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```
<!-- ************************************************************* -->
<!--                3.0 Major BSML Document Divisions              -->
<!-- ************************************************************* -->
<!ELEMENT Bsml (Attribute*,Info*,Definitions?,Display?)              >
<!--
  Note: For the top level Bsml element, the following Attribute
        elements (name/content pairs) are commonly defined:
           document-title="title of document"
           project="name of project" (used with project manager)
           project-id="unique project identifer for this document"
           author="originator of document"
           storage="primary storage location"
           owner="user who has complete access"
           password="security manager term to validate owner"
           owner-access="(none|read-only|read-write)"
           user-access="(none|read-only|read-write)"
           create-date="date of origination (yyyy-mm-dd)"
           update-date="date of last modification (yyyy-mm-dd)"
                                                                   -->
<!ELEMENT Attribute EMPTY >
<!ATTLIST Attribute
  name     CDATA  #REQUIRED
  content  CDATA  #IMPLIED >
<!-- ************************************************************* -->
<!--                 4.0  Definitions Sub-divisions                -->
<!-- ************************************************************* -->
<!--
     Notes:

        1. The Definitions section may be used without a Display
           section if the goal is simply to encode sequence data;
           for convenience, a few elements in the Definitions
           section have display-related attributes, but these
           attributes are never required. Thus a BSML document may
           be used to convey data independently of a BSML browser,
           and the document may be read and processed by any
           suitable XML parsing software.

        2. The Display section provides information that is mainly
           relevant for the graphical display of bioinformatic data
           and for accessing links in other network resources. Much
           of the content of the Display section only has meaning
           for a browser that works specifically with BSML and has
           been customized to display the widgets defined in the
           BSML standard.
-->
<!-- ************************************************************* -->
<!ELEMENT Definitions (Attribute*,Sequences?,Sets?,Tables?)          >

<!-- ************************************************************* -->
<!--                             7.0 Tables                        -->
<!-- ************************************************************* -->
<!ELEMENT Tables (Attribute|Table|Motif-table|
            Seq-pair-alignment|Alignment-point-set|Table-import)*   >
<!ATTLIST Tables
  %attrs;                                    -- attributes     -->
<!-- ************************************************************* -->
```

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```
<!--                    7.1 Multiple-alignment-table                -->
<!-- ************************************************************* -->
<!ELEMENT Table-data EMPTY -- locally supplied data for import -->
<!ATTLIST Table-data
   %attrs;   --        use title to name table row, if appropriate --
             -- uses value for comma separated data table row list -->

<!ELEMENT Table-import (Attribute*,Table-data*)
     -- internal, if table-data, or external file or internet href -->
<!ATTLIST Table-import
  %attrs;
  format CDATA #IMPLIED -- acceptable formats=bsml|html|txt|sdf|db --
       --     if data in Table-data elements, no format needed     --
  read-field-desc  %yesorno; #IMPLIED           -- use for txt,sdf --
       -- if read-field-desc=yes, read field descriptions at start --
       -- of file = Num (number of fields on first line)           --
       --           FieldName,Type(=T,N,L),Width,Decimals          --
       --           with one line per field                        --
       -- list of columns to include; use all if not defined       --
  column-numbers   CDATA     #IMPLIED
                        -- comma separated list of column headings --
  column-headers   CDATA     #IMPLIED          --  use for txt,sdf --
       -- comma separated lists of start positions and field widths--
  column-starts    CDATA     #IMPLIED          -- used for txt     --
  column-widths    CDATA     #IMPLIED          -- used for txt     --
  header-count     %integer; #IMPLIED          -- text skip lines  --
  display-widths   CDATA     #IMPLIED      -- comma separated
                  list of column widths for display in grid viewer --
  alignments       CDATA     #IMPLIED      -- comma separated
        list of L (left=text) or R (right=numeric) for each column --
  font             IDREF     #IMPLIED           -- font for grid   --
  add-row-numbers  %yesorno; #IMPLIED           -- number grid rows--
  locked-columns   %integer; #IMPLIED           --# to lock at left--
  source           %url;     #REQUIRED          -- file/remote     --
  refs             IDREFS    #IMPLIED  -- element cross-references -->

<!-- ************************************************************* -->
<!--                          7.2 Table                            -->
<!-- ************************************************************* -->
<!-- IETF HTML table standard, see RFC1942                         -->
<!ENTITY % tframe
                "(void|above|below|hsides|lhs|rhs|vsides|box|border)">
<!ENTITY % trules "(none | groups | rows | cols | all)">
<!-- horizontal placement of table relative to document            -->
<!ENTITY % talign "(left|center|right)"                              >
<!-- horizontal alignment attributes for cell contents             -->
<!ENTITY % cellhalign
  "align (left|center|right|justify|char) #IMPLIED
   char    %character;  #IMPLIED  -- alignment char, e.g. char=':' --
   charoff %length;     #IMPLIED  -- offset for alignment char --"
>

<!-- vertical alignment attributes for cell contents               -->
<!ENTITY % cellvalign "valign (top|middle|bottom|baseline) #IMPLIED" >

<!ELEMENT Table (Caption?,(Col*|Colgroup*),Thead?,Tfoot?,Tbody+)     >
<!ELEMENT Caption  (#PCDATA)  -- table caption                     -->
```

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```
<!ELEMENT Thead    (Tr)+      -- table header                      -->
<!ELEMENT Tfoot    (Tr)+      -- table footer                      -->
<!ELEMENT Tbody    (Tr)+      -- table body                        -->
<!ELEMENT Colgroup (Col)*     -- table column group                -->
<!ELEMENT Col      EMPTY      -- table column                      -->
<!ELEMENT Tr       (Th|Td)+   -- table row                         -->
<!ELEMENT Th       (#PCDATA)  -- table header or data cell         -->
<!ELEMENT Th       (#PCDATA)  -- table header or data cell         -->

<!ATTLIST Table                   -- table element --
  %attrs;                         -- %coreattrs, %events --
  summary     %text;     #IMPLIED -- purpose/structure for speech  --
  width       %length;   #IMPLIED -- table width relative to window--
  border      CDATA      #IMPLIED -- frame width around table      --
  frame       %tframe;   #IMPLIED -- include which parts of framee --
  rules       %trules;   #IMPLIED -- rulings between rows and cols --
  cellspacing %length;   #IMPLIED -- spacing between cells         --
  cellpadding %length;   #IMPLIED -- spacing within cells          -->

<!ENTITY % calign "(top|bottom|left|right)"                          >

<!ATTLIST Caption
  %attrs;                                   -- %coreattrs, %events -->
<!--
  COLGROUP groups a set of COL elements. It allows you to group
  several semantically related columns together.
-->
<!ATTLIST Colgroup
  %attrs;                       -- attributes                      --
  span        %integer;  "1"    -- default # of columns in group   --
  width       %length; #IMPLIED -- default width for enclosed COLs --
  %cellhalign;                  -- horizontal alignment in cells   --
  %cellvalign;                  -- vertical alignment in cells     -->
<!--
  COL elements define the alignment properties for cells in
  one or more columns. The WIDTH attribute specifies the width of
  the columns, e.g.
     width=64        width in screen pixels
     width=0.5*      relative width of 0.5
  The REPEAT attribute allows you to repeat the effects of
  a COL element as if the same element was repeated n times.
  There are no grouping semantics for repeated columns.
-->
<!ATTLIST Col                     -- column groups and properties  --
  %attrs;                         -- attributes                    --
  repeat      %integer;  "1"      -- repeat count for COL          --
  width       %length; #IMPLIED   -- column width specification    --
  %cellhalign;                    -- horizontal alignment in cells --
  %cellvalign;                     -- vertical alignment in cells  -->
<!--
  Use THEAD to duplicate headers when breaking table across page
  boundaries, or for static headers when TBODY sections are rendered
  in scrolling panel.

  Use TFOOT to duplicate footers when breaking table across page
  boundaries, or for static footers when TBODY sections are rendered
  in scrolling panel.
```

```
  Use multiple TBODY sections when rules are needed between groups
  of table rows.
-->
<!ATTLIST Thead                  -- table section                  --
  %attrs;                        -- attributes                     --
  %cellhalign;                   -- horizontal alignment in cells  --
  %cellvalign;                   -- vertical alignment in cells    --
  >
<!ATTLIST Tbody                  -- table section                  --
  %attrs;                        -- attributes                     --
  %cellhalign;                   -- horizontal alignment in cells  --
  %cellvalign;                   -- vertical alignment in cells    --
  >
<!ATTLIST Tfoot                  -- table section                  --
  %attrs;                        -- attributes                     --
  %cellhalign;                   -- horizontal alignment in cells  --
  %cellvalign;                   -- vertical alignment in cells    --
  >

<!ATTLIST Tr                     -- table row                      --
  %attrs;                        -- attributes                     --
  %cellhalign;                   -- horizontal alignment in cells  --
  %cellvalign;                   -- vertical alignment in cells    -->

<!-- Scope is simpler than axes attribute for common tables        -->
<!ENTITY % scope "(row|col|rowgroup|colgroup)"                      >

<!-- TH is for headers, TD for data, but for cells as both use TD  -->
<!ATTLIST Th                     -- header or data cell            --
  %attrs;                        -- attributes                     --
  abbr        %text;    #IMPLIED -- abbreviation for header cell   --
  axis        CDATA     #IMPLIED -- names groups of related headers--
  headers     IDREFS    #IMPLIED -- list of id's for header cells  --
  scope       %scope;   #IMPLIED -- scope covered by header cells  --
  width       %length;  #IMPLIED -- width relative to table        --
  rowspan     %integer; "1"      -- number of rows spanned by cell --
  colspan     %integer; "1"      -- number of cols spanned by cell --
  %cellhalign;                    -- horizontal alignment in cells --
  %cellvalign;                    -- vertical alignment in cells   -->

<!ATTLIST Td                     -- header or data cell            --
  %attrs;                        -- attributes                     --
  abbr        %text;    #IMPLIED -- abbreviation for header cell   --
  axis        CDATA     #IMPLIED -- names groups of related headers--
  headers     IDREFS    #IMPLIED -- list of id's for header cells  --
  scope       %scope;   #IMPLIED -- scope covered by header cells  --
  width       %length;  #IMPLIED -- width relative to table        --
  rowspan     %integer; "1"      -- number of rows spanned by cell --
  colspan     %integer; "1"      -- number of cols spanned by cell --
  %cellhalign;                    -- horizontal alignment in cells --
  %cellvalign;                    -- vertical alignment in cells   -->

<!-- ************************************************************* -->
<!--                          7.3 Motif-table                      -->
<!-- ************************************************************* -->
<!ELEMENT Motif-data (Motif-data*)                                  >
```

```
<!ATTLIST Motif-data
  %attrs;
  -- if hierachical, top level owns next level, etc.               --
  -- if flat, use comma-separated lists                            --
  -- if flat and site series for 1-element motif, one-element=true --
  one-element %yesorno; "0"   -- by default, multi-element is true --
  positions   CDATA #REQUIRED -- ,-separated list of positions     --
  widths      CDATA #IMPLIED  -- ,-separated list of motif widths  --
  strands     CDATA #IMPLIED  -- ,-separated list of plus=1,minus=0--
  titles      CDATA #IMPLIED  -- ,-separated list of titles        --
  values      CDATA #IMPLIED  -- ,-separated list of values        --
  markers     CDATA #IMPLIED  -- ,-separated 5 prime offsets       --
  overhangs   CDATA #IMPLIED  -- ,-separated overhang on minus std --
  refs        CDATA #IMPLIED  -- space-separated list of IDs       -->

<!ELEMENT Sequence-motif (Interval-loc*,Motif-data*)                 >
<!ATTLIST Sequence-motif
  %attrs;
       -- if display-auto, create default display widget and show  --
  display-auto %yesorno; #IMPLIED
       -- auto-view is view to which to attach display widget      --
       -- if not defined, feature added to first view for this seq --
  auto-view   IDREF      #IMPLIED
  seqref      IDREF      #REQUIRED -- reference sequence           --
  alignment   %integer;  #IMPLIED  -- alignment pos on global seq  --
  startpos    %integer;  #IMPLIED  -- optional start of seq range  --
  endpos      %integer;  #IMPLIED  -- optional end of seq range    --
  refs        CDATA      #IMPLIED  -- space-separated list of IDs  -->

<!ELEMENT Motif-element EMPTY    -- describes one element of motif -->
<!ATTLIST Motif-element
  %attrs;
       -- if display-auto, create default display widget and show  --
  display-auto      %yesorno; #IMPLIED
  -- fill applies to intervals --
  border-color      %color;   #IMPLIED  -- edge of rectangle        --
  fill-fg-color     %color;   #IMPLIED  -- foreground of fill area --
  fill-bg-color     %color;   #IMPLIED  -- background of fill area --
  fill-pattern      (clear|horiz|vert|fdiag|bdiag|
                      cross|diagcross|solid) #IMPLIED
  column-width      %length;  #IMPLIED -- if non-positional display--
  show-values       %yesorno; #IMPLIED -- if 1, show data values   --
  show-titles       %yesorno; #IMPLIED -- if 1, show titles        --
  show-no-position  %yesorno; #IMPLIED -- if 1, show at side       --
  state-names       CDATA     #IMPLIED
  -- state names are ,separated list for position values= -1,-2,   --
  value-scale       %integer; #IMPLIED  -- divide by power of 10   --
  value-min         %integer; #IMPLIED    -- to show as saturation --
  value-max         %integer; #IMPLIED    -- to show as saturation -->

<!ELEMENT Motif-table (Attribute*,Numbering?,
                       Interval-loc*,Motif-element*,Sequence-motif*) >
<!ATTLIST Motif-table
  %attrs;
  display-height     %length;  #IMPLIED  -- each line of display   --
  display-gap        %length;  #IMPLIED  -- distance between lines --
  point-width        %length;  #IMPLIED  -- line width for points  --
```

```
  title-width        %length;  #IMPLIED  -- if defined, show titles--
  value-width        %length;  #IMPLIED  -- if defined, show values--
  values-as-color    %yesorno; #IMPLIED  -- values as saturation   --
  value-scale        %integer; #IMPLIED  -- divide by power of 10  --
  global-length      %integer; #IMPLIED  -- =longest seq otherwise --
  refs               IDREFS    #IMPLIED  --element cross-references-->
<!-- Note: For further information on the use of the display
           parameters, see the browser motif viewer description;
           the display attributes are all optional if the goal
           is simply to convey information content.                -->

<!-- ************************************************************* -->
<!--                   7.4 Alignment-point-set                     -->
<!-- ************************************************************* -->

<!ELEMENT Alignment-point-set  (Attribute*,Numbering?)               >
<!ATTLIST Alignment-point-set
  %attrs;
  seqids     IDREFS    #REQUIRED       -- ids of sequencess        --
  featids    CDATA     #REQUIRED
  -- ids of corresponding features, points or intervals, or actual
                position values; value="NONE" means not included --
  captions   CDATA     #IMPLIED   -- n - 1 comma separated
                   captions to be shown on lines connecting points --
  consensus %yesorno;  #IMPLIED        --true if 1st=consensus seq --
       -- next 4 borrowed attributes from Dense-seg in ncbi asn.1  --
  numseg     %integer; #IMPLIED           -- number of segments    --
  starts     CDATA     #IMPLIED           -- offsets               --
  strands    CDATA     #IMPLIED           -- "P" or "M" - strand   --
  seglens    CDATA     #IMPLIED           -- lengths of segments   --
  refs       IDREFS    #IMPLIED        -- element cross-references -->

<!-- ************************************************************* -->
<!--                     7.5 Seq-pair-alignment                    -->
<!-- ************************************************************* -->

<!ELEMENT Seq-pair-run (Attribute*)          -- run of similarity  -->
<!ATTLIST Seq-pair-run
  id             IDREF     #IMPLIED         -- unique identifier   --
  translated     %yesorno; #IMPLIED         -- compared translated --
  runlength      %integer; #REQUIRED        -- length on ref seq   --
  comprunlength  %integer; #IMPLIED         -- if <> runlength     --
  refpos         %integer; #REQUIRED        -- position on ref     --
  refcomplement  %yesorno; #IMPLIED         -- true if comp strand --
  comppos        %integer; #REQUIRED        -- position on comp    --
  compcomplement %integer; #IMPLIED         -- true if comp strand --
  runscore       CDATA     #IMPLIED         -- displayable value   --
  runprob        CDATA     #IMPLIED         -- probability         --
  alignment      CDATA     #IMPLIED         -- transform compseq   --
  -- The alignment transforms the reference sequence into
     the comparison sequence; it uses following terminology:
       =N      next N bases/residues are identical
       -N:Mcc...replace next N bases/residues with following M
       for example =5-3:2ac-0:4acgt=20-4:0                    --
  refs          IDREFS     #IMPLIED    -- element cross-references -->

<!ELEMENT Seq-pair-alignment (Attribute*,Seq-pair-run*)              >
```

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```
<!ATTLIST Seq-pair-alignment
  %attrs;
  refseq        IDREF     #REQUIRED    -- reference sequence       --
  refxref       CDATA     #IMPLIED     -- database reference       --
  refcaption    CDATA     #IMPLIED     -- display caption          --
  refstart      %integer; #IMPLIED     -- overall region searched  --
  refend        %integer; #IMPLIED     -- end of search region     --
  reflength     %integer; #IMPLIED     -- complete seq length      --
  compseq       IDREF     #IMPLIED     -- comparison sequence      --
  compxref      CDATA     #IMPLIED     -- database reference       --
  compcaption   CDATA     #IMPLIED     -- display caption          --
  compstart     %integer; #IMPLIED     -- overall region searched  --
  compend       %integer; #IMPLIED     -- end of search region     --
  complength    %integer; #IMPLIED     -- complete seq length      --
  method        CDATA     #IMPLIED     -- comparison notes         --
  runminscore   CDATA     #IMPLIED     -- minimum run score        --
  runmaxscore   CDATA     #IMPLIED     -- maximum run score        --
  totalscore    CDATA     #IMPLIED     -- total alignment score    --
  refs          IDREFS    #IMPLIED     -- element cross-references -->
```