```
<?xml version="1.0" encoding="iso-8859-1"?>
<?xml-stylesheet type="text/xsl" href="stylesheet_PGD.xsl"?>


<!-- for aligned data and all ind in one population has the same data type (same loci/ loci
combination) -->
<!-- fill the text in the tags and delete not used optional (empty) tags!!! -->

<PGD>

  <header title="">
    <organism></organism>         <!-- optional -->
    <numPop></numPop>
    <numReads></numReads>         <!-- mixed/ 1/ 2/ ... -->
    <aligned></aligned>           <!-- yes/ no -->
    <missing></missing>
    <gap></gap>
    <gameticPhase></gameticPhase>           <!-- optional;  known/ unknown -->
    <recessiveData></recessiveData>         <!-- optional;  yes/ no -->
  </header>


  <loci>
    <lociNum></lociNum>
    <lociDataType></lociDataType>           <!-- mixed/ DNA/ Microsat/ RFLP/ AFLP/ Standard/
Frequency/... -->

    <!-- locus block can exist multiple (same number as the number of loci) -->
    <locus id="">
      <locusDataType></locusDataType>       <!-- if lociDataType = mixed;  DNA/ Microsat/
RFLP/ AFLP/ Standard/ Frequency/... -->
      <locusChromosom></locusChromosom>     <!-- optional;  number/ X/ Y/ V/ W/ mtDNA/ ...
-->
      <locusLocation></locusLocation>       <!-- optional -->
      <locusGenic></locusGenic>             <!-- optional;  coding/ noncoding -->
      <locusLength></locusLength>           <!-- optional -->
      <locusLinks></locusLinks>             <!-- optional -->
      <locusComments></locusComments>       <!-- optional -->
    </locus>
  </loci>

  <!-- population block can exist multiple (same number as the number of populations) -->
  <population name="">
    <popSize></popSize>
    <popGeogCoord></popGeogCoord>           <!-- optional, (for all ind in this pop the
same);  lon, lat -->
    <popLingGroup></popLingGroup>           <!-- optional, (for all ind in this pop the
same) -->
    <popNumReads></popNumReads>             <!-- if numReads = mixed;  mixed/ 1/ 2/ ... -->
    <popLoci></popLoci>                     <!-- locus, locus, ...   (all locus of same data
type,
                                                 if nucleotid data only one locus (one
sequence) is allowed) -->

    <!-- ind block can exist multiple (same number as the populatin size) -->
    <ind name="">
      <indGeogCoord></indGeogCoord>         <!-- optional;  lon, lat -->
      <indLingGroup></indLingGroup>         <!-- optional -->
      <indNumReads></indNumReads>           <!-- if popNumReads = mixed;  1/ 2/ ... -->
      <indFreq></indFreq>                   <!-- optional;  absolute frequency -->

      <!-- data block can exist multiple (same number as the number of reads) -->
      <data></data>                   <!-- data of locus, data of locus, ... -->
    </ind>
  </population>


  <!-- optional block -->
  <structure name="">
    <numGroups></numGroups>
    <group name=""></group>           <!-- population name, population name, ... -->
  </structure>


  <!-- optional block -->
  <distanceMatrix name="">
```

```
    <matrixSize></matrixSize>
    <matrixLabels></matrixLabels>     <!-- name, name, ... -->
    <matrix>                          <!-- lowertriangle matrix with diagonals -->
    </matrix>                         <!-- number (line break), number, number (line break),
... -->
  </distanceMatrix>

</PGD>
```