

```
<?xml version="1.0" encoding="iso-8859-1"?>
```

```
<?xml-stylesheet type="text/xsl" href="stylesheet_PGD.xsl"?>
```

```
<!-- for aligned data and ind in one population has the different data type (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/... -->
  <locusChromosome></locusChromosome> <!-- 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 -->
  <popLangGroup></popLangGroup>    <!-- optional, (for all ind in this pop the
same) -->
  <popNumReads></popNumReads>      <!-- if numReads = mixed; mixed/ 1/ 2/ ... -->
```

```
<!-- ind block can exist multiple (same number as the population size) -->
<ind name="">
  <indGeogCoord></indGeogCoord>    <!-- optional; lon, lat -->
  <indLangGroup></indLangGroup>    <!-- optional -->
  <indLoci></indLoci>              <!-- locus, locus, ... (all locus of same data
type,
sequence) per tag is allowed) -->
  <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>
```