Heterozygoti i insemineringsplan

- Der er beskrevet og testet hvordan heterozygoti kan inkluderes i insemineringsplanen på den fagligt korrekte måde. Nedenfor er vist programmer som anvendes til test

Forfatter

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Baggrund for formlerne for bidraget fra heterozygoti, forudsætninger for anvendelse:

--Jersey

select CKRDYRNR, NTMKO, STBNR, NAVN, SUM, Rank, NTM, NYNTM, NYSUM, NyRank, rank-nyrank forskel, heterozygoti from (

Select s.CKRDYRNR, NTMKO, s.STBNR, NAVN, SUM, RANK() OVER (PARTITION BY s.ckrdyrnr ORDER BY sum DESC) rank, NTM, heterozygoti, mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti)

 nyntm, SÆDBEHKODE||KATEGORI||FORTEGN||PRIORITEREDE||NTM+(mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti))||KSS||YINDEKS||s.stbnr nysum

, RANK() OVER (PARTITION BY s.ckrdyrnr ORDER BY SÆDBEHKODE||KATEGORI||FORTEGN||PRIORITEREDE||NTM+mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti)||KSS||YINDEKS||s.stbnr DESC) nyrank from h6601.v_ipdok_sum s

join h6601.dyr d on d.ckrdyrnr = s.ckrdyrnr

join h6601.heterozygoti z on z.DAM_DYR_ID = d.id

join h6601.tyr t on t.dyr_id = z.sire_dyr_id and s.stbnr = t.stbnr

where ipde_id = 39873 order by ckrdyrnr);

--RDM

select CKRDYRNR, NTMKO, STBNR, NAVN, SUM, Rank, NTM, NYNTM, NYSUM, NyRank, rank-nyrank forskel, heterozygoti from (

Select s.CKRDYRNR, NTMKO, s.STBNR, NAVN, SUM, RANK() OVER (PARTITION BY s.ckrdyrnr ORDER BY sum DESC) rank, NTM, heterozygoti, mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti)

 nyntm, SÆDBEHKODE||KATEGORI||FORTEGN||PRIORITEREDE||NTM+(mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti))||KSS||YINDEKS||s.stbnr nysum

, RANK() OVER (PARTITION BY s.ckrdyrnr ORDER BY SÆDBEHKODE||KATEGORI||FORTEGN||PRIORITEREDE||NTM+mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti)||KSS||YINDEKS||s.stbnr DESC) nyrank from h6601.v_ipdok_sum s

```sql
join h6601.dyr d on d.ckrdyrnr = s.ckrdyrnr

join h6601.heterozygoti z on z.DAM_DYR_ID = d.id

join h6601.tyr t on t.dyr_id = z.sire_dyr_id and s.stbnr = t.stbnr

where ipde_id = 3277 order by ckrdyrnr);
```

--HOL

```sql
select CKRDYRNR, NTMKO, STBNR, NAVN, SUM, Rank, NTM, NYNTM, NYSUM, NyRank, rank-nyrank forskel, heterozygoti from (

Select s.CKRDYRNR, NTMKO, s.STBNR, NAVN, SUM, RANK() OVER (PARTITION BY s.ckrdyrnr ORDER BY sum DESC ) rank, NTM, heterozygoti, mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti)

 nyntm, SÆDBEHKODE||KATEGORI||FORTEGN||PRIORITEREDE||NTM+(mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti))||KSS||YINDEKS||s.stbnr nysum

, RANK() OVER ( PARTITION BY s.ckrdyrnr ORDER BY SÆDBEHKODE||KATEGORI||FORTEGN||PRIORITEREDE||NTM+mirmod.hz2prod_ntm_addition(substr(dam_idnor,1,3),substr(sire_idnor,1,3),z.heterozygoti)||KSS||YINDEKS||s.stbnr DESC ) nyrank from h6601.v_ipdok_sum s

join h6601.dyr d on d.ckrdyrnr = s.ckrdyrnr

join h6601.heterozygoti z on z.DAM_DYR_ID = d.id

join h6601.tyr t on t.dyr_id = z.sire_dyr_id and s.stbnr = t.stbnr

where ipde_id = 31051 order by ckrdyrnr);
```

Identifikation af kombination af hundyr/tyr til beregning af heterozygoti grad:

```sql
select *
  from (select distinct d.id dam_dyr_id, h6601.func_idnor(d.id) dam_idnor
          from h6601.dyr d
          join h6601.genomiskselektiontest g on d.id = g.dyr_id
          where d.bes_id is not null
            and d.konk_id in (122,124)) dam
  join (select distinct tyr.dyr_id sire_dyr_id, func_idnor(tyr.dyr_id) sire_idnor
          from h6601.tyr tyr
          join h6601.produkttyr prodtyr on (prodtyr.tyr_id = tyr.id)
          join h6601.relprodtyrtyrkat rpttk on (rpttk.prodtyr_id = prodtyr.id)
          where tyr.race_id in (1201, 1202, 1203, 1204, 1205)
            and (rpttk.kviepct > 0 or rpttk.koerpct > 0)) sire on (1=1)
  where not exists (select 1
                      from navsnpdb.hz_compute_queue h
                      where h.dam_idnor = dam.dam_idnor
                        and h.sire_dyr_id = sire.sire_dyr_id)
    and not exists (select 1
                      from h6601.heterozygoti h
                      where h.dam_idnor = dam.dam_idnor
                        and h.sire_idnor = sire.sire_idnor)
    and rownum <= cantal;
```

Opdatere beregnet heterozygoti grad i tabel til videre brug i insemineringsplan.

```sql
merge into h6601.heterozygoti d
  using (select * from navsnpdb.hz_compute_result) s  on (d.dam_idnor =
s.dam_idnor and
                                                          d.sire_idnor =
s.sire_idnor)
  when matched then
  update
    set heterozygoti = s.heterozygoti
  when not matched then
  insert
    (dam_idnor,
     sire_idnor,
     dam_dyr_id,
     sire_dyr_id,
     heterozygoti)
  values
    (s.dam_idnor,
     s.sire_idnor,
     s.dam_dyr_id,
     s.sire_dyr_id,
     s.heterozygoti);
```

Tast af heterozygoti grad i sum beregning i Insemineringsplan.

```
function fntm_addition (piphundyrid in number, piptyrid in number) return
number is

    cursor cHeterozygoti is
        select hz.heterozygoti, hundyr.ckrdyrnr, sire_breed.raceforkor-
telse_international, dam_breed.raceforkortelse_international, ipt.stbnr,
ipt.k10navn1
            from h6601.iptyre ipt
            join h6601.iphundyr iph on (1=1)
            join h6601.heterozygoti hz on (hz.dam_dyr_id = iph.dyr_id and
hz.sire_dyr_id = ipt.dyr_id)
            join h6601.dyr hundyr on (hundyr.id = iph.dyr_id)
            join h6601.racer sire_breed on (sire_breed.id = ipt.race_id)
            join h6601.racer dam_breed on (dam_breed.id = iph.race_id)
        where ipt.id = piptyrid
            and iph.id = piphundyrid;


    wheterozygoti          number;
    wckrdyrnr              number;
    wstbnr                 number;
    wnavn                  varchar2(10);
    wheterozygoti_vaerdi   number;
    wsire_breed            varchar2(3);
    wdam_breed             varchar2(3);
  begin
    apptrace.proc_entry('fntm_addition');
    apptrace.proc_parm('iphundyrid', piphundyrid);
    apptrace.proc_parm('iptyrid', piptyrid);


    open cHeterozygoti;
    fetch cHeterozygoti into wheterozygoti, wckrdyrnr, wsire_breed,
wdam_breed, wstbnr, wnavn;
    close cHeterozygoti;


    if wheterozygoti is not null then
        wheterozygoti_vaerdi := h6601.hz2prod_ntm_addition (sire_breed =>
wsire_breed, dam_breed => wdam_breed, hz => wheterozygoti);
    end if;


    if wheterozygoti_vaerdi is not null then
        dbms_output.put_line('Hundyr '||wckrdyrnr||', tyr
'||wstbnr||'/'||wnavn||' - heterozygoti_vaerdi: '||wheterozygoti_vaerdi);
```
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```
    end if;
    apptrace.proc_parm('wheterozygoti_vaerdi', wckrdyrnr||' # '||wheterozy-
goti_vaerdi);
    return nvl(wheterozygoti_vaerdi,0);

  end;
```

```
if nvl(pheterozygotiflag,0) = 1 then
        wntmindeks := wntmindeks + round(fntm_addition (piphundyrid =>
piphundyrid, piptyrid => piptyrid)); --  omregningsfaktor
      end if;
```

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