remaining after drying

EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
INSTRUME	Instrument code to identify the final chemical analysis method(s) used for analyzing the sample
MEAS_BAS	Result is wet or dry weight basis (see also P)
NSIREVCD	Preliminary evaluation code (A=Reviewed in QA/QC of Preliminary Evaluation, U=Only one (1) observation of this chemical in source, X=Deleted based on QA/QC of Preliminary Evaluation (first run), Y=Duplicate Data, Z=Deleted based on QA/QC of Preliminary Evaluation (second run))
P	Result associated with PARM (µg/kg, ppb)
PARM	Analyte measured (see also P and R)
R	Remark code associated with PARM and P
SAMP_DTL	Depth to bottom of sample interval (m)
SAMP_DTU	Depth to top of sample interval (m)
SMP_EQP	Sampling equipment code
SPHERE	Sphere (i.e., environment) code from which the sample came
WET_WGT	Total wet weight of sample (g)

ALLTISS.DBF	Tissue residue
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
SEQ	Computer-generated sequence number when multiple samples were taken; SOURCE, AGENCY, STATION, and DATE were identical; and no SAMPLE, SUBSAMPL, or REPLICAT codes were provided
REPLICAT	Unique replicate identifier code
ANATOMY	Organ/tissue sampled
ANAT_CD	Organ/tissue sampled code
CAS	CAS number for analyte
CLEANUP	Sample cleanup code to indicate an additional step taken to further purify the sample extracts or digestates
COMPOSIT	A unique identifier to indicate a sample created by compositing tissues from several individuals
DRY_WGT	Percent of total sample remaining after drying
EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
INSTRUME	Instrument code to identify the final chemical analysis method(s) used for analyzing the sample
NSIREVCD	Preliminary evaluation code (F=Field test, L=Lab test, W=Species cannot be resolved, Y=Duplicate Data)
LENGTH	Length of specimen
LIFE_STA	Life stage code to identify the life stage of the sample
MEAS_BAS	Result is wet or dry weight basis (see also P)
NUMB_IND	Number of organisms in sample
P	Result associated with PARM
PARM	Analyte measured (see also P and R)
P_STD	Standard deviation of P associated with repeated measurements of PARM
R	Remark code associated with PARM and P

SAMPTYPE	Sample type
SEX	Sex code used to identify sex of sample
SMP_EQP	Sampling equipment code
SPECCODE	Species code
SPECIMEN	Unique identifier for the individual organism being analyzed
TOT_REP	Number of replicates
WEIGHT	Weight of organism
WET_WGT	Total weight of sample
LIPIDS	% Extractable lipids
SPEC_BIO	STORET taxonomic code

ALLBIOT.DBF	Biotoxicity
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
REPLICAT	Unique replicate identifier code
SEQ	Computer-generated sequence number when multiple samples were taken; SOURCE, AGENCY, STATION, and DATE were identical; and no SAMPLE, SUBSAMPL, or REPLICAT codes were provided
AMMONIA	Ammonia concentration (mg/L)
ABNORMAL	Abnormality
BIOASS_DA	Bioassay date
BIOASSAY	Type of bioassay reported
BIOMASS	Biomass
COMMENTS	Comments
COM_NAME	Common name
DIL_UNIT	Concentration/Dilution units
DILUTION	Concentration/Dilution
DOX	Dissolved oxygen (mL/L)
ENDPOIN2	Endpoint #2 of bioassay test
ENDPOINT	Endpoint of bioassay test
E_QUALIF	EMERGENC qualifier
EMERGENC	Emergence after 10 days
EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
FEEDING	Feeding of species tested
FLUSH	Flushing rate in percent of chamber volume exchanged/24 hours
GENUS	Organism genus
HARDNESS	Hardness
HOLD_TIM	Holding time of sample prior to analysis (weeks)
LFSTG_EN	Life stage end—for bioassays that span more than one life stage, record predominant life stage at the end of the bioassay
LFSTG_ST	Life stage start—for bioassays that span more than one life stage, record predominant life stage at the start of the bioassay
MEASURED	Measured (Y/N)
NAME	Genus and species name (linked to PHASE)
NUM_ORGA	Number of organisms
P	Result associated with ENDPOINT

P_CC	Control-corrected analytical result associated with P
P2	Result associated with ENDPOIN2
PH	pH
PHASE	Phase code to indicate the phase (i.e., medium) in which the bioassay organisms are housed
PHOTO_PE	Photoperiod: Number of light hours vs. number of dark hours (e.g., 1608 = 16 hours light, 8 hours dark)
QASAMP1	Control sample no. 1
QASAMP2	Control sample no. 2
QASAMP3	Control sample no. 3
RENEWAL	Renewal (Y/N)
R	Remark code associated with ENDPOINT and P
REBURIAL	ET50 (mean reburial time)
RESPO_TY	Type of bioassay response
SALINITY	Salinity of water in test chamber (ppt)
SAMP_DTL	Depth to bottom of sample interval (m)
SAMP_DTU	Depth to top of sample interval (m)
SERIES	Bioassay series number
SIGNIF	Significant difference from control
SMP_EQP	Sampling equipment code
SPECCODE	Species code
SPECIES	Organism species
SPHERE	Sphere (i.e., environment) code from which the sample came
STD_TOX	Standard Toxicant Result code to indicate whether the results of the standard toxicant bioassay were acceptable
TEMP	Water temperature (deg C)
TESTDUR	Test duration (days)
TESTTYPE	Test used
TESTEXP	Test exposure periods
UNITS	Units associated with ENDPOINT and P
UNITS2	Units associated with ENDPOIN2 and P2
WATERTYP	Water type
YOUNG	Number of young produced per adult female over 4 weeks

ALLSEDM.DBF	Sediment grain size and miscellaneous sediment chemistry
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
SUBSAMPL	Unique subsample identifier code
REPLICAT	Unique replicate identifier code
SEQ	Computer-generated sequence number when multiple samples were taken; SOURCE, AGENCY, STATION, and DATE were identical; and no SAMPLE, SUBSAMPL, or REPLICAT codes were provided
CAS	CAS number for analyte
CLEANUP	Sample cleanup code to indicate an additional step taken to further purify the sample extracts or digestates
COARSE_M	Method of analysis for analysis of coarse particles. Left blank if sample was not split into fractions.
COMMENTS	Comments

DRY_WGT	Percent of total sample remaining after drying
EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
FINE_MTH	Method of analysis for analysis of fine particles. Left blank if sample was not split into fractions.
INSTRUME	Instrument code to identify the final chemical analysis method(s) used for analyzing the sample
MEAS_BAS	Result is wet or dry weight basis (see also P)
P	Result associated with PARM
PARM	Analyte measured (see also P and R)
PHI_B	Phi boundaries in phi units, between the coarse and fine fractions
PHI_MAX	Phi boundary maximum at the fine end of the analyzed range
PHI_MIN	Phi boundary minimum at the coarse end of the analyzed range
R	Remark code associated with PARM and P
SAMP_DTL	Depth to bottom of sample interval (m)
SAMP_DTU	Depth to top of sample interval (m)
SMP_EQP	Sampling equipment code
SPHERE	Sphere (i.e., environment) code from which the sample came
TOT_WGT	Total weight of sample (g)
UNITS	Units associated with PARM, P, and R
WET_WGT	Total wet weight of sample (g)
P_ALP	Nonnumeric result associated with PARM

ALLTISM.DBF	Miscellaneous tissue residue
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
SEQ	Computer-generated sequence number when multiple samples were taken; SOURCE, AGENCY, STATION, and DATE were identical; and no SAMPLE, SUBSAMPL, or REPLICAT codes were provided
REPLICAT	Unique replicate identifier code
ANAT_CD	Organ/tissue sampled code
CAS	CAS number for analyte
CLEANUP	Sample cleanup code to indicate an additional step taken to further purify the sample extracts or digestates
COMPOSIT	A unique identifier to indicate a sample created by compositing tissues from several individuals.
DRY_WGT	Percent of total sample remaining after drying
EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
INSTRUME	Instrument code to identify the final chemical analysis method(s) used for analyzing the sample
LENGTH	Length of specimen
LIPIDS	Lipids (%)
LIFE_STA	Life stage code to identify the life stage of sample
MEAS_BAS	Result is wet or dry weight basis (see also P)
NUMB_IND	Number of organisms in sample
P	Result associated with PARM

PARM	Analyte measured (see also P and R)
R	Remark code associated with PARM and P
SEX	Sex code used to identify sex of sample
SMP_EQP	Sampling equipment code
SPECCODE	Species code
SPEC_SCI	Species scientific name
SPECIMEN	Unique identifier for the individual organism being analyzed
UNITS	Units associated with PARM, P, and R
WET_WGT	Total weight of sample
P_ALP	Nonnumeric result associated with PARM

ALLELUT.DBF	Elutriate
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
SEQ	Computer-generated sequence number when multiple samples were taken; SOURCE, AGENCY, STATION, and DATE were identical; and no SAMPLE, SUBSAMPL, or REPLICAT codes were provided.
SUBSAMPL	Unique subsample identifier code
REPLICAT	Unique replicate identifier code
CAS	CAS number for analyte
EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
INSTRUME	Instrument code to identify the final chemical analysis method(s) used for analyzing the sample
P	Result associated with PARM (µg/L)
PARM	Analyte measured (see also P and R)
R	Remark code associated with PARM and P
SAMP_DTL	Depth to bottom of sample interval (m)
SAMP_DTU	Depth to top of sample interval (m)
SAMP_EQP	Sampling equipment code

LOADD.DBF	PCS/TRI loadings
ID	Facility identification number
CAS	CAS number for analyte
CHEMICAL	Analyte name
SIC	SIC code for facility
E3KGY0	PCS loadings using below detection limit (dl) equal to 0.0 assumption
E3KGYE	PCS loadings using below detection limit equal to 0.5-dl assumption
E3KGY1	PCS loadings using below detection limit equal to dl assumption
E3FLO0	PCS flow using below detection limit equal to 0.0 assumption
E3FLOE	PCS flow using below detection limit equal to 0.5-dl assumption
E3FLO1	PCS flow using below detection limit equal to dl assumption
E6KGYE	TRI POTW transfers
E6KGY75	75 percent of TRI POTW transfers

LOADS.DBF **PCS/TRI facilities (have loadings data)**

ID	Facility identification number
CODE	“PCS” or “TRI”
SPC	State postal code
LAT	Latitude (decimal degrees)
LNG	Longitude (decimal degrees)
NSIREACH	Reach File 1 Reach

LOADO.DBF **Other PCS/TRI facilities (no associated loadings data)**

ID	Facility identification number
SPC	State postal code
LAT	Latitude (decimal degrees)
LNG	Longitude (decimal degrees)
NSIREACH	Reach File 1 Reach

BIOTCODE.DBF **Toxicity phase for biotoxicity table (ALLBIOT)**

NAME	Genus and species name
PHASE	Toxicity phase listed in source of data (when available)
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
NSIPHASE	Toxicity phase used by NSI

ELUTPARM.DBF **List of analytes for elutriate table (ALLELUT)**

SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
PARM	Analyte measured (see also P and R)
CAS	CAS number for analyte
LNAME	Analyte long name

SED_PARM.DBF **List of analytes for sediment tables (ALLSEDI, ALLSEDM)**

SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
PARM	Analyte measured (see also P and R)
CAS	CAS number for analyte
LNAME	Analyte long name

TIS_CODE.DBF **List of species for tissue tables (ALLTISS, ALLTISM)**

SPECCODE	Species code
SPEC_SCI	Species scientific name
SPEC_COM	Species common name
RES_MIG	Species resident, migratory, or either
BOT_PEL	Species benthic, pelagic, or either
EDIBLE	Species considered edible by humans

TIS_PARM.DBF **List of analytes for tissue tables (ALLTISS, ALLTISM)**

SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
PARM	Analyte measured (see also P and R)

CAS	CAS number for analyte
LNAME	Analyte long name

ALLSUPR.DBF	Superfund facilities
STATE	State postal code
ID	Superfund identification
NAME	Facility name
COUNTY	County name
CNTY_FIP	3-digit county FIPS code
C0305	C0305
C0326	C0326
LAT	Latitude (decimal degrees)
LNG	Longitude (decimal degrees)
NSIREACH	Reach File 1 Reach

ALLBENA.DBF	Benthic species abundance
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
REPLICAT	Unique replicate identifier code
BOTTOM	Bottom type
AREA_BAS	Area basis for reported data
COMM_BAS	Basis for community abundance measurements
EXT_MTHO	Extraction method code to indicate the method used to extract or digest the sample matrix and remove or isolate the chemical of concern
GENUS	Organism genus
MESH_SZ	Seive mesh size
N_REP	Number of replicate samples
NUMB_IND	Total number of individuals
NUMB_SPE	Total number of unique species
ORDER	Organism order
P	Result associated with PARM
PARM	Analyte measured (see also P and R)
P_MEAN	Mean P
P_STD	Standard deviation of P
R	Remark code associated with P and PARM
SAMP_DTL	Depth to bottom of sample interval (m)
SAMP_DTU	Depth to top of sample interval (m)
SPECIES	Organism species
SPECCODE	Species code
UNITS	Units associated with PARM, P, and R

ALLBENC.DBF	Benthic community
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)

AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
SAMPLE	Unique sample identifier code
AMPHIPOD	Number of amphipod
AMPHMABN	Mean abundance of amphipods
AREA_BAS	Area basis for reported data
ARTHROPO	Number of arthropods in the sample
BIOM_TOT	Total biomass (g)
BIOMMEAN	Mean biomass per grab (g)
BIV_MABN	Mean abundance of bivalves (g)
BSPINDEX	Benthic species index
BSP_GRAB	Number of grabs
BSP_MABN	Mean abundance per grab
BSP_MDIV	Mean Shannon-Wiener diversity index
BSP_MEAN	Mean number of species per grab
BSP_MEXP	Expected mean number of species
BSP_TABN	Total abundance
BSP_TDIV	Pooled Shannon-Wiener diversity index
BSP_TOT	Total number of species
CAPIMABN	Mean abundance of capitellids
COMM_BAS	Basis for community abundance measurements
CRUSTACE	Number of crustaceans in the sample
DECAMABN	Mean abundance of decapods
DOMINANC	Numeric dominance in the sample
ECHINODE	Number of echinoderms in the sample
EVENESS	Eveness
ITI	ITI
MED_DIAM	50% quartile diameter (phi)
MISC_TAX	Number of miscellaneous taxa in sample
MOIST_M	Sediment moisture content (%)
MOLLUSCS	Number of molluscs in the sample
NEMATODE	Number of nematodes in the sample
OLIGOCHA	Number of oligochaetes in the sample
PABN_AMP	Percent abundance amphipods
PABN_BIV	Percent abundance bivalves
PABN_GAS	Percent abundance gastropods
PABN_TUB	Percent abundance tubificids
PLYC_MWT	Mean biomass per polychaete (g)
PLYCMABN	Mean abundance of polychaetes
P_SENSIT	Abundance of pollution sensitive organisms (%)
P_TOLERA	Abundance of pollution tolerant organisms (%)
POLYCHAE	Number of polychaetes in the sample
QUARDVTM	Phi quartile deviation
Q1_PHI	25% quartile diameter (phi)
Q3_PHI	75% quartile diameter (phi)
RPDDEP_M	Mean RPD in mm
SICL_B_M	Mean silt/clay content (%)
SKEWNESS	Phi quartile skewness
TUBIMABN	Mean abundance of tubificids

ALLHIST.DBF	Histopathology
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
BODYPATH	Number of fish with body pathologies
BRNCPATH	Number of fish with branchial pathologies
BUCCPATH	Number of fish with buccal pathologies
FSP_ABN	Abundance (number/rawl)
FSP_TOT	Number of species
MNMDTRSH	Manmade trash (Y/N)
ALLFISA.DBF	Fish abundance
SOURCE	Identification of data origin (e.g., REG4 is the Region 4 Pilot Study)
AGENCY	Identification of group responsible for collecting data (e.g., NS&T is NOAA's National Status and Trends Program)
STATION	Monitoring station identification code. (ODES NOTE: STATION = <i>STN_CD</i> ' ' <i>STATION</i> DATE. DMATS NOTE: STATION = <i>ID</i> ' ' <i>STATIONI</i> ' ' <i>SERIES</i> ' ' <i>SCAN</i> .)
DATE	Date of sample collection
LEN_MEAN	Mean length (in)
LEN_STD	Standard deviation length (in)
P	Result associated with PARM
PARM	Analyte measured (see also P)
SPECCODE	Species code
UNITS	Units associated with PARM and P
SPEC-CD.DBF	Species codes for benthic data
SPECCODE	Species code
SPEC_SCI	Species scientific name
SPEC_COM	Species common name
FISH-CD.DBF	Species codes for fish abundance data
SPECCODE	Species code
SPEC_SCI	Species scientific name
SPEC_COM	Species common name