

**nf-core/** 

**bytesize**

**#31**

Troubleshooting a failed pipeline

Phil Ewels, SciLifeLab Sweden

Because at some point, things will go wrong..



1

Start small

2

Categorise the type of error

3

Read the log, check the work directory

4

Check Slack, Google, ask for help

5

Report a bug

1

Start small

2

```
nextflow run nf-core/xxx -profile test,docker
```

3

4

5





1

Start small

Check the basics

2

✓ Nextflow up to date ( `nextflow -self-update` )

✓ Haven't run out of disk space

3

✓ Docker demon is running (*if you're using Docker*)

4

✓ ...

5



1

Start small

Check the basics

2

Check the troubleshooting docs:

<https://nf-co.re/usage/troubleshooting>

3

4

5



1

2

Categorise the type of error

3

4

5



1

2

 *Warning:*

3

*Note that just because Nextflow reports a particular tool failed, this does not necessarily mean it's an issue with the tool itself.*

4

5





Categorise the type of error

1

Before the first process

2

First process

3

During run

4

5

Problem with outputs

## Categorise the type of error

1

2

Before the first process

3

```
N E X T F L O W ~ version 0.27.3
Launching `./main.nf` [prickly_snyder] - revision: bb0fa33a13
ERROR ~ Unknown config attribute: projectDir -- check config file:
nextflow.config
```

```
null
```

4

```
-- Check '.nextflow.log' file for details
```

5

**✗** Nextflow not up to date

1

```
* The pipeline
https://doi.org/10.5281/zenodo.1400710

* The nf-core framework
https://doi.org/10.1038/s41587-020-0439-x

* Software dependencies
https://github.com/nf-core/rnaseq/blob/master/CITATIONS.md
```

2

```
-----
WARN: =====
Both '--gtf' and '--gff' parameters have been provided.
Using GTF file as priority.
=====
```

3

```
WARN: =====
When using '--additional_fasta <FASTA_FILE>' the aligner index will not
be re-built with the transgenes incorporated by default since you have
already provided an index via '--star_index <INDEX>'.
=====
```

4

```
Set '--additional_fasta <FASTA_FILE> --star_index false --save_reference' to
re-build the index with transgenes included and the index will be saved in
'results/genome/index/star/' for re-use with '--star_index'.

Ignore this warning if you know that the index already contains transgenes.

Please see:
https://github.com/nf-core/rnaseq/issues/556
```

5

```
-----
Module compilation error
- file : /Users/phil/GitHub/nf-core/rnaseq/./workflows/./modules/local/bedtools_genomecov.nf
- cause: end of line reached within a simple string 'x' or "x" or /x/;
  solution: for multi-line literals, use triple quotes '''x''' or ""x"" or /x/ or $/x/$ @ line 6, column 108.
ularity_pull_docker_container ?
      ^
```

1 error

✗ Nextflow not up to date

1

```
NEXTFLOW ~ version 20.07.0
Launching `./main.nf` [furious_hamilton] - revision: bb0fa33a13
```

```

graph TD
  A(( )) --> B(( ))
  A --> C(( ))
  B --> D(( ))
  C --> D
  D --> E(( ))
  E --> F(( ))
  F --> G(( ))
  F --> H(( ))
  G --> I(( ))
  H --> I
  I --> J(( ))
  J --> K(( ))
  K --> L(( ))
  K --> M(( ))
  L --> N(( ))
  M --> N
  N --> O(( ))
  O --> P(( ))
  O --> Q(( ))
  P --> R(( ))
  Q --> R
  R --> S(( ))
  S --> T(( ))
  S --> U(( ))
  T --> V(( ))
  U --> V
  V --> W(( ))
  W --> X(( ))
  W --> Y(( ))
  X --> Z(( ))
  Y --> Z
  Z --> AA(( ))
  AA --> AB(( ))
  AA --> AC(( ))
  AB --> AD(( ))
  AC --> AD
  AD --> AE(( ))
  AE --> AF(( ))
  AE --> AG(( ))
  AF --> AH(( ))
  AG --> AH
  AH --> AI(( ))
  AI --> AJ(( ))
  AI --> AK(( ))
  AJ --> AL(( ))
  AK --> AL
  AL --> AM(( ))
  AM --> AN(( ))
  AM --> AO(( ))
  AN --> AP(( ))
  AO --> AP
  AP --> AQ(( ))
  AQ --> AR(( ))
  AQ --> AS(( ))
  AR --> AT(( ))
  AS --> AT
  AT --> AU(( ))
  AU --> AV(( ))
  AU --> AW(( ))
  AV --> AX(( ))
  AW --> AX
  AX --> AY(( ))
  AY --> AZ(( ))
  AY --> BA(( ))
  AZ --> BB(( ))
  BA --> BB
  BA --> BC(( ))
  BB --> BD(( ))
  BC --> BD
  BD --> BE(( ))
  BE --> BF(( ))
  BE --> BG(( ))
  BF --> BH(( ))
  BG --> BH
  BH --> BI(( ))
  BI --> BJ(( ))
  BI --> BK(( ))
  BJ --> BL(( ))
  BK --> BL
  BL --> BM(( ))
  BM --> BN(( ))
  BM --> BO(( ))
  BN --> BP(( ))
  BO --> BP
  BP --> BQ(( ))
  BQ --> BR(( ))
  BQ --> BS(( ))
  BR --> BT(( ))
  BS --> BT
  BT --> BU(( ))
  BU --> BV(( ))
  BU --> BW(( ))
  BV --> BX(( ))
  BW --> BX
  BX --> BY(( ))
  BY --> BZ(( ))
  BY --> CA(( ))
  BZ --> CB(( ))
  CA --> CB
  CA --> CC(( ))
  CB --> CD(( ))
  CC --> CD
  CD --> CE(( ))
  CE --> CF(( ))
  CE --> CG(( ))
  CF --> CH(( ))
  CG --> CH
  CH --> CI(( ))
  CI --> CJ(( ))
  CI --> CK(( ))
  CJ --> CL(( ))
  CK --> CL
  CL --> CM(( ))
  CM --> CN(( ))
  CM --> CO(( ))
  CN --> CP(( ))
  CO --> CP
  CP --> CQ(( ))
  CQ --> CR(( ))
  CQ --> CS(( ))
  CR --> CT(( ))
  CS --> CT
  CT --> CU(( ))
  CU --> CV(( ))
  CU --> CW(( ))
  CV --> CX(( ))
  CW --> CX
  CX --> CY(( ))
  CY --> CZ(( ))
  CY --> DA(( ))
  CZ --> DB(( ))
  DA --> DB
  DA --> DC(( ))
  DB --> DD(( ))
  DC --> DD
  DD --> DE(( ))
  DE --> DF(( ))
  DE --> DG(( ))
  DF --> DH(( ))
  DG --> DH
  DH --> DI(( ))
  DI --> DJ(( ))
  DI --> DK(( ))
  DJ --> DL(( ))
  DK --> DL
  DL --> DM(( ))
  DM --> DN(( ))
  DM --> DO(( ))
  DN --> DP(( ))
  DO --> DP
  DP --> DQ(( ))
  DQ --> DR(( ))
  DQ --> DS(( ))
  DR --> DT(( ))
  DS --> DT
  DT --> DU(( ))
  DU --> DV(( ))
  DU --> DW(( ))
  DV --> DX(( ))
  DW --> DX
  DX --> DY(( ))
  DY --> DZ(( ))
  DY --> EA(( ))
  DZ --> EB(( ))
  EA --> EB
  EA --> EC(( ))
  EB --> ED(( ))
  EC --> ED
  ED --> EE(( ))
  EE --> EF(( ))
  EE --> EG(( ))
  EF --> EH(( ))
  EG --> EH
  EH --> EI(( ))
  EI --> EJ(( ))
  EI --> EK(( ))
  EJ --> EL(( ))
  EK --> EL
  EL --> EM(( ))
  EM --> EN(( ))
  EM --> EO(( ))
  EN --> EP(( ))
  EO --> EP
  EP --> EQ(( ))
  EQ --> ER(( ))
  EQ --> ES(( ))
  ER --> ET(( ))
  ES --> ET
  ET --> EU(( ))
  EU --> EV(( ))
  EU --> EW(( ))
  EV --> EX(( ))
  EW --> EX
  EX --> EY(( ))
  EY --> EZ(( ))
  EY --> FA(( ))
  EZ --> FB(( ))
  FA --> FB
  FA --> FC(( ))
  FB --> FD(( ))
  FC --> FD
  FD --> FE(( ))
  FE --> FF(( ))
  FE --> FG(( ))
  FF --> FH(( ))
  FG --> FH
  FH --> FI(( ))
  FI --> FJ(( ))
  FI --> FK(( ))
  FJ --> FL(( ))
  FK --> FL
  FL --> FM(( ))
  FM --> FN(( ))
  FM --> FO(( ))
  FN --> FP(( ))
  FO --> FP
  FP --> FQ(( ))
  FQ --> FR(( ))
  FQ --> FS(( ))
  FR --> FT(( ))
  FS --> FT
  FT --> FU(( ))
  FU --> FV(( ))
  FU --> FW(( ))
  FV --> FX(( ))
  FW --> FX
  FX --> FY(( ))
  FY --> FZ(( ))
  FY --> GA(( ))
  FZ --> GB(( ))
  GA --> GB
  GA --> GC(( ))
  GB --> GD(( ))
  GC --> GD
  GD --> GE(( ))
  GE --> GF(( ))
  GE --> GG(( ))
  GF --> GH(( ))
  GG --> GH
  GH --> GI(( ))
  GI --> GJ(( ))
  GI --> GK(( ))
  GJ --> GL(( ))
  GK --> GL
  GL --> GM(( ))
  GM --> GN(( ))
  GM --> GO(( ))
  GN --> GP(( ))
  GO --> GP
  GP --> GQ(( ))
  GQ --> GR(( ))
  GQ --> GS(( ))
  GR --> GT(( ))
  GS --> GT
  GT --> GU(( ))
  GU --> GV(( ))
  GU --> GW(( ))
  GV --> GX(( ))
  GW --> GX
  GX --> GY(( ))
  GY --> GZ(( ))
  GY --> HA(( ))
  GZ --> HB(( ))
  HA --> HB
  HA --> HC(( ))
  HB --> HD(( ))
  HC --> HD
  HD --> HE(( ))
  HE --> HF(( ))
  HE --> HG(( ))
  HF --> HH(( ))
  HG --> HH
  HH --> HI(( ))
  HI --> HJ(( ))
  HI --> HK(( ))
  HJ --> HL(( ))
  HK --> HL
  HL --> HM(( ))
  HM --> HN(( ))
  HM --> HO(( ))
  HN --> HP(( ))
  HO --> HP
  HP --> HQ(( ))
  HQ --> HR(( ))
  HQ --> HS(( ))
  HR --> HT(( ))
  HS --> HT
  HT --> HU(( ))
  HU --> HV(( ))
  HU --> HW(( ))
  HV --> HX(( ))
  HW --> HX
  HX --> HY(( ))
  HY --> HZ(( ))
  HY --> IA(( ))
  HZ --> IB(( ))
  IA --> IB
  IA --> IC(( ))
  IB --> ID(( ))
  IC --> ID
  ID --> IE(( ))
  IE --> IF(( ))
  IE --> IG(( ))
  IF --> IH(( ))
  IG --> IH
  IH --> II(( ))
  II --> IJ(( ))
  II --> IK(( ))
  IJ --> IL(( ))
  IK --> IL
  IL --> IM(( ))
  IM --> IN(( ))
  IM --> IO(( ))
  IN --> IP(( ))
  IO --> IP
  IP --> IQ(( ))
  IQ --> IR(( ))
  IQ --> IS(( ))
  IR --> IT(( ))
  IS --> IT
  IT --> IU(( ))
  IU --> IV(( ))
  IU --> IW(( ))
  IV --> IX(( ))
  IW --> IX
  IX --> IY(( ))
  IY --> IZ(( ))
  IY --> JA(( ))
  IZ --> JB(( ))
  JA --> JB
  JA --> JC(( ))
  JB --> JD(( ))
  JC --> JD
  JD --> JE(( ))
  JE --> JF(( ))
  JE --> JG(( ))
  JF --> JH(( ))
  JG --> JH
  JH --> JI(( ))
  JI --> JJ(( ))
  JI --> JK(( ))
  JJ --> JL(( ))
  JK --> JL
  JL --> JM(( ))
  JM --> JN(( ))
  JM --> JO(( ))
  JN --> JP(( ))
  JO --> JP
  JP --> JQ(( ))
  JQ --> JR(( ))
  JQ --> JS(( ))
  JR --> JT(( ))
  JS --> JT
  JT --> JU(( ))
  JU --> JV(( ))
  JU --> JW(( ))
  JV --> JX(( ))
  JW --> JX
  JX --> JY(( ))
  JY --> JZ(( ))
  JY --> KA(( ))
  JZ --> KB(( ))
  KA --> KB
  KA --> KC(( ))
  KB --> KD(( ))
  KC --> KD
  KD --> KE(( ))
  KE --> KF(( ))
  KE --> KG(( ))
  KF --> KH(( ))
  KG --> KH
  KH --> KI(( ))
  KI --> KJ(( ))
  KI --> KK(( ))
  KJ --> KL(( ))
  KK --> KL
  KL --> KM(( ))
  KM --> KN(( ))
  KM --> KO(( ))
  KN --> KP(( ))
  KO --> KP
  KP --> KQ(( ))
  KQ --> KR(( ))
  KQ --> KS(( ))
  KR --> KT(( ))
  KS --> KT
  KT --> KU(( ))
  KU --> KV(( ))
  KU --> KW(( ))
  KV --> KX(( ))
  KW --> KX
  KX --> KY(( ))
  KY --> KZ(( ))
  KY --> LA(( ))
  KZ --> LB(( ))
  LA --> LB
  LA --> LC(( ))
  LB --> LD(( ))
  LC --> LD
  LD --> LE(( ))
  LE --> LF(( ))
  LE --> LG(( ))
  LF --> LH(( ))
  LG --> LH
  LH --> LI(( ))
  LI --> LJ(( ))
  LI --> LK(( ))
  LJ --> LL(( ))
  LK --> LL
  LL --> LM(( ))
  LM --> LN(( ))
  LM --> LO(( ))
  LN --> LP(( ))
  LO --> LP
  LP --> LQ(( ))
  LQ --> LR(( ))
  LQ --> LS(( ))
  LR --> LT(( ))
  LS --> LT
  LT --> LU(( ))
  LU --> LV(( ))
  LU --> LW(( ))
  LV --> LX(( ))
  LW --> LX
  LX --> LY(( ))
  LY --> LZ(( ))
  LY --> MA(( ))
  LZ --> MB(( ))
  MA --> MB
  MA --> MC(( ))
  MB --> MD(( ))
  MC --> MD
  MD --> ME(( ))
  ME --> MF(( ))
  ME --> MG(( ))
  MF --> MH(( ))
  MG --> MH
  MH --> MI(( ))
  MI --> MJ(( ))
  MI --> MK(( ))
  MJ --> ML(( ))
  MK --> ML
  ML --> MM(( ))
  MM --> MN(( ))
  MM --> MO(( ))
  MN --> MP(( ))
  MO --> MP
  MP --> MQ(( ))
  MQ --> MR(( ))
  MQ --> MS(( ))
  MR --> MT(( ))
  MS --> MT
  MT --> MU(( ))
  MU --> MV(( ))
  MU --> MW(( ))
  MV --> MX(( ))
  MW --> MX
  MX --> MY(( ))
  MY --> MZ(( ))
  MY --> NA(( ))
  MZ --> NB(( ))
  NA --> NB
  NA --> NC(( ))
  NB --> ND(( ))
  NC --> ND
  ND --> NE(( ))
  NE --> NF(( ))
  NE --> NG(( ))
  NF --> NH(( ))
  NG --> NH
  NH --> NI(( ))
  NI --> NJ(( ))
  NI --> NK(( ))
  NJ --> NL(( ))
  NK --> NL
  NL --> NM(( ))
  NM --> NN(( ))
  NM --> NO(( ))
  NN --> NP(( ))
  NO --> NP
  NP --> NQ(( ))
  NQ --> NR(( ))
  NQ --> NS(( ))
  NR --> NT(( ))
  NS --> NT
  NT --> NU(( ))
  NU --> NV(( ))
  NU --> NW(( ))
  NV --> NX(( ))
  NW --> NX
  NX --> NY(( ))
  NY --> NZ(( ))
  NY --> OA(( ))
  NZ --> OB(( ))
  OA --> OB
  OA --> OC(( ))
  OB --> OD(( ))
  OC --> OD
  OD --> OE(( ))
  OE --> OF(( ))
  OE --> OG(( ))
  OF --> OH(( ))
  OG --> OH
  OH --> OI(( ))
  OI --> OJ(( ))
  OI --> OK(( ))
  OJ --> OL(( ))
  OK --> OL
  OL --> OM(( ))
  OM --> ON(( ))
  OM --> OO(( ))
  ON --> OP(( ))
  OO --> OP
  OP --> OQ(( ))
  OQ --> OR(( ))
  OQ --> OS(( ))
  OR --> OT(( ))
  OS --> OT
  OT --> OU(( ))
  OU --> OV(( ))
  OU --> OW(( ))
  OV --> OX(( ))
  OW --> OX
  OX --> OY(( ))
  OY --> OZ(( ))
  OY --> PA(( ))
  OZ --> PB(( ))
  PA --> PB
  PA --> PC(( ))
  PB --> PD(( ))
  PC --> PD
  PD --> PE(( ))
  PE --> PF(( ))
  PE --> PG(( ))
  PF --> PH(( ))
  PG --> PH
  PH --> PI(( ))
  PI --> PJ(( ))
  PI --> PK(( ))
  PJ --> PL(( ))
  PK --> PL
  PL --> PM(( ))
  PM --> PN(( ))
  PM --> PO(( ))
  PN --> PP(( ))
  PO --> PP
  PP --> PQ(( ))
  PQ --> PR(( ))
  PQ --> PS(( ))
  PR --> PT(( ))
  PS --> PT
  PT --> PU(( ))
  PU --> PV(( ))
  PU --> PW(( ))
  PV --> PX(( ))
  PW --> PX
  PX --> PY(( ))
  PY --> PZ(( ))
  PY --> QA(( ))
  PZ --> QB(( ))
  QA --> QB
  QA --> QC(( ))
  QB --> QD(( ))
  QC --> QD
  QD --> QE(( ))
  QE --> QF(( ))
  QE --> QG(( ))
  QF --> QH(( ))
  QG --> QH
  QH --> QI(( ))
  QI --> QJ(( ))
  QI --> QK(( ))
  QJ --> QL(( ))
  QK --> QL
  QL --> QM(( ))
  QM --> QN(( ))
  QM --> QO(( ))
  QN --> QP(( ))
  QO --> QP
  QP --> QQ(( ))
  QQ --> QR(( ))
  QQ --> QS(( ))
  QR --> QT(( ))
  QS --> QT
  QT --> QU(( ))
  QU --> QV(( ))
  QU --> QW(( ))
  QV --> QX(( ))
  QW --> QX
  QX --> QY(( ))
  QY --> QZ(( ))
  QY --> RA(( ))
  QZ --> RB(( ))
  RA --> RB
  RA --> RC(( ))
  RB --> RD(( ))
  RC --> RD
  RD --> RE(( ))
  RE --> RF(( ))
  RE --> RG(( ))
  RF --> RH(( ))
  RG --> RH
  RH --> RI(( ))
  RI --> RJ(( ))
  RI --> RK(( ))
  RJ --> RL(( ))
  RK --> RL
  RL --> RM(( ))
  RM --> RN(( ))
  RM --> RO(( ))
  RN --> RP(( ))
  RO --> RP
  RP --> RQ(( ))
  RQ --> RR(( ))
  RQ --> RS(( ))
  RR --> RT(( ))
  RS --> RT
  RT --> RU(( ))
  RU --> RV(( ))
  RU --> RW(( ))
  RV --> RX(( ))
  RW --> RX
  RX --> RY(( ))
  RY --> RZ(( ))
  RY --> SA(( ))
  RZ --> SB(( ))
  SA --> SB
  SA --> SC(( ))
  SB --> SD(( ))
  SC --> SD
  SD --> SE(( ))
  SE --> SF(( ))
  SE --> SG(( ))
  SF --> SH(( ))
  SG --> SH
  SH --> SI(( ))
  SI --> SJ(( ))
  SI --> SK(( ))
  SJ --> SL(( ))
  SK --> SL
  SL --> SM(( ))
  SM --> SN(( ))
  SM --> SO(( ))
  SN --> SP(( ))
  SO --> SP
  SP --> SQ(( ))
  SQ --> SR(( ))
  SQ --> SS(( ))
  SR --> ST(( ))
  SS --> ST
  ST --> SU(( ))
  SU --> SV(( ))
  SU --> SW(( ))
  SV --> SX(( ))
  SW --> SX
  SX --> SY(( ))
  SY --> SZ(( ))
  SY --> TA(( ))
  SZ --> TB(( ))
  TA --> TB
  TA --> TC(( ))
  TB --> TD(( ))
  TC --> TD
  TD --> TE(( ))
  TE --> TF(( ))
  TE --> TG(( ))
  TF --> TH(( ))
  TG --> TH
  TH --> TI(( ))
  TI --> TJ(( ))
  TI --> TK(( ))
  TJ --> TL(( ))
  TK --> TL
  TL --> TM(( ))
  TM --> TN(( ))
  TM --> TO(( ))
  TN --> TP(( ))
  TO --> TP
  TP --> TQ(( ))
  TQ --> TR(( ))
  TQ --> TS(( ))
  TR --> TT(( ))
  TS --> TT
  TT --> TU(( ))
  TU --> TV(( ))
  TU --> TW(( ))
  TV --> TX(( ))
  TW --> TX
  TX --> TY(( ))
  TY --> TZ(( ))
  TY --> UA(( ))
  TZ --> UB(( ))
  UA --> UB
  UA --> UC(( ))
  UB --> UD(( ))
  UC --> UD
  UD --> UE(( ))
  UE --> UF(( ))
  UE --> UG(( ))
  UF --> UH(( ))
  UG --> UH
  UH --> UI(( ))
  UI --> UJ(( ))
  UI --> UK(( ))
  UJ --> UL(( ))
  UK --> UL
  UL --> UM(( ))
  UM --> UN(( ))
  UM --> UO(( ))
  UN --> UP(( ))
  UO --> UP
  UP --> UQ(( ))
  UQ --> UR(( ))
  UQ --> US(( ))
  UR --> UT(( ))
  US --> UT
  UT --> UU(( ))
  UU --> UV(( ))
  UU --> UW(( ))
  UV --> UX(( ))
  UW --> UX
  UX --> UY(( ))
  UY --> UZ(( ))
  UY --> VA(( ))
  UZ --> VB(( ))
  VA --> VB
  VA --> VC(( ))
  VB --> VD(( ))
  VC --> VD
  VD --> VE(( ))
  VE --> VF(( ))
  VE --> VG(( ))
  VF --> VH(( ))
  VG --> VH
  VH --> VI(( ))
  VI --> VJ(( ))
  VI --> VK(( ))
  VJ --> VL(( ))
  VK --> VL
  VL --> VM(( ))
  VM --> VN(( ))
  VM --> VO(( ))
  VN --> VP(( ))
  VO --> VP
  VP --> VQ(( ))
  VQ --> VR(( ))
  VQ --> VS(( ))
  VR --> VT(( ))
  VS --> VT
  VT --> VU(( ))
  VU --> VV(( ))
  VU --> VW(( ))
  VV --> VX(( ))
  VW --> VX
  VX --> VY(( ))
  VY --> VZ(( ))
  VY --> WA(( ))
  VZ --> WB(( ))
  WA --> WB
  WA --> WC(( ))
  WB --> WD(( ))
  WC --> WD
  WD --> WE(( ))
  WE --> WF(( ))
  WE --> WG(( ))
  WF --> WH(( ))
  WG --> WH
  WH --> WI(( ))
  WI --> WJ(( ))
  WI --> WK(( ))
  WJ --> WL(( ))
  WK --> WL
  WL --> WM(( ))
  WM --> WN(( ))
  WM --> WO(( ))
  WN --> WP(( ))
  WO --> WP
  WP --> WQ(( ))
  WQ --> WR(( ))
  WQ --> WS(( ))
  WR --> WT(( ))
  WS --> WT
  WT --> WU(( ))
  WU --> WV(( ))
  WU --> WW(( ))
  WV --> WX(( ))
  WW --> WX
  WX --> WY(( ))
  WY --> WZ(( ))
  WY --> XA(( ))
  WZ --> XB(( ))
  XA --> XB
  XA --> XC(( ))
  XB --> XD(( ))
  XC --> XD
  XD --> XE(( ))
  XE --> XF(( ))
  XE --> XG(( ))
  XF --> XH(( ))
  XG --> XH
  XH --> XI(( ))
  XI --> XJ(( ))
  XI --> XK(( ))
  XJ --> XL(( ))
  XK --> XL
  XL --> XM(( ))
  XM --> XN(( ))
  XM --> XO(( ))
  XN --> XP(( ))
  XO --> XP
  XP --> XQ(( ))
  XQ --> XR(( ))
  XQ --> XS(( ))
  XR --> XT(( ))
  XS --> XT
  XT --> XU(( ))
  XU --> XV(( ))
  XU --> XW(( ))
  XV --> XX(( ))
  XW --> XX
  XX --> XY(( ))
  XY --> XZ(( ))
  XY --> YA(( ))
  XZ --> YB(( ))
  YA --> YB
  YA --> YC(( ))
  YB --> YD(( ))
  YC --> YD
  YD --> YE(( ))
  YE --> YF(( ))
  YE --> YG(( ))
  YF --> YH(( ))
  YG --> YH
  YH --> YI(( ))
  YI --> YJ(( ))
  YI --> YK(( ))
  YJ --> YL(( ))
  YK --> YL
  YL --> YM(( ))
  YM --> YN(( ))
  YM --> YO(( ))
  YN --> YP(( ))
  YO --> YP
  YP --> YQ(( ))
  YQ --> YR(( ))
  YQ --> YS(( ))
  YR --> YT(( ))
  YS --> YT
  YT --> YU(( ))
  YU --> YV(( ))
  YU --> YW(( ))
  YV --> YX(( ))
  YW --> YX
  YX --> YY(( ))
  YY --> YZ(( ))
  YY --> ZA(( ))
  YZ --> ZB(( ))
  ZA --> ZB
  ZA --> ZC(( ))
  ZB --> ZD(( ))
  ZC --> ZD
  ZD --> ZE(( ))
  ZE --> ZF(( ))
  ZE --> ZG(( ))
  ZF --> ZH(( ))
  ZG --> ZH
  ZH --> ZI(( ))
  ZI --> ZJ(( ))
  ZI --> ZK(( ))
  ZJ --> ZL(( ))
  ZK --> ZL
  ZL --> ZM(( ))
  ZM --> ZN(( ))
  ZM --> ZO(( ))
  ZN --> ZP(( ))
  ZO --> ZP
  ZP --> ZQ(( ))
  ZQ --> ZR(( ))
  ZQ --> ZS(( ))
  ZR --> ZT(( ))
  ZS --> ZT
  ZT --> ZU(( ))
  ZU --> ZV(( ))
  ZU --> ZW(( ))
  ZV --> ZX(( ))
  ZW --> ZX
  ZX --> ZY(( ))
  ZY --> ZZ(( ))
  ZY --> [ ]
```

nf-core/rnaseq v3.6dev

2

**Core Nextflow options**

runName	: furious_hamilton
containerEngine	: docker
launchDir	: /Users/phil/GitHub/nf-core/rnaseq
workDir	: /Users/phil/GitHub/nf-core/rnaseq/work
projectDir	: /Users/phil/GitHub/nf-core/rnaseq
userName	: phil
profile	: test,docker
configFiles	: /Users/phil/GitHub/nf-core/rnaseq/nextflow.config

3

**Input/output options**

input	: https://raw.githubusercontent.com/nf-core/test-datasets/rnaseq/samplesheet/v3.4/samplesheet_test.csv
-------	--

4

**UMI options**

umitools_bc_pattern	: NNNN
---------------------	--------

5

**Read filtering options**

bbsplit_fasta_list	: https://github.com/nf-core/test-datasets/raw/rnaseq/reference/bbsplit_fasta_list.txt
skip_bbsplit	: false

**Reference genome options**

fasta	: https://github.com/nf-core/test-datasets/raw/rnaseq/reference/genome.fa
gtf	: https://github.com/nf-core/test-datasets/raw/rnaseq/reference/genes.gtf.gz
gff	: https://github.com/nf-core/test-datasets/raw/rnaseq/reference/genes.gff.gz
transcript_fasta	: https://github.com/nf-core/test-datasets/raw/rnaseq/reference/transcriptome.fasta



## Categorise the type of error

1

First process

2

Remember that you need to tell Nextflow how to handle software dependencies..

3

```
-profile test,docker
```

4

No spaces between profile names

5

# Categorise the type of error

1

## First process

2

Command exit status:  
127

Command output:  
(empty)

3

Command error:  
.command.sh: line 3: rsem-prepare-reference: command not found

Work dir:  
/home/lfaller/nextflow/rnaseq/work/f7/b6ef5a3f12f5efbf641f19046aca74

4

Tip: you can try to figure out what's wrong by changing to the process work dir and showing the script file named ``.command.sh``

Unexpected error [AbortedException]

-- Check script `'/home/lfaller/.nextflow/assets/nf-core/rnaseq/./workflows/rnaseq.nf'` at line: 603 or see `'./nextflow.log'` file for more details

5

# Categorise the type of error

1

## First process

2

Command exit status:  
127

Command output:  
(empty)

3

Command error:  
.command.sh: line 3: rsem-prepare-reference: **command not found**

Work dir:  
/home/lfaller/nextflow/rnaseq/work/f7/b6ef5a3f12f5efbf641f19046aca74

4

Tip: you can try to figure out what's wrong by changing to the process work dir and showing the script file named ``.command.sh``

5

Unexpected error [AbortedException]

-- Check script '/home/lfaller/.nextflow/assets/nf-core/rnaseq/./workflows/rnaseq.nf' at line: 603 or see ``.nextflow.log`` file for more details

# Categorise the type of error

1

## First process

2

Error executing process > 'NFCORE\_SSDS:SSDS:BEDTOOLS\_MAKEWINDOWS (mm10rn6)'

Caused by:

Failed to submit process to grid scheduler for execution

Command executed:

```
sbatch .command.run
```

Command exit status:

```
1
```

Command output:

```
sbatch: error: Invalid --signal specification
```

Work dir:

```
/gpfs/gsfs9/users/RDC0pipes/010101_Fulgent_1010_SE7599/010101_1010_newVersionSS_ssds/ssds__20211215_155733_rn077168/work/84/3deb9b6cf726a27c167bb775028b09
```

Tip: view the complete command output by changing to the process work dir and entering the command  
`cat .command.out`

3

4

5





1

2

3

Read the log, check the work directory

4

5

1

[6:16 PM] Error executing process > 'FASTQC (hct116\_h3k4me1\_IP\_R1\_T1)'

Caused by:

Missing output file(s) `\*.{zip,html}` expected by process `FASTQC (hct116\_h3k4me1\_IP\_R1\_T1)`

Command executed:

2

```
[ ! -f hct116_h3k4me1_IP_R1_T1.fastq.gz ] && ln -s hct116_h3k4me1_clean.fastq.gz
hct116_h3k4me1_IP_R1_T1.fastq.gz
fastqc -q -t 6 hct116_h3k4me1_IP_R1_T1.fastq.gz
```

Command exit status:

0

3

Command output:  
(empty)

Command error:

WARNING: Your kernel does not support swap limit capabilities or the cgroup is not mounted.  
Memory limited without swap.

4

Failed to process file hct116\_h3k4me1\_IP\_R1\_T1.fastq.gz  
uk.ac.babraham.FastQC.Sequence.SequenceFormatException: Ran out of data in the middle of a  
fastq entry. Your file is probably truncated

at uk.ac.babraham.FastQC.Sequence.FastQFile.readNext(FastQFile.java:179)

at uk.ac.babraham.FastQC.Sequence.FastQFile.next(FastQFile.java:125)

at uk.ac.babraham.FastQC.Analysis.AnalysisRunner.run(AnalysisRunner.java:77)

at java.base/java.lang.Thread.run(Thread.java:834)

5

1

## Where in the pipeline and what type of error

2

```
[6:16 PM] Error executing process > 'FASTQC (hct116_h3k4me1_IP_R1_T1)'  
Caused by:  
  Missing output file(s) `*.{zip,html}` expected by process `FASTQC (hct116_h3k4me1_IP_R1_T1)`  
Command executed:  
  
  [ ! -f hct116_h3k4me1_IP_R1_T1.fastq.gz ] && ln -s hct116_h3k4me1_clean.fastq.gz  
  hct116_h3k4me1_IP_R1_T1.fastq.gz  
  fastqc -q -t 6 hct116_h3k4me1_IP_R1_T1.fastq.gz  
Command exit status:  
  0
```

3

Command output:  
(empty)

4

Command error:  
WARNING: Your kernel does not support swap limit capabilities or the cgroup is not mounted.  
Memory limited without swap.  
Failed to process file hct116\_h3k4me1\_IP\_R1\_T1.fastq.gz  
uk.ac.babraham.FastQC.Sequence.SequenceFormatException: Ran out of data in the middle of a  
fastq entry. Your file is probably truncated  
at uk.ac.babraham.FastQC.Sequence.FastQFile.readNext(FastQFile.java:179)  
at uk.ac.babraham.FastQC.Sequence.FastQFile.next(FastQFile.java:125)  
at uk.ac.babraham.FastQC.Analysis.AnalysisRunner.run(AnalysisRunner.java:77)  
at java.base/java.lang.Thread.run(Thread.java:834)

5

1

```
[6:16 PM] Error executing process > 'FASTQC (hct116_h3k4me1_IP_R1_T1)'
```

Caused by:

```
Missing output file(s) `*.{zip,html}` expected by process `FASTQC (hct116_h3k4me1_IP_R1_T1)`
```

Command executed:

```
[ ! -f hct116_h3k4me1_IP_R1_T1.fastq.gz ] && ln -s hct116_h3k4me1_clean.fastq.gz  
hct116_h3k4me1_IP_R1_T1.fastq.gz  
fastqc -q -t 6 hct116_h3k4me1_IP_R1_T1.fastq.gz
```

Command exit status:

```
0
```

2

3

Command output:  
(empty)

Command error:

```
WARNING: Your kernel does not support swap limit capabilities or the cgroup is not mounted.  
Memory limited without swap.
```

```
Failed to process file hct116_h3k4me1_IP_R1_T1.fastq.gz
```

```
uk.ac.babraham.FastQC.Sequence.SequenceFormatException: Ran out of data in the middle of a  
fastq entry. Your file is probably truncated
```

```
at uk.ac.babraham.FastQC.Sequence.FastQFile.readNext(FastQFile.java:179)
```

```
at uk.ac.babraham.FastQC.Sequence.FastQFile.next(FastQFile.java:125)
```

```
at uk.ac.babraham.FastQC.Analysis.AnalysisRunner.run(AnalysisRunner.java:77)
```

```
at java.base/java.lang.Thread.run(Thread.java:834)
```

4

5

## Log output from the tool



1

```
[6:16 PM] Error executing process > 'FASTQC (hct116_h3k4me1_IP_R1_T1)'
```

Caused by:

```
Missing output file(s) `*.{zip,html}` expected by process `FASTQC (hct116_h3k4me1_IP_R1_T1)`
```

Command executed:

```
[ ! -f hct116_h3k4me1_IP_R1_T1.fastq.gz ] && ln -s hct116_h3k4me1_clean.fastq.gz  
hct116_h3k4me1_IP_R1_T1.fastq.gz  
fastqc -q -t 6 hct116_h3k4me1_IP_R1_T1.fastq.gz
```

Command exit status:

```
0
```

2

3

Command output:  
(empty)

Command error:

```
WARNING: Your kernel does not support swap limit capabilities or the cgroup is not mounted.  
Memory limited without swap.
```

```
Failed to process file hct116_h3k4me1_IP_R1_T1.fastq.gz
```

```
uk.ac.babraham.FastQC.Sequence.SequenceFormatException: Ran out of data in the middle of a  
fastq entry. Your file is probably truncated
```

```
at uk.ac.babraham.FastQC.Sequence.FastQFile.readNext(FastQFile.java:179)
```

```
at uk.ac.babraham.FastQC.Sequence.FastQFile.next(FastQFile.java:125)
```

```
at uk.ac.babraham.FastQC.Analysis.AnalysisRunner.run(AnalysisRunner.java:77)
```

```
at java.base/java.lang.Thread.run(Thread.java:834)
```

4

5

## Log output from the tool

Error executing process > 'NFCORE\_RNASEQ:RNASEQ:ALIGN\_STAR:BAM\_SORT\_SAMTOOLS:SAMTOOLS\_SORT (bln1\_t16\_rep1)'

Caused by:

Process `NFCORE\_RNASEQ:RNASEQ:ALIGN\_STAR:BAM\_SORT\_SAMTOOLS:SAMTOOLS\_SORT (bln1\_t16\_rep1)` terminated with an error exit status (1)

Command executed:

```
samtools sort -@ 36 -o bln1_t16_rep1.sorted.bam -T bln1_t16_rep1.sorted
bln1_t16_rep1.Aligned.out.bam
cat <<-END_VERSIONS > versions.yml
SAMTOOLS_SORT:
  samtools: $(echo $(samtools --version 2>&1) | sed 's/^. *samtools //; s/Using.*$//')
END_VERSIONS
```

Command exit status:

1

Command output:  
(empty)

Command error:

```
[E::bgzf_read_block] Invalid BGZF header at offset 1083189972
[E::bgzf_read] Read block operation failed with error 6 after 131 of 197 bytes
samtools sort: truncated file. Aborting
```

Work dir:

/lustre/scratch123/tol/teams/tolit/users/ps22/work/eb/4d3c6811645c4730ea79d1bca11ff1

Tip: you can try to figure out what's wrong by changing to the process work dir and showing the script file named `.command.sh`

Process `NFCORE\_RNASEQ:RNASEQ:ALIGN\_STAR:BAM\_SORT\_SAMTOOLS:SAMTOOLS\_SORT (bln1\_t16\_rep1)`  
(bln1\_t16\_rep1) `  
Caused by:  
Process `NFCORE\_RNASEQ:RNASEQ:ALIGN\_STAR:BAM\_SORT\_SAMTOOLS:SAMTOOLS\_SORT (bln1\_t16\_rep1)`  
terminated with an error exit status (1)

1

Command executed:

```
samtools sort -@ 36 -o bln1_t16_rep1.sorted.bam -T bln1_t16_rep1.sorted
bln1_t16_rep1.Aligned.out.bam
cat <<-END_VERSIONS > versions.yml
SAMTOOLS_SORT:
  samtools: $(echo $(samtools --version 2>&1) | sed 's/^.*/samtools //; s/Using.*$//')
END_VERSIONS
```

2

Command exit status:  
1

3

Command output:  
(empty)

Command error:

```
[E::bgzf_read_block] Invalid BGZF header at offset 1083189972
[E::bgzf_read] Read block operation failed with error 6 after 131 of 197 bytes
samtools sort: truncated file. Aborting
```

4

Work dir:  
/lustre/scratch123/tol/teams/tolit/users/ps22/work/eb/4d3c6811645c4730ea79d1bca11ff1

Tip: you can try to figure out what's wrong by changing to the process work dir and showing the script file named `.command.sh`

5

## Where the work directory is on the disk

## Anatomy of a work directory..

1

- `command.out` - STDOUT from tool

2

- `command.err` - STDERR from tool

- `command.log` - STDOUT and STDERR from tool

3

- `command.begin` - Created as soon as the job launches

- `exitcode` - Created when the job ends, with exit code

- `command.trace` - Logs of compute resource usage

4

- `command.run` - Wrapper script used to run the job

5

- `command.sh` - Process command used for this task



1

2

3

4

Search Slack, Google, ask for help

5



1

2

3

4

5

nf-core ▾

- # coproid
- # cutandrun
- # demultiplex
- # denovo hybrid
- # diaproteomics
- # dualnaseq
- # eager
- # fetchngs
- # gwas
- # hic
- # hicar
- # kmermaid
- # liverctanalysis
- # mag
- # magmap
- # metaboigniter
- # metapep
- # metatdenovo
- # methylseq
- # mnaseq
- # nanoseq
- # nascent
- # pangenome
- # pgdb
- # proteomicslfq
- # quantms
- # raredisease
- # rnafusion
- # rnaseq
- # rnavar

Search: `samtools sort: truncated file. Aborting` Clear X

Search: `samtools sort: truncated file. Aborting` X

Not the results you expected? [Give feedback](#) or [learn more](#)

People ▾ Channels & DMs ▾ Date ▾ Reactions ▾ [More filters](#)

Sort: Newest message ▾ Show: 20 results per page ▾

# rnaseq - Dec 20th

**Priyanka Surana** 10:55  
Hello everyone. I need help with another error. I am running 3.4 version of rnaseq, its already ran ...

```
Error executing process > 'NFCORE_RNASEQ:RNASEQ:ALIGN_STAR:BAM_SORT_SAMTOOLS:SAMTOOLS_SORT (b1n1_t16_rep1)'
```

Caused by:  
Process `NFCORE\_RNASEQ:RNASEQ:ALIGN\_STAR ...`

```
... offset 1083189972
[E::bgzf_read] Read block operation failed with error 6 after 131 of 197 bytes
samtools ... Show more
```

7 replies

# rnaseq - Jan 25th, 2021

**Oliver Ziff** 17:46  
Hi all, Any ideas how to correct this error with `samtools sort`? Some online forums suggest it is a memory issue.

```
Error executing process > 'RNASEQ:ALIGN_STAR:BAM_SORT_SAMTOOLS: ... Show more
```

# sarek - Sep 15th, 2020

**Cem Sievers** 16:04  
Thank you both for the suggestions. I ran into some problems with bwa-mem2 using `--bwa=false`. In this case the index gets build and the alignment finishes but `samtools sort` returns an error as the `file` is corrupted (`[W::sam_read1] Parse error at line 27093655` ... Show more

# viralrecon - Apr 22nd, 2020

**Michael Heuer** 19:23

```
Error executing process > 'IVAR_TRIM (SAMPLE3_SE)'
```

...  
Command error:



Google

samtools sort: truncated file. Aborting



All

Images

Videos

Shopping

News

More

Tools

About 1 880 results (0,47 seconds)

<https://github.com> › [samtools](#) › [samtools](#) › [issues](#) ⋮

## Samtools sort: truncated file Aborting · Issue #824 - GitHub

20 Apr 2018 — [W::sam\_read1] Parse error at line 2 **samtools sort: truncated file. Aborting** I am getting above error while sorting the bam file.

<https://www.biostars.org> › ... ⋮

## samtools sort: truncated file. Aborting - Biostars

9 Apr 2019 · 1 answer

**Samtools** expect a bam file and you have provided a sam file (see usage below). Usage: **samtools sort** [options...] [in.bam]. So, first try converting sam to ...

Error when trying to use **samtools** to convert a sam files to a ... 11 Dec 2015

**Samtools** gives "truncated file" when trying to view a ... - Biostars 6 Sept 2017

**Truncated sam file** - Parse error - Biostars 25 Aug 2017

**Truncated File, When Converting Sam To Bam** - Biostars 14 Apr 2014

More results from [www.biostars.org](http://www.biostars.org)

1

2

3

4

5

1

## Ask for help

2

- Pick the correct Slack channel to post in
- Provide as much information as you can
  - As a minimum, the command and configs you used
  - Use a thread under your message if in doubt

3

- Use markdown code blocks

4

- Narrow the issue down as much as possible before asking
- Explain the steps to reproduce if possible

5

1

# Ask for help

2



**Phil Ewels** 1 day ago

markdownhelp



Custom response



**Slackbot** 1 day ago

Here are some tips about how to format code snippets nicely in Slack:

<https://slack.com/intl/en-se/help/articles/202288908-Format-your-messages>

<https://slack.com/intl/en-se/help/articles/204145658-Create-a-snippet>



**Slack Help Center**

**Format your messages**

Formatting helps add detail and clarity to your messages in Slack. You can use the formatting toolbar in the message field, or use markup and surround text with special characters.

Formatting to...



**Slack Help Center**



3

4

5

1

2

3

4

5

Report a bug

1

2

3


4

5

nf-core / rnaseq Public

Watch 83 Fork 394 Star 409

Code Issues 28 Pull requests 3 Discussions Actions Security

 **Bug report** [Get started](#)  
Report something that is broken or incorrect

**Feature request** [Get started](#)  
Suggest an idea for the nf-core/rnaseq pipeline

**Join nf-core** [Open](#)  
Please join the nf-core community here

**Slack #rnaseq channel** [Open](#)  
Discussion about the nf-core/rnaseq pipeline

Don't see your issue here? [Open a blank issue.](#) [Edit templates](#)



# Issue: Bug report

Report something that is broken or incorrect. If this doesn't look right, [choose a different type](#).



Title

Before you post this issue, please check the documentation:

- [nf-core website: troubleshooting](#)
- [nf-core/rnaseq pipeline documentation](#)

## Description of the bug \*

A clear and concise description of what the bug is.

## Command used and terminal output

Steps to reproduce the behaviour. Please paste the command you used to launch the pipeline and the output from your terminal.

```
$ nextflow run ...  
  
Some output where something broke
```

## Relevant files

Please drag and drop the relevant files here. Create a `.zip` archive if the extension is not allowed.

Your verbose log file `.nextflow.log` is often useful (*this is a hidden file in the directory where you launched the pipeline*) as well as custom Nextflow configuration files.

Assignees



No one—assign yourself

Labels



bug

Projects



None yet

Milestone



No milestone

Linked pull requests

Successfully merging a pull request may close this issue.

Helpful resources

[Contributing](#)

[Code of conduct](#)

[GitHub Community Guidelines](#)

Beta

You're using an **issue form**, a new type of issue template.

1

2

3

4

5



1

2

3

4

5

Report a bug

- Fill in the bug issue template
- Narrow the issue down as much as possible before asking
- Explain the steps to reproduce
- If you think you know the solution, please say so
- If you think you can fix the problem, please make a pull request



# nf-core



## Phil Ewels

<https://phil.ewels.co.uk>



<https://ngisweden.scilifelab.se>



<https://nf-co.re/join>