Testing `rmelting`

2019-01-16

Contents

Basic usage

```
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-159000.00000
Entropy..cal.	-430.00000
Enthalpy..J.	-664620.00000
Entropy..J.	-1797.40000
Melting.temperature..C.	73.35168

Approximate method

```
# Approximative mode - default (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGT
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	wetdna91
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05

Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	87.82455

```
# Approximative mode - wetdna91 (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "wetdna91")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am wetdna91"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGTA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	wetdna91
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	87.82455

```
# Approximative mode - ahs01 (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "ahs01")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am ahs01"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGT
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	ahs01
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	87.325

```
# Approximative mode - che93 (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "che93")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am che93"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGT
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	che93
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02

Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	77.575


```
# Approximative mode - che93corr (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "che93corr")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am che93corr
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGT
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0

dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	che93corr
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	79.0125

```r
# Approximative mode - schdot (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "schdot")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am schdot"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGT
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	schdot
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05

Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	89.4625

```
# Approximative mode - owe69 (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "owe69")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am owe69"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGTA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	owe69
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	100.96

```
# Approximative mode - san98 (DNA/DNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "san98")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnadna -P 2e-06 -E Na=1 -T 60 -am san98"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGATTACACGACAATCTACATAGGTCTCTATCGGCTCGTATTTGAAGTTGTGTGCTCTGCAACTAACCTAAATTGGT
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	san98
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	86.9

```
# Approximative mode - default (RNA/RNA)
out <- melting(sequence = "UUAAUCUCCGUCAUCUUUAAGCCGUGGAGAGACUGUAGACUUGAACAGGGGUAAGCGGAGGCACGUAGGAUUCACAUCAU",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S UUAAUCUCCGUCAUCUUUAAGCCGUGGAGAGACUGUAGACUUGAACAGGGGUAAGCGGAGGCACGUAGGAUUCACAUCAU -H dnadna -P 2e-06 -E Na=1 -T 60"
```

Sequence	UUAAUCUCCGUCAUCUUUAAGCCGUGGAGAGACUGUAGACUUGAACAGGGGUAAGCGGAGGCACGUAGGAUUCAC
Complementary.sequence	AATTAGAGGCAGTAGAAATTCGGCACCTCTCTGACATCTGAACTTGTCCCCATTCGCCTCCGTGCATCCTAAGTGTA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	wetdna91
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04

Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	90.89955


```
# Approximative mode - wetrna91 (RNA/RNA)
out <- melting(sequence = "UUAAUCUCCGUCAUCUUUAAGCCGUGGAGAGACUGUAGACUUGAACAGGGGUAAGCGGAGGCACGUAGGAUUCACAUCAU",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnadna", Na.conc = 1,
               method.approx = "wetrna91")
```

```
## [1] "-S UUAAUCUCCGUCAUCUUUAAGCCGUGGAGAGACUGUAGACUUGAACAGGGGUAAGCGGAGGCACGUAGGAUUCACAUCAU -H dnadna -P 2e-06 -E Na=1 -T 60 -am wetrna91"
```

Sequence	UUAAUCUCCGUCAUCUUUAAGCCGUGGAGAGACUGUAGACUUGAACAGGGGUAAGCGGAGGCACGUAGGAUUCAC
Complementary.sequence	AATTAGAGGCAGTAGAAATTCGGCACCTCTCTGACATCTGAACTTGTCCCCATTCGCCTCCGTGCATCCTAAGTGTA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0

DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	wetrna91
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	101.1745

```r
# Approximative mode - default (DNA/RNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnarna", Na.conc = 1)
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnarna -P 2e-06 -E Na=1 -T 60"
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGAUUACACGACAAUCUACAUAGGUCUCUAUCGGCUCGUAUUUGAAGUUGUGUGCUCUGCAACUAACCUAAAUUG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	wetdnarna91
Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA

Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	88.92455

```
# Approximative mode - wetdnarna91 (DNA/RNA)
out <- melting(sequence = "TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG",
               nucleic.acid.conc = 2e-06,
               hybridisation.type = "dnarna", Na.conc = 1,
               method.approx = "wetdnarna91")
```

```
## [1] "-S TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCATAG -H dnarna -P 2e-06 -E Na=1 -T 60 -am wetdnarna
```

Sequence	TCTAATGTGCTGTTAGATGTATCCAGAGATAGCCGAGCATAAACTTCAACACACGAGACGTTGATTGGATTTAACCA
Complementary.sequence	AGAUUACACGACAAUCUACAUAGGUCUCUAUCGGCUCGUAUUUGAAGUUGUGUGCUCUGCAACUAACCUAAAUUG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	wetdnarna91

Nearest.neighbour.model	NA
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	A

Enthalpy..cal.	NA
Entropy..cal.	NA
Enthalpy..J.	NA
Entropy..J.	NA
Melting.temperature..C.	88.92455

Nearest neighbour methods

Perfectly matching sequences

No Self-Complementarity

```
# Nearest neighbour method - default (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-159000.00000
Entropy..cal.	-430.00000
Enthalpy..J.	-664620.00000
Entropy..J.	-1797.40000

Melting.temperature..C.	73.35168

```
# Nearest neighbour method - bre86 (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "all97")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn all97"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-159000.00000
Entropy..cal.	-430.00000
Enthalpy..J.	-664620.00000
Entropy..J.	-1797.40000
Melting.temperature..C.	73.35168

```
# Nearest neighbour method - bre86 (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "bre86")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn bre86"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	bre86
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-140400.0000
Entropy..cal.	-365.1000
Enthalpy..J.	-586872.0000
Entropy..J.	-1526.1180
Melting.temperature..C.	83.2203

```
# Nearest neighbour method - san04 (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
```

```
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "san04")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn san04"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	san04
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-158700.00000
Entropy..cal.	-429.20000
Enthalpy..J.	-663366.00000
Entropy..J.	-1794.05600
Melting.temperature..C.	73.30191

```
# Nearest neighbour method - san96 (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "san96")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn san96"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	san96
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-147000.0000
Entropy..cal.	-392.5000
Enthalpy..J.	-614460.0000
Entropy..J.	-1640.6500
Melting.temperature..C.	75.7102

```
# Nearest neighbour method - sug96 (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "sug96")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn sug96"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug96
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-161600.00000
Entropy..cal.	-431.10000
Enthalpy..J.	-675488.00000
Entropy..J.	-1801.99800
Melting.temperature..C.	78.17556

```
# Nearest neighbour method - tan04 (DNA/DNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "tan04")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn tan04"
```

Sequence	CAGTGAGACAGCAATGGTCG

Complementary.sequence	GTCACTCTGTCGTTACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tan04
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-167400.00000
Entropy..cal.	-457.10000
Enthalpy..J.	-699732.00000
Entropy..J.	-1910.67800
Melting.temperature..C.	71.31413

```
# Nearest neighbour method - default (RNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGUGAGACAGCAAUGGUCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "rnarna", Na.conc = 1)
```

```
## [1] "-S CAGUGAGACAGCAAUGGUCG -H rnarna -P 2e-06 -E Na=1 -T 60"
```

Sequence	CAGUGAGACAGCAAUGGUCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06

Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-206660.00000
Entropy..cal.	-545.30000
Enthalpy..J.	-863838.80000
Entropy..J.	-2279.35400
Melting.temperature..C.	86.77685

```
# Nearest neighbour method - xia98 (RNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGUGAGACAGCAAUGGUCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "rnarna", Na.conc = 1, method.nn = "xia98")
```

```
## [1] "-S CAGUGAGACAGCAAUGGUCG -H rnarna -P 2e-06 -E Na=1 -T 60 -nn xia98"
```

Sequence	CAGUGAGACAGCAAUGGUCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	1

Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-206660.00000
Entropy..cal.	-545.30000
Enthalpy..J.	-863838.80000
Entropy..J.	-2279.35400
Melting.temperature..C.	86.77685

```
# Nearest neighbour method - fre86 (RNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGUGAGACAGCAAUGGUCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "rnarna", Na.conc = 1, method.nn = "fre86")
```

```
## [1] "-S CAGUGAGACAGCAAUGGUCG -H rnarna -P 2e-06 -E Na=1 -T 60 -nn fre86"
```

Sequence	CAGUGAGACAGCAAUGGUCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0

K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	fre86
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-192500.00000
Entropy..cal.	-510.40000
Enthalpy..J.	-804650.00000
Entropy..J.	-2133.47200
Melting.temperature..C.	83.81257

```
# Nearest neighbour method - default (mRNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGUGAGACAGCAAUGGUCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "mrnarna", Na.conc = 1)
```

```
## [1] "-S CAGUGAGACAGCAAUGGUCG -H mrnarna -P 2e-06 -E Na=1 -T 60"
```

Sequence	CAGUGAGACAGCAAUGGUCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0

DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-180120.00000
Entropy..cal.	-455.10032
Enthalpy..J.	-752901.60000
Entropy..J.	-1902.31936
Melting.temperature..C.	99.01986

```
# Nearest neighbour method - tur06 (mRNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGUGAGACAGCAAUGGUCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "mrnarna", Na.conc = 1, method.nn = "tur06")
```

```
## [1] "-S CAGUGAGACAGCAAUGGUCG -H mrnarna -P 2e-06 -E Na=1 -T 60 -nn tur06"
```

Sequence	CAGUGAGACAGCAAUGGUCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0

Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-180120.00000
Entropy..cal.	-455.10032
Enthalpy..J.	-752901.60000
Entropy..J.	-1902.31936
Melting.temperature..C.	99.01986

```
# Nearest neighbour method - default (DNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnarna", Na.conc = 1)
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnarna -P 2e-06 -E Na=1 -T 60"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE

Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug95
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-164000.00000
Entropy..cal.	-453.60000
Enthalpy..J.	-685520.00000
Entropy..J.	-1896.04800
Melting.temperature..C.	66.77049

```
# Nearest neighbour method - sug95 (DNA/RNA: No Self-Complimentarity)
out <- melting(sequence = "CAGTGAGACAGCAATGGTCG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnarna", Na.conc = 1, method.nn = "sug95")
```

```
## [1] "-S CAGTGAGACAGCAATGGTCG -H dnarna -P 2e-06 -E Na=1 -T 60 -nn sug95"
```

Sequence	CAGTGAGACAGCAATGGTCG
Complementary.sequence	GUCACUCUGUCGUUACCAGC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug95
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-164000.00000
Entropy..cal.	-453.60000
Enthalpy..J.	-685520.00000
Entropy..J.	-1896.04800
Melting.temperature..C.	66.77049

Self-Complementarity

```
# Nearest neighbour method - default (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-102800.00000
Entropy..cal.	-286.20000
Enthalpy..J.	-429704.00000
Entropy..J.	-1196.31600
Melting.temperature..C.	56.00644

```
# Nearest neighbour method - bre86 (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "all97")
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn all97"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97

GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-102800.00000
Entropy..cal.	-286.20000
Enthalpy..J.	-429704.00000
Entropy..J.	-1196.31600
Melting.temperature..C.	56.00644

```
# Nearest neighbour method - bre86 (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "bre86")
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn bre86"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	bre86
GU.model	NA
Single.mismatch.model	allsanpey

Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-102700.00000
Entropy..cal.	-279.00000
Enthalpy..J.	-429286.00000
Entropy..J.	-1166.22000
Melting.temperature..C.	63.44605

```
# Nearest neighbour method - san04 (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "san04")
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn san04"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	san04
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00

Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-102800.00000
Entropy..cal.	-284.50000
Enthalpy..J.	-429704.00000
Entropy..J.	-1189.21000
Melting.temperature..C.	57.80792

```
# Nearest neighbour method - san96 (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "san96")
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn san96"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	san96
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02

Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-92700.0000
Entropy..cal.	-256.3000
Enthalpy..J.	-387486.0000
Entropy..J.	-1071.3340
Melting.temperature..C.	55.0921

```
# Nearest neighbour method - sug96 (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "sug96")
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn sug96"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	sug96
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04

Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-100100.00000
Entropy..cal.	-275.20000
Enthalpy..J.	-418418.00000
Entropy..J.	-1150.33600
Melting.temperature..C.	59.06213

```
# Nearest neighbour method - tan04 (DNA/DNA: Self-Complimentarity)
out <- melting(sequence = "CATATGGCCATATG", nucleic.acid.conc = 2e-06,
        hybridisation.type = "dnadna", Na.conc = 1, method.nn = "tan04")
```

```
## [1] "-S CATATGGCCATATG -H dnadna -P 2e-06 -E Na=1 -T 60 -nn tan04"
```

Sequence	CATATGGCCATATG
Complementary.sequence	GTATACCGGTATAC
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	tan04
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA

Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-106900.00000
Entropy..cal.	-299.00000
Enthalpy..J.	-446842.00000
Entropy..J.	-1249.82000
Melting.temperature..C.	55.65824

```
# Nearest neighbour method - default (RNA/RNA: Self-Complimentarity)
out <- melting(sequence = "AUGUACAU", nucleic.acid.conc = 2e-06,
        hybridisation.type = "rnarna", Na.conc = 1)
```

```
## [1] "-S AUGUACAU -H rnarna -P 2e-06 -E Na=1 -T 60"
```

Sequence	AUGUACAU
Complementary.sequence	UACAUGUA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA

Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-59080.00000
Entropy..cal.	-168.60000
Enthalpy..J.	-246954.40000
Entropy..J.	-704.74800
Melting.temperature..C.	30.27015

```
# Nearest neighbour method - xia98 (RNA/RNA: Self-Complimentarity)
out <- melting(sequence = "AUGUACAU", nucleic.acid.conc = 2e-06,
        hybridisation.type = "rnarna", Na.conc = 1, method.nn = "xia98")
```

```
## [1] "-S AUGUACAU -H rnarna -P 2e-06 -E Na=1 -T 60 -nn xia98"
```

Sequence	AUGUACAU
Complementary.sequence	UACAUGUA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA

Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-59080.00000
Entropy..cal.	-168.60000
Enthalpy..J.	-246954.40000
Entropy..J.	-704.74800
Melting.temperature..C.	30.27015

```
# Nearest neighbour method - fre86 (RNA/RNA: Self-Complimentarity)
out <- melting(sequence = "AUGUACAU", nucleic.acid.conc = 2e-06,
        hybridisation.type = "rnarna", Na.conc = 1, method.nn = "fre86")
```

```
## [1] "-S AUGUACAU -H rnarna -P 2e-06 -E Na=1 -T 60 -nn fre86"
```

Sequence	AUGUACAU
Complementary.sequence	UACAUGUA
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	fre86
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01

DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	NN

Enthalpy..cal.	-60900.00000
Entropy..cal.	-173.80000
Enthalpy..J.	-254562.00000
Entropy..J.	-726.48400
Melting.temperature..C.	31.48175

GU wobble base pairs effect

```
# Nearest neighbour method - default (RNA/RNA)
out <- melting(sequence = "CCAGCGUCCU", nucleic.acid.conc = 0.0001,
        hybridisation.type = "rnarna", Na.conc = 1)
```

```
## [1] "-S CCAGCGUCCU -H rnarna -P 1e-04 -E Na=1 -T 60"
```

Sequence	CCAGCGUCCU
Complementary.sequence	GGUCGCAGGA
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01

DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-100210.00000
Entropy..cal.	-263.10000
Enthalpy..J.	-418877.80000
Entropy..J.	-1099.75800
Melting.temperature..C.	79.46955

```
# Nearest neighbour method - ser12 (RNA/RNA)
out <- melting(sequence = "CCAGCGUCCU", nucleic.acid.conc = 0.0001,
        hybridisation.type = "rnarna", Na.conc = 1, method.GU = "ser12")
```

```
## [1] "-S CCAGCGUCCU -H rnarna -P 1e-04 -E Na=1 -T 60 -GU ser12"
```

Sequence	CCAGCGUCCU
Complementary.sequence	GGUCGCAGGA
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96

Mode	def

Enthalpy..cal.	-100210.00000
Entropy..cal.	-263.10000
Enthalpy..J.	-418877.80000
Entropy..J.	-1099.75800
Melting.temperature..C.	79.46955

```
# Nearest neighbour method - tur99 (RNA/RNA)
out <- melting(sequence = "CCAGCGUCCU", nucleic.acid.conc = 0.0001,
        hybridisation.type = "rnarna", Na.conc = 1, method.GU = "tur99")
```

```
## [1] "-S CCAGCGUCCU -H rnarna -P 1e-04 -E Na=1 -T 60 -GU tur99"
```

Sequence	CCAGCGUCCU
Complementary.sequence	GGUCGCAGGA
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	tur99
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-100210.00000
Entropy..cal.	-263.10000
Enthalpy..J.	-418877.80000
Entropy..J.	-1099.75800
Melting.temperature..C.	79.46955

Single mismatch effect

```
# Single mismatch effect - default (DNA/DNA)
out <- melting(sequence = "CAACTTGATATTAATA", comp.sequence = "GTTGAACTCTAATTAT",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S CAACTTGATATTAATA -H dnadna -P 4e-04 -E Na=1 -C GTTGAACTCTAATTAT -T 60"
```

Sequence	CAACTTGATATTAATA
Complementary.sequence	GTTGAACTCTAATTAT
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-99400.00000
Entropy..cal.	-287.40000
Enthalpy..J.	-415492.00000
Entropy..J.	-1201.33200
Melting.temperature..C.	51.97499

```
# Single mismatch effect - allsanpey (DNA/DNA)
out <- melting(sequence = "CAACTTGATATTAATA", comp.sequence = "GTTGAACTCTAATTAT",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1, method.singleMM = "allsanpey")
```

```
## [1] "-S CAACTTGATATTAATA -H dnadna -P 4e-04 -E Na=1 -C GTTGAACTCTAATTAT -T 60 -sinMM allsanpey"
```

Sequence	CAACTTGATATTAATA
Complementary.sequence	GTTGAACTCTAATTAT
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-99400.00000

Entropy..cal.	-287.40000
Enthalpy..J.	-415492.00000
Entropy..J.	-1201.33200
Melting.temperature..C.	51.97499

```
# Single mismatch effect - default (RNA/RNA)
out <- melting(sequence = "GACAGGCUG", comp.sequence = "CUGUGCGAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna", Na.conc = 1)
```

```
## [1] "-S GACAGGCUG -H rnarna -P 1e-04 -E Na=1 -C CUGUGCGAC -T 60"
```

Sequence	GACAGGCUG
Complementary.sequence	CUGUGCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-86470.00000
Entropy..cal.	-242.90000
Enthalpy..J.	-361444.60000

Entropy..J.	-1015.32200
Melting.temperature..C.	54.40363

```
# Single mismatch effect - zno07 (RNA/RNA)
out <- melting(sequence = "GACAGGCUG", comp.sequence = "CUGUGCGAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.singleMM = "zno07")
```

```
## [1] "-S GACAGGCUG -H rnarna -P 1e-04 -E Na=1 -C CUGUGCGAC -T 60 -sinMM zno07"
```

Sequence	GACAGGCUG
Complementary.sequence	CUGUGCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-86470.00000
Entropy..cal.	-242.90000
Enthalpy..J.	-361444.60000
Entropy..J.	-1015.32200

Melting.temperature..C.	54.40363

```
# Single mismatch effect - zno08 (RNA/RNA)
out <- melting(sequence = "CAGUACGUC", comp.sequence = "GUCGGGCAG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.singleMM = "zno08")
```

```
## [1] "-S CAGUACGUC -H rnarna -P 1e-04 -E Na=1 -C GUCGGGCAG -T 60 -sinMM zno08"
```

Sequence	CAGUACGUC
Complementary.sequence	GUCGGGCAG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno08
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-63680.00000
Entropy..cal.	-183.40000
Enthalpy..J.	-266182.40000
Entropy..J.	-766.61200

Melting.temperature..C.	38.26298

```
# Single mismatch effect - tur06 (RNA/RNA)
out <- melting(sequence = "GACAGGCUG", comp.sequence = "CUGUGCGAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.singleMM = "tur06")
```

```
## [1] "-S GACAGGCUG -H rnarna -P 1e-04 -E Na=1 -C CUGUGCGAC -T 60 -sinMM tur06"
```

Sequence	GACAGGCUG
Complementary.sequence	CUGUGCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	tur06
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-79870.00000
Entropy..cal.	-219.90000
Enthalpy..J.	-333856.60000
Entropy..J.	-919.18200

Melting.temperature..C.	58.27825

```
# Single mismatch effect - default (DNA/RNA)
out <- melting(sequence = "CCATAACTACC", comp.sequence = "GGUAAUGAUGG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnarna", Na.conc = 1)
```

```
## [1] "-S CCATAACTACC -H dnarna -P 1e-04 -E Na=1 -C GGUAAUGAUGG -T 60"
```

Sequence	CCATAACTACC
Complementary.sequence	GGUAAUGAUGG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug95
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-73600.00000
Entropy..cal.	-213.70000
Enthalpy..J.	-307648.00000
Entropy..J.	-893.26600
Melting.temperature..C.	40.32976

```r
# Single mismatch effect - wat11 (DNA/RNA)
out <- melting(sequence = "CCATAACTACC", comp.sequence = "GGUAAUGAUGG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnarna",
        Na.conc = 1, method.singleMM = "wat11")
```

```
## [1] "-S CCATAACTACC -H dnarna -P 1e-04 -E Na=1 -C GGUAAUGAUGG -T 60 -sinMM wat11"
```

Sequence	CCATAACTACC
Complementary.sequence	GGUAAUGAUGG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug95
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-73600.00000
Entropy..cal.	-213.70000
Enthalpy..J.	-307648.00000
Entropy..J.	-893.26600
Melting.temperature..C.	40.32976

Tandem mismatches effect

```
# Tandem mismatches effect - default (DNA/DNA)
out <- melting(sequence = "GACGTTGGAC", comp.sequence = "CTGCGGCCTG",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna", Na.conc = 1)
```

```
## [1] "-S GACGTTGGAC -H dnadna -P 4e-04 -E Na=1 -C CTGCGGCCTG -T 60"
```

Sequence	GACGTTGGAC
Complementary.sequence	CTGCGGCCTG
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-54300.00000
Entropy..cal.	-149.60000
Enthalpy..J.	-226974.00000
Entropy..J.	-625.32800
Melting.temperature..C.	50.20175

```r
# Tandem mismatches effect - allsanpey (DNA/DNA)
out <- melting(sequence = "GACGTTGGAC", comp.sequence = "CTGCGGCCTG",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1, method.tandemMM = "allsanpey")
```

```
## [1] "-S GACGTTGGAC -H dnadna -P 4e-04 -E Na=1 -C CTGCGGCCTG -T 60"
```

Sequence	GACGTTGGAC
Complementary.sequence	CTGCGGCCTG
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-54300.00000
Entropy..cal.	-149.60000
Enthalpy..J.	-226974.00000
Entropy..J.	-625.32800
Melting.temperature..C.	50.20175

```r
# Tandem mismatches effect - default (RNA/RNA)
out <- melting(sequence = "GAGCGGAG", comp.sequence = "CUCCACUC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna", Na.conc = 1)

# Tandem mismatches effect -  tur06 (RNA/RNA)
out <- melting(sequence = "GAGCGGAG", comp.sequence = "CUCCACUC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.tandemMM = "tur99")
```

```
## [1] "-S GAGCGGAG -H rnarna -P 1e-04 -E Na=1 -C CUCCACUC -T 60"
```

Sequence	GAGCGGAG
Complementary.sequence	CUCCACUC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-53530.00000
Entropy..cal.	-160.85000
Enthalpy..J.	-223755.40000
Entropy..J.	-672.35300

Melting.temperature..C.	21.07224

Single dangling end effect

```
# Single dangling end effect - default (DNA/DNA)
out <- melting(sequence = "-GTAGCTACA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S -GTAGCTACA -H dnadna -P 4e-04 -E Na=1 -T 60"
```

Sequence	-GTAGCTACA
Complementary.sequence	ACATCGATG-
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-68200.00000
Entropy..cal.	-193.80000
Enthalpy..J.	-285076.00000

Entropy..J.	-810.08400
Melting.temperature..C.	52.58935

```
# Single dangling end effect - bom00 (DNA/DNA)
out <- melting(sequence = "-GTAGCTACA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1, method.single.dangle = "bom00")
```

```
## [1] "-S -GTAGCTACA -H dnadna -P 4e-04 -E Na=1 -T 60 -sinDE bom00"
```

Sequence	-GTAGCTACA
Complementary.sequence	ACATCGATG-
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-68200.00000
Entropy..cal.	-193.80000
Enthalpy..J.	-285076.00000
Entropy..J.	-810.08400

Melting.temperature..C.	52.58935

```
# Single dangling end effect - sugdna02 (DNA/DNA)
out <- melting(sequence = "-GTAGCTACA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1, method.single.dangle = "sugdna02")
```

```
## [1] "-S -GTAGCTACA -H dnadna -P 4e-04 -E Na=1 -T 60 -sinDE sugdna02"
```

Sequence	-GTAGCTACA
Complementary.sequence	ACATCGATG-
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	sugdna02
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-59400.00000
Entropy..cal.	-167.80000
Enthalpy..J.	-248292.00000
Entropy..J.	-701.40400

Melting.temperature..C.	50.78548

```
# Single dangling end effect - default (RNA/RNA)
out <- melting(sequence = "-GGCGCUG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S -GGCGCUG -H rnarna -P 1e-04 -E Na=1 -T 60"
```

Sequence	GGCGCUG
Complementary.sequence	CCGCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-71100.0000
Entropy..cal.	-188.7000
Enthalpy..J.	-297198.0000
Entropy..J.	-788.7660
Melting.temperature..C.	65.7647

```r
# Single dangling end effect -  ser08 (RNA/RNA)
out <- melting(sequence = "-GGCGCUG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.single.dangle = "ser08")
```

```
## [1] "-S -GGCGCUG -H rnarna -P 1e-04 -E Na=1 -T 60 -sinDE ser08"
```

Sequence	GGCGCUG
Complementary.sequence	CCGCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-71100.0000
Entropy..cal.	-188.7000
Enthalpy..J.	-297198.0000
Entropy..J.	-788.7660
Melting.temperature..C.	65.7647

```r
# Single dangling end effect -  sugrna02 (RNA/RNA)
out <- melting(sequence = "-GGCGCUG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.single.dangle = "sugrna02")
```

```
## [1] "-S -GGCGCUG -H rnarna -P 1e-04 -E Na=1 -T 60 -sinDE sugrna02"
```

Sequence	GGCGCUG
Complementary.sequence	CCGCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	sugrna02
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-71100.0000
Entropy..cal.	-188.7000
Enthalpy..J.	-297198.0000
Entropy..J.	-788.7660
Melting.temperature..C.	65.7647

Double dangling end effect

```
# Double dangling end effect - default (DNA/DNA)
out <- melting(sequence = "--ATGCATAA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S --ATGCATAA -H dnadna -P 4e-04 -E Na=1 -T 60"
```

Sequence	–ATGCATAA
Complementary.sequence	AATACGTA–
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-38600.00000
Entropy..cal.	-105.80000
Enthalpy..J.	-161348.00000
Entropy..J.	-442.24400
Melting.temperature..C.	44.88615

```r
# Double dangling end effect - sugdna02 (DNA/DNA)
out <- melting(sequence = "--ATGCATAA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1, method.double.dangle = "sugdna02")
```

```
## [1] "-S --ATGCATAA -H dnadna -P 4e-04 -E Na=1 -T 60 -secDE sugdna02"
```

Sequence	–ATGCATAA
Complementary.sequence	AATACGTA–
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-38600.00000
Entropy..cal.	-105.80000
Enthalpy..J.	-161348.00000
Entropy..J.	-442.24400
Melting.temperature..C.	44.88615

```r
# Double dangling end effect - default (RNA/RNA)
out <- melting(sequence = "--AUGCAUAA",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)

# Double dangling end effect -  ser06 (RNA/RNA)
out <- melting(sequence = "--AUGCAUAA",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.double.dangle = "ser06")
```

```
## [1] "-S --AUGCAUAA -H rnarna -P 1e-04 -E Na=1 -T 60 -secDE ser06"
```

Sequence	–AUGCAUAA
Complementary.sequence	AAUACGUA–
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-58870.00000
Entropy..cal.	-168.00000
Enthalpy..J.	-246076.60000

Entropy..J.	-702.24000
Melting.temperature..C.	42.79724

```
# Double dangling end effect -  sugrna02 (RNA/RNA)
out <- melting(sequence = "--AUGCAUAA",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.double.dangle = "sugrna02")
```

```
## [1] "-S --AUGCAUAA -H rnarna -P 1e-04 -E Na=1 -T 60 -secDE sugrna02"
```

Sequence	–AUGCAUAA
Complementary.sequence	AAUACGUA–
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	sugrna02
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-49870.00000
Entropy..cal.	-140.00000
Enthalpy..J.	-208456.60000
Entropy..J.	-585.20000

Melting.temperature..C.	41.82788

```
# Double dangling end effect -  ser05 (RNA/RNA)
out <- melting(sequence = "--AUGCAUAA",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.double.dangle = "ser05")
```

```
## [1] "-S --AUGCAUAA -H rnarna -P 1e-04 -E Na=1 -T 60 -secDE ser05"
```

Sequence	–AUGCAUAA
Complementary.sequence	AAUACGUA–
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser05
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-62470.00000
Entropy..cal.	-179.40000
Enthalpy..J.	-261124.60000
Entropy..J.	-749.89200

Melting.temperature..C.	42.78815

Long dangling end effect

```
# Long dangling end effect - default (DNA/DNA)
out <- melting(sequence = "----GCATATGCAAAA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S ----GCATATGCAAAA -H dnadna -P 4e-04 -E Na=1 -T 60"
```

Sequence	—-GCATATGCAAAA
Complementary.sequence	AAAACGTATACG—-
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-67700.00000
Entropy..cal.	-190.30000
Enthalpy..J.	-282986.00000

Entropy..J.	-795.45400
Melting.temperature..C.	55.69854

```
# Long dangling end effect - sugdna02 (DNA/DNA)
out <- melting(sequence = "----GCATATGCAAAA",
        nucleic.acid.conc = 0.0004, hybridisation.type = "dnadna",
        Na.conc = 1, method.long.dangle = "sugdna02")
```

```
## [1] "-S ----GCATATGCAAAA -H dnadna -P 4e-04 -E Na=1 -T 60 -lonDE sugdna02"
```

Sequence	—-GCATATGCAAAA
Complementary.sequence	AAAACGTATACG—-
Nucleic.acid.concentration..M.	4e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-67700.00000
Entropy..cal.	-190.30000
Enthalpy..J.	-282986.00000
Entropy..J.	-795.45400

Melting.temperature..C.	55.69854

```
# Long dangling end effect - default (RNA/RNA)
out <- melting(sequence = "AAAAGCAUAUGC----",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S AAAAGCAUAUGC---- -H rnarna -P 1e-04 -E Na=1 -T 60"
```

Sequence	AAAAGCAUAUGC—-
Complementary.sequence	—-CGUAUACGAAAA
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-99680.00000
Entropy..cal.	-283.40000
Enthalpy..J.	-416662.40000
Entropy..J.	-1184.61200
Melting.temperature..C.	57.21314

```
# Long dangling end effect -  sugrna02 (RNA/RNA)
out <- melting(sequence = "AAAAGCAUAUGC----",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.long.dangle = "sugrna02")
```

```
## [1] "-S AAAAGCAUAUGC---- -H rnarna -P 1e-04 -E Na=1 -T 60 -lonDE sugrna02"
```

Sequence	AAAAGCAUAUGC—-
Complementary.sequence	—-CGUAUACGAAAA
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	TRUE
Correction.factor	1

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-99680.00000
Entropy..cal.	-283.40000
Enthalpy..J.	-416662.40000
Entropy..J.	-1184.61200
Melting.temperature..C.	57.21314

Internal loop effect

```
# Internal loop effect - default (DNA/DNA)
out <- melting(sequence = "GCGATTGGCACTTTGGTGAAC", comp.sequence = "CGCTACATATGAAACCACTTG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S GCGATTGGCACTTTGGTGAAC -H dnadna -P 1e-04 -E Na=1 -C CGCTACATATGAAACCACTTG -T 60"
```

Sequence	GCGATTGGCACTTTGGTGAAC
Complementary.sequence	CGCTACATATGAAACCACTTG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-121100.00000
Entropy..cal.	-333.40000
Enthalpy..J.	-506198.00000
Entropy..J.	-1393.61200
Melting.temperature..C.	84.09052

```r
# Internal loop effect - san04 (DNA/DNA)
out <- melting(sequence = "GCGATTGGCACTTTGGTGAAC", comp.sequence = "CGCTACATATGAAACCACTTG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.internal.loop = "san04")
```

```
## [1] "-S GCGATTGGCACTTTGGTGAAC -H dnadna -P 1e-04 -E Na=1 -C CGCTACATATGAAACCACTTG -T 60 -intLP san04"
```

Sequence	GCGATTGGCACTTTGGTGAAC
Complementary.sequence	CGCTACATATGAAACCACTTG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-121100.00000
Entropy..cal.	-333.40000
Enthalpy..J.	-506198.00000
Entropy..J.	-1393.61200
Melting.temperature..C.	84.09052

```r
# Internal loop effect - default (RNA/RNA)
out <- melting(sequence = "GACAC-GCUG", comp.sequence = "CUGUAUCGAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S GACAC-GCUG -H rnarna -P 1e-04 -E Na=1 -C CUGUAUCGAC -T 60"
```

Sequence	GACAC-GCUG
Complementary.sequence	CUGUAUCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-68770.00000
Entropy..cal.	-194.40000
Enthalpy..J.	-287458.60000
Entropy..J.	-812.59200
Melting.temperature..C.	45.98713

```r
# Internal loop effect -  zno07 (RNA/RNA)
out <- melting(sequence = "GACAC-GCUG", comp.sequence = "CUGUAUCGAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.internal.loop = "zno07")
```

```
## [1] "-S GACAC-GCUG -H rnarna -P 1e-04 -E Na=1 -C CUGUAUCGAC -T 60 -intLP zno07"
```

Sequence	GACAC-GCUG
Complementary.sequence	CUGUAUCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	zno07
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-66770.00000
Entropy..cal.	-191.80000
Enthalpy..J.	-279098.60000
Entropy..J.	-801.72400
Melting.temperature..C.	40.49012

```r
# Internal loop effect -  tur06 (RNA/RNA)
out <- melting(sequence = "GACAC-GCUG", comp.sequence = "CUGUAUCGAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.internal.loop = "tur06")
```

```
## [1] "-S GACAC-GCUG -H rnarna -P 1e-04 -E Na=1 -C CUGUAUCGAC -T 60 -intLP tur06"
```

Sequence	GACAC-GCUG
Complementary.sequence	CUGUAUCGAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-68770.00000
Entropy..cal.	-194.40000
Enthalpy..J.	-287458.60000
Entropy..J.	-812.59200
Melting.temperature..C.	45.98713

Single bulge loop effect

```
# Single bulge loop effect - default (DNA/DNA)
out <- melting(sequence = "TCGATTAGCGACACAGG", comp.sequence = "AGCTAATC-CTGTGTCC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S TCGATTAGCGACACAGG -H dnadna -P 1e-04 -E Na=1 -C AGCTAATC-CTGTGTCC -T 60"
```

Sequence	TCGATTAGCGACACAGG
Complementary.sequence	AGCTAATC-CTGTGTCC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-98700.00000
Entropy..cal.	-265.60000
Enthalpy..J.	-412566.00000
Entropy..J.	-1110.20800
Melting.temperature..C.	71.12754

```r
# Single bulge loop effect - tan04 (DNA/DNA)
out <- melting(sequence = "TCGATTAGCGACACAGG", comp.sequence = "AGCTAATC-CTGTGTCC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.single.bulge.loop = "tan04")
```

```
## [1] "-S TCGATTAGCGACACAGG -H dnadna -P 1e-04 -E Na=1 -C AGCTAATC-CTGTGTCC -T 60 -sinBU tan04"
```

Sequence	TCGATTAGCGACACAGG
Complementary.sequence	AGCTAATC-CTGTGTCC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-98700.00000
Entropy..cal.	-265.60000
Enthalpy..J.	-412566.00000
Entropy..J.	-1110.20800
Melting.temperature..C.	71.12754

```r
# Single bulge loop effect - san04 (DNA/DNA)
out <- melting(sequence = "TCGATTAGCGACACAGG", comp.sequence = "AGCTAATC-CTGTGTCC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.single.bulge.loop = "san04")
```

```
## [1] "-S TCGATTAGCGACACAGG -H dnadna -P 1e-04 -E Na=1 -C AGCTAATC-CTGTGTCC -T 60 -sinBU san04"
```

Sequence	TCGATTAGCGACACAGG
Complementary.sequence	AGCTAATC-CTGTGTCC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	san04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-120500.0000
Entropy..cal.	-338.4000
Enthalpy..J.	-503690.0000
Entropy..J.	-1414.5120
Melting.temperature..C.	62.0496

```r
# Single bulge loop effect - default (RNA/RNA)
out <- melting(sequence = "GACUCUGUC", comp.sequence = "CUGA-ACAG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S GACUCUGUC -H rnarna -P 1e-04 -E Na=1 -C CUGA-ACAG -T 60"
```

Sequence	GACUCUGUC
Complementary.sequence	CUGA-ACAG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-64710.00000
Entropy..cal.	-185.90000
Enthalpy..J.	-270487.80000
Entropy..J.	-777.06200
Melting.temperature..C.	39.47787

```r
# Single bulge loop effect -  tur06 (RNA/RNA)
out <- melting(sequence = "GACUCUGUC", comp.sequence = "CUGA-ACAG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.single.bulge.loop = "tur06")
```

```
## [1] "-S GACUCUGUC -H rnarna -P 1e-04 -E Na=1 -C CUGA-ACAG -T 60 -sinBU tur06"
```

Sequence	GACUCUGUC
Complementary.sequence	CUGA-ACAG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-64710.00000
Entropy..cal.	-185.90000
Enthalpy..J.	-270487.80000
Entropy..J.	-777.06200
Melting.temperature..C.	39.47787

```r
# Single bulge loop effect -  ser07 (RNA/RNA)
out <- melting(sequence = "GACUCUGUC", comp.sequence = "CUGA-ACAG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.single.bulge.loop = "ser07")
```

```
## [1] "-S GACUCUGUC -H rnarna -P 1e-04 -E Na=1 -C CUGA-ACAG -T 60 -sinBU ser07"
```

Sequence	GACUCUGUC
Complementary.sequence	CUGA-ACAG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	ser07
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-60790.00000
Entropy..cal.	-178.50000
Enthalpy..J.	-254102.20000
Entropy..J.	-746.13000
Melting.temperature..C.	31.42849

Long bulge loop effect

```
# Long bulge loop effect - default (DNA/DNA)
out <- melting(sequence = "ATATGACGCCACAGCG", comp.sequence = "TATAC---GGTGTCGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S ATATGACGCCACAGCG -H dnadna -P 1e-04 -E Na=1 -C TATAC---GGTGTCGC -T 60"
```

Sequence	ATATGACGCCACAGCG
Complementary.sequence	TATAC—GGTGTCGC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-89300.0000
Entropy..cal.	-253.8000
Enthalpy..J.	-373274.0000
Entropy..J.	-1060.8840
Melting.temperature..C.	51.7104

```
# Long bulge loop effect - san04 (DNA/DNA)
out <- melting(sequence = "ATATGACGCCACAGCG", comp.sequence = "TATAC---GGTGTCGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.long.bulge.loop = "san04")
```

```
## [1] "-S ATATGACGCCACAGCG -H dnadna -P 1e-04 -E Na=1 -C TATAC---GGTGTCGC -T 60 -lonBU san04"
```

Sequence	ATATGACGCCACAGCG
Complementary.sequence	TATAC—GGTGTCGC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-89300.0000
Entropy..cal.	-253.8000
Enthalpy..J.	-373274.0000
Entropy..J.	-1060.8840
Melting.temperature..C.	51.7104

```r
# Long bulge loop effect - default (RNA/RNA)
out <- melting(sequence = "AUAUGACGCCACAGCG", comp.sequence = "UAUAC---GGUGUCGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S AUAUGACGCCACAGCG -H rnarna -P 1e-04 -E Na=1 -C UAUAC---GGUGUCGC -T 60"
```

Sequence	AUAUGACGCCACAGCG
Complementary.sequence	UAUAC—GGUGUCGC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-104130.0000
Entropy..cal.	-285.9000
Enthalpy..J.	-435263.4000
Entropy..J.	-1195.0620
Melting.temperature..C.	66.0497

```
# Long bulge loop effect -  tur06 (RNA/RNA)
out <- melting(sequence = "AUAUGACGCCACAGCG", comp.sequence = "UAUAC---GGUGUCGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.long.bulge.loop = "tur06")
```

```
## [1] "-S AUAUGACGCCACAGCG -H rnarna -P 1e-04 -E Na=1 -C UAUAC---GGUGUCGC -T 60 -lonBU tur06"
```

Sequence	AUAUGACGCCACAGCG
Complementary.sequence	UAUAC—GGUGUCGC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-104130.0000
Entropy..cal.	-285.9000
Enthalpy..J.	-435263.4000
Entropy..J.	-1195.0620
Melting.temperature..C.	66.0497

CNG repeats effect

```
# CNG repeats effect - default (RNA/RNA)
out <- melting(sequence = "GCGGCGGCGGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S GCGGCGGCGGC -H rnarna -P 1e-04 -E Na=1 -T 60"
```

Sequence	GCGGCGGCGGC
Complementary.sequence	CGCCGCCGCCG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-128000.00000
Entropy..cal.	-327.30000
Enthalpy..J.	-535040.00000
Entropy..J.	-1368.11400
Melting.temperature..C.	94.25719

```r
# CNG repeats effect -  bro05 (RNA/RNA)
out <- melting(sequence = "GCGGCGGCGGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.CNG = "bro05")
```

```
## [1] "-S GCGGCGGCGGC -H rnarna -P 1e-04 -E Na=1 -T 60 -CNG bro05"
```

Sequence	GCGGCGGCGGC
Complementary.sequence	CGCCGCCGCCG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-128000.00000
Entropy..cal.	-327.30000
Enthalpy..J.	-535040.00000
Entropy..J.	-1368.11400
Melting.temperature..C.	94.25719

Inosine bases effect

```
# Inosine bases effect - default (DNA/DNA)
out <- melting(sequence = "CCGICTGTIGCG", comp.sequence = "GGCCGACACCGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S CCGICTGTIGCG -H dnadna -P 1e-04 -E Na=1 -C GGCCGACACCGC -T 60"
```

Sequence	CCGICTGTIGCG
Complementary.sequence	GGCCGACACCGC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-89500.00000
Entropy..cal.	-243.30000
Enthalpy..J.	-374110.00000
Entropy..J.	-1016.99400
Melting.temperature..C.	65.36853

```r
# Inosine bases effect - san05 (DNA/DNA)
out <- melting(sequence = "CCGICTGTIGCG", comp.sequence = "GGCCGACACCGC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.inosine = "san05")
```

```
## [1] "-S CCGICTGTIGCG -H dnadna -P 1e-04 -E Na=1 -C GGCCGACACCGC -T 60 -ino san05"
```

Sequence	CCGICTGTIGCG
Complementary.sequence	GGCCGACACCGC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-89500.00000
Entropy..cal.	-243.30000
Enthalpy..J.	-374110.00000
Entropy..J.	-1016.99400
Melting.temperature..C.	65.36853

```r
# Inosine bases effect - default (RNA/RNA)
out <- melting(sequence = "GCAICGC", comp.sequence = "CGUUGCG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1)
```

```
## [1] "-S GCAICGC -H rnarna -P 1e-04 -E Na=1 -C CGUUGCG -T 60"
```

Sequence	GCAICGC
Complementary.sequence	CGUUGCG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-70470.00000
Entropy..cal.	-199.20000
Enthalpy..J.	-294564.60000
Entropy..J.	-832.65600
Melting.temperature..C.	46.75042

```r
# Inosine bases effect -  zno07 (RNA/RNA)
out <- melting(sequence = "GCAICGC", comp.sequence = "CGUUGCG",
        nucleic.acid.conc = 0.0001, hybridisation.type = "rnarna",
        Na.conc = 1, method.inosine = "zno07")
```

```
## [1] "-S GCAICGC -H rnarna -P 1e-04 -E Na=1 -C CGUUGCG -T 60 -ino zno07"
```

Sequence	GCAICGC
Complementary.sequence	CGUUGCG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	rnarna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-70470.00000
Entropy..cal.	-199.20000
Enthalpy..J.	-294564.60000
Entropy..J.	-832.65600
Melting.temperature..C.	46.75042

Hydroxyadenine bases effect

```
# Hydroxyadenine bases effect - default (DNA/DNA)
out <- melting(sequence = "AGAAATGA*CACGGTG", comp.sequence = "TCTTTACCGTGCCAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S AGAAATGA*CACGGTG -H dnadna -P 1e-04 -E Na=1 -C TCTTTACCGTGCCAC -T 60"
```

Sequence	AGAAATGA*CACGGTG
Complementary.sequence	TCTTTACC GTGCCAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-95100.00000
Entropy..cal.	-257.30000
Enthalpy..J.	-397518.00000
Entropy..J.	-1075.51400
Melting.temperature..C.	68.46041

```r
# Hydroxyadenine bases effect - sug01 (DNA/DNA)
out <- melting(sequence = "AGAAATGA*CACGGTG", comp.sequence = "TCTTTACCGTGCCAC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.hydroxyadenine = "sug01")
```

```
## [1] "-S AGAAATGA*CACGGTG -H dnadna -P 1e-04 -E Na=1 -C TCTTTACCGTGCCAC -T 60 -ha sug01"
```

Sequence	AGAAATGA*CACGGTG
Complementary.sequence	TCTTTACC GTGCCAC
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-95100.00000
Entropy..cal.	-257.30000
Enthalpy..J.	-397518.00000
Entropy..J.	-1075.51400
Melting.temperature..C.	68.46041

Azobenzenes effect

```
# Azobenzenes effect - default (DNA/DNA)
out <- melting(sequence = "CTX_CTTAAX_CGAAGX_CGAGAX_CTATAX_CCC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S CTX_CTTAAX_CGAAGX_CGAGAX_CTATAX_CCC -H dnadna -P 1e-04 -E Na=1 -T 60"
```

Sequence	CTX_CTTAAX_CGAAGX_CGAGAX_CTATAX_CCC
Complementary.sequence	GA AATT CTTC CTCT ATAT GG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-56300.00000
Entropy..cal.	-154.30000
Enthalpy..J.	-235334.00000
Entropy..J.	-644.97400
Melting.temperature..C.	47.85385

```r
# Azobenzenes effect - asa05 (DNA/DNA)
out <- melting(sequence = "CTX_CTTAAX_CGAAGX_CGAGAX_CTATAX_CCC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.azobenzenes = "asa05")
```

```
## [1] "-S CTX_CTTAAX_CGAAGX_CGAGAX_CTATAX_CCC -H dnadna -P 1e-04 -E Na=1 -T 60 -azo asa05"
```

Sequence	CTX_CTTAAX_CGAAGX_CGAGAX_CTATAX_CCC
Complementary.sequence	GA AATT CTTC CTCT ATAT GG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-56300.00000
Entropy..cal.	-154.30000
Enthalpy..J.	-235334.00000
Entropy..J.	-644.97400
Melting.temperature..C.	47.85385

Locked nucleic acids effect

```
# Locked nucleic acids effect - default (DNA/DNA)
out <- melting(sequence = "CCATTLGCTACC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1)
```

```
## [1] "-S CCATTLGCTACC -H dnadna -P 1e-04 -E Na=1 -T 60"
```

Sequence	CCATTLGCTACC
Complementary.sequence	GGTAA CGATGG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-80314.00000
Entropy..cal.	-217.40000
Enthalpy..J.	-335712.52000
Entropy..J.	-908.73200
Melting.temperature..C.	63.61426

```r
# Locked nucleic acids effect - sug01 (DNA/DNA)
out <- melting(sequence = "CCATTLGCTACC",
        nucleic.acid.conc = 0.0001, hybridisation.type = "dnadna",
        Na.conc = 1, method.locked = "mct04")
```

```
## [1] "-S CCATTLGCTACC -H dnadna -P 1e-04 -E Na=1 -T 60 -lck mct04"
```

Sequence	CCATTLGCTACC
Complementary.sequence	GGTAA CGATGG
Nucleic.acid.concentration..M.	1e-04
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-80314.00000
Entropy..cal.	-217.40000
Enthalpy..J.	-335712.52000
Entropy..J.	-908.73200
Melting.temperature..C.	63.61426

Corrections

Ion corrections

Sodium corrections

```
# Na correction - default (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069)
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000

Entropy..J.	-1287.85800
Melting.temperature..C.	56.70492

```
# Na correction - owc2204 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "owc2204")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion owc2204"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	owc2204
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800

Melting.temperature..C.	56.70492

```
# Na correction - ahs01 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "ahs01")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion ahs01"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	ahs01
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.0000
Entropy..cal.	-321.8689
Enthalpy..J.	-479864.0000
Entropy..J.	-1345.4121
Melting.temperature..C.	54.1569

```r
# Na correction - kam71 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "kam71")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion kam71"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	kam71
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	51.72963

```r
# Na correction - marschdot (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "marschdot")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion marschdot"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	marschdot
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	49.18075

```r
# Na correction - owc1904 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "owc1904")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion owc1904"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	owc1904
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	56.18571

```r
# Na correction - owc2004 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "owc2004")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion owc2004"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	owc2004
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	56.67553

```r
# Na correction - owc2104 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "owc2104")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion owc2104"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	owc2104
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	56.63967

```r
# Na correction - san96 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "san96")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion san96"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	san96
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	53.01651

```r
# Na correction - san04 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "san04")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion san04"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	san04
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-321.87464
Enthalpy..J.	-479864.00000
Entropy..J.	-1345.43599
Melting.temperature..C.	54.15157

```r
# Na correction - schlif (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "schlif")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion schlif"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	schlif
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	48.25579

```r
# Na correction - tanna06 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "tanna06")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion tanna06"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	tanna06
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-320.68325
Enthalpy..J.	-479864.00000
Entropy..J.	-1340.45597
Melting.temperature..C.	55.26711

```r
# Na correction - wet91 (DNA/DNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, correction.ion = "wet91")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnadna -P 2e-06 -E Na=0.069 -T 60 -ion wet91"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGTCGGTCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	wet91
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-114800.00000
Entropy..cal.	-308.10000
Enthalpy..J.	-479864.00000
Entropy..J.	-1287.85800
Melting.temperature..C.	51.74573

```r
# Na correction - default (RNA/RNA)
out <- melting(sequence = "CCAGCCAGUCUCUCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Na.conc = 0.069)
```

```
## [1] "-S CCAGCCAGUCUCUCC -H rnarna -P 2e-06 -E Na=0.069 -T 60"
```

Sequence	CCAGCCAGUCUCUCC
Complementary.sequence	GGUCGGUCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-162960.0000
Entropy..cal.	-438.9933
Enthalpy..J.	-681172.8000
Entropy..J.	-1834.9920
Melting.temperature..C.	75.1552

```r
# Na correction -  tanna07 (RNA/RNA)
out <- melting(sequence = "CCAGCCAGUCUCUCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Na.conc = 0.069, correction.ion = "tanna07")
```

```
## [1] "-S CCAGCCAGUCUCUCC -H rnarna -P 2e-06 -E Na=0.069 -T 60 -ion tanna07"
```

Sequence	CCAGCCAGUCUCUCC
Complementary.sequence	GGUCGGUCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	tanna07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-162960.0000
Entropy..cal.	-438.9933
Enthalpy..J.	-681172.8000
Entropy..J.	-1834.9920
Melting.temperature..C.	75.1552

```r
# Na correction -  wet91 (RNA/RNA)
out <- melting(sequence = "CCAGCCAGUCUCUCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Na.conc = 0.069, correction.ion = "wet91")
```

```
## [1] "-S CCAGCCAGUCUCUCC -H rnarna -P 2e-06 -E Na=0.069 -T 60 -ion wet91"
```

Sequence	CCAGCCAGUCUCUCC
Complementary.sequence	GGUCGGUCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	wet91
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-162960.00000
Entropy..cal.	-425.70000
Enthalpy..J.	-681172.80000
Entropy..J.	-1779.42600
Melting.temperature..C.	69.55572

```r
# Na correction - default (mRNA/RNA)
out <- melting(sequence = "UACGCGUCAAUAACGCUA",
        nucleic.acid.conc = 0.000002, hybridisation.type = "mrnarna",
        Na.conc = 0.069)
```

```
## [1] "-S UACGCGUCAAUAACGCUA -H mrnarna -P 2e-06 -E Na=0.069 -T 60"
```

Sequence	UACGCGUCAAUAACGCUA
Complementary.sequence	AUGCGCAGUUAUUGCGAU
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-143140.00000
Entropy..cal.	-374.64864
Enthalpy..J.	-598325.20000
Entropy..J.	-1566.03130
Melting.temperature..C.	81.57763

```r
# Na correction -  tanna07 (mRNA/RNA)
out <- melting(sequence = "UACGCGUCAAUAACGCUA",
        nucleic.acid.conc = 0.000002, hybridisation.type = "mrnarna",
        Na.conc = 0.069, correction.ion = "tanna07")
```

```
## [1] "-S UACGCGUCAAUAACGCUA -H mrnarna -P 2e-06 -E Na=0.069 -T 60 -ion tanna07"
```

Sequence	UACGCGUCAAUAACGCUA
Complementary.sequence	AUGCGCAGUUAUUGCGAU
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	tanna07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-143140.00000
Entropy..cal.	-374.64864
Enthalpy..J.	-598325.20000
Entropy..J.	-1566.03130
Melting.temperature..C.	81.57763

```r
# Na correction - default (DNA/RNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnarna",
        Na.conc = 0.069)
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnarna -P 2e-06 -E Na=0.069 -T 60"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGUCGGUCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug95
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-119900.00000
Entropy..cal.	-312.70000
Enthalpy..J.	-501182.00000
Entropy..J.	-1307.08600
Melting.temperature..C.	62.08869

```r
# Na correction - wet91 (DNA/RNA)
out <- melting(sequence = "CCAGCCAGTCTCTCC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnarna",
        Na.conc = 0.069, correction.ion = "wet91")
```

```
## [1] "-S CCAGCCAGTCTCTCC -H dnarna -P 2e-06 -E Na=0.069 -T 60 -ion wet91"
```

Sequence	CCAGCCAGTCTCTCC
Complementary.sequence	GGUCGGUCAGAGAGG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	sug95
GU.model	NA
Single.mismatch.model	wat11
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	wet91
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-119900.00000
Entropy..cal.	-312.70000
Enthalpy..J.	-501182.00000
Entropy..J.	-1307.08600
Melting.temperature..C.	62.08869

Magnesium corrections

```
# Mg correction - default (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Mg.conc = 0.0015)
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Mg=0.0015 -T 60"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.52043

```r
# Mg correction - owcmg08 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Mg.conc = 0.0015, correction.ion = "owcmg08")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Mg=0.0015 -T 60 -ion owcmg08"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	owcmg08
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.52043

```r
# Mg correction - tanmg06 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Mg.conc = 0.0015, correction.ion = "tanmg06")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Mg=0.0015 -T 60 -ion tanmg06"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	tanmg06
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-336.77490
Enthalpy..J.	-516648.00000
Entropy..J.	-1407.71908
Melting.temperature..C.	64.88082

```r
# Mg correction - default (RNA/RNA)
out <- melting(sequence = "CAGCCUCGUCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Mg.conc = 0.0015)
```

```
## [1] "-S CAGCCUCGUCGCAGC -H rnarna -P 2e-06 -E Mg=0.0015 -T 60"
```

Sequence	CAGCCUCGUCGCAGC
Complementary.sequence	GUCGGAGCAGCGUCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-164300.0000
Entropy..cal.	-433.6455
Enthalpy..J.	-686774.0000
Entropy..J.	-1812.6383
Melting.temperature..C.	82.0796

```r
# Mg correction -  tanmg07 (RNA/RNA)
out <- melting(sequence = "CAGCCUCGUCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Mg.conc = 0.0015, correction.ion = "tanmg07")
```

```
## [1] "-S CAGCCUCGUCGCAGC -H rnarna -P 2e-06 -E Mg=0.0015 -T 60 -ion tanmg07"
```

Sequence	CAGCCUCGUCGCAGC
Complementary.sequence	GUCGGAGCAGCGUCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	tanmg07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-164300.0000
Entropy..cal.	-433.6455
Enthalpy..J.	-686774.0000
Entropy..J.	-1812.6383
Melting.temperature..C.	82.0796

```r
# Mg correction - default (mRNA/RNA)
out <- melting(sequence = "UACGCGUCAAUAACGCUA",
        nucleic.acid.conc = 0.000002, hybridisation.type = "mrnarna",
        Mg.conc = 0.0015)
```

```
## [1] "-S UACGCGUCAAUAACGCUA -H mrnarna -P 2e-06 -E Mg=0.0015 -T 60"
```

Sequence	UACGCGUCAAUAACGCUA
Complementary.sequence	AUGCGCAGUUAUUGCGAU
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-143140.00000
Entropy..cal.	-365.21571
Enthalpy..J.	-598325.20000
Entropy..J.	-1526.60167
Melting.temperature..C.	90.06842

```r
# Mg correction -  tanmg07 (mRNA/RNA)
out <- melting(sequence = "UACGCGUCAAUAACGCUA",
        nucleic.acid.conc = 0.000002, hybridisation.type = "mrnarna",
        Mg.conc = 0.0015, correction.ion = "tanmg07")
```

```
## [1] "-S UACGCGUCAAUAACGCUA -H mrnarna -P 2e-06 -E Mg=0.0015 -T 60 -ion tanmg07"
```

Sequence	UACGCGUCAAUAACGCUA
Complementary.sequence	AUGCGCAGUUAUUGCGAU
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	0
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	tanmg07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-143140.00000
Entropy..cal.	-365.21571
Enthalpy..J.	-598325.20000
Entropy..J.	-1526.60167
Melting.temperature..C.	90.06842

Mixed Sodium and Magnesium corrections

```
# Mixed Na & Mg correction - default (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015)
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.83371

```r
# Mixed Na & Mg correction - owcmix08 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015, correction.ion = "owcmix08")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -ion owcmix08"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	owcmix08
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.83371

```r
# Mixed Na & Mg correction - tanmix07 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015, correction.ion = "tanmix07")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -ion tanmix07"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	tanmix07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-338.58330
Enthalpy..J.	-516648.00000
Entropy..J.	-1415.27819
Melting.temperature..C.	63.21723

```r
# Mixed Na & Mg correction - default (RNA/RNA)
out <- melting(sequence = "CAGCCUCGUCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Na.conc = 0.069, Mg.conc = 0.0015)
```

```
## [1] "-S CAGCCUCGUCGCAGC -H rnarna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60"
```

Sequence	CAGCCUCGUCGCAGC
Complementary.sequence	GUCGGAGCAGCGUCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-164300.00000
Entropy..cal.	-437.15938
Enthalpy..J.	-686774.00000
Entropy..J.	-1827.32622
Melting.temperature..C.	79.40119

```r
# Mixed Na & Mg correction - tanmix07 (RNA/RNA)
out <- melting(sequence = "CAGCCUCGUCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "rnarna",
        Na.conc = 0.069, Mg.conc = 0.0015, correction.ion = "tanmix07")
```

```
## [1] "-S CAGCCUCGUCGCAGC -H rnarna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -ion tanmix07"
```

Sequence	CAGCCUCGUCGCAGC
Complementary.sequence	GUCGGAGCAGCGUCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	rnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	xia98
GU.model	ser12
Single.mismatch.model	zno07
Tandem.mismatch.model	tur06
Single.dangling.end.model	ser08
Double.dangling.end.model	ser06
Long.dangling.end.model	sugrna02
Internal.loop.model	tur06
Single.bulge.loop.model	tur06
Long.bulge.loop.model	tur06
CNG.repeats.model	NA
Inosine.bases.model	zno07
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	tanmix07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-164300.00000
Entropy..cal.	-437.15938
Enthalpy..J.	-686774.00000
Entropy..J.	-1827.32622
Melting.temperature..C.	79.40119

```r
# Mixed Na & Mg correction - default (mRNA/RNA)
out <- melting(sequence = "UACGCGUCAAUAACGCUA",
        nucleic.acid.conc = 0.000002, hybridisation.type = "mrnarna",
        Na.conc = 0.069, Mg.conc = 0.0015)
```

```
## [1] "-S UACGCGUCAAUAACGCUA -H mrnarna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60"
```

Sequence	UACGCGUCAAUAACGCUA
Complementary.sequence	AUGCGCAGUUAUUGCGAU
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-143140.00000
Entropy..cal.	-358.39889
Enthalpy..J.	-598325.20000
Entropy..J.	-1498.10736
Melting.temperature..C.	96.46186

```r
# Mixed Na & Mg correction - tanmix07 (mRNA/RNA)
out <- melting(sequence = "UACGCGUCAAUAACGCUA",
        nucleic.acid.conc = 0.000002, hybridisation.type = "mrnarna",
        Na.conc = 0.069, Mg.conc = 0.0015, correction.ion = "tanmix07")
```

```
## [1] "-S UACGCGUCAAUAACGCUA -H mrnarna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -ion tanmix07"
```

Sequence	UACGCGUCAAUAACGCUA
Complementary.sequence	AUGCGCAGUUAUUGCGAU
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	mrnarna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	tur06
GU.model	NA
Single.mismatch.model	NA
Tandem.mismatch.model	NA
Single.dangling.end.model	NA
Double.dangling.end.model	NA
Long.dangling.end.model	NA
Internal.loop.model	NA
Single.bulge.loop.model	NA
Long.bulge.loop.model	NA
CNG.repeats.model	NA
Inosine.bases.model	NA
Hydroxyadenine.bases.model	NA
Azobenzenes.model	NA
Locked.nucleic.acids.model	NA
Ion.correction.method	tanmix07
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-143140.00000
Entropy..cal.	-358.39889
Enthalpy..J.	-598325.20000
Entropy..J.	-1498.10736
Melting.temperature..C.	96.46186

Sodium equivalent concentration methods

```
# Na equivalent concentration method - default (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015)
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.83371

```r
# Na equivalent concentration method - ahs01 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015, method.Naeq = "ahs01")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -naeq ahs01"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.83371

```r
# Na equivalent concentration method - mit96 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015, method.Naeq = "mit96")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -naeq mit96"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	mit96
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.83371

```r
# Na equivalent concentration method - pey00 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 0.069, Mg.conc = 0.0015, method.Naeq = "pey00")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=0.069:Mg=0.0015 -T 60 -naeq pey00"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	0.069
Mg.concentration..M.	0.0015
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	pey00
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.83371

Denaturing agent corrections

DMSO corrections

```
# DMSO correction - default (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, DMSO.conc = 10)
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:DMSO=10 -T 60"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	10
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.40154

```r
# DMSO correction - ahs01 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, DMSO.conc = 10, correction.DMSO = "ahs01")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:DMSO=10 -T 60 -DMSO ahs01"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	10
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	65.40154

```r
# DMSO correction - cul76 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, DMSO.conc = 10, correction.DMSO = "cul76")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:DMSO=10 -T 60 -DMSO cul76"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	10
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	cul76
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	67.90154

```r
# DMSO correction - esc80 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, DMSO.conc = 10, correction.DMSO = "esc80")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:DMSO=10 -T 60 -DMSO esc80"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	10
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	esc80
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	66.15154

```r
# DMSO correction - mus80 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, DMSO.conc = 10, correction.DMSO = "mus81")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:DMSO=10 -T 60 -DMSO mus81"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	10
Formamide.concentration..M.or. . .	0
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	mus81
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	66.90154

Formamide corrections

```
# Formamide correction - default (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, formamide.conc = 0.06)
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:formamide=0.06 -T 60"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration....	0
Formamide.concentration..M.or...	0.06
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	72.74867

```r
# Formamide correction - bla96 (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, formamide.conc = 0.06, correction.formamide = "bla96")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:formamide=0.06 -T 60 -for bla96"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	0.06
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	bla96
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	72.74867

```r
# Formamide correction - lincorr (DNA/DNA)
out <- melting(sequence = "CAGCCTCGTCGCAGC",
        nucleic.acid.conc = 0.000002, hybridisation.type = "dnadna",
        Na.conc = 1, formamide.conc = 10, correction.formamide = "lincorr")
```

```
## [1] "-S CAGCCTCGTCGCAGC -H dnadna -P 2e-06 -E Na=1:formamide=10 -T 60 -for lincorr"
```

Sequence	CAGCCTCGTCGCAGC
Complementary.sequence	GTCGGAGCAGCGTCG
Nucleic.acid.concentration..M.	2e-06
Hybridization.type	dnadna
Na.concentration..M.	1
Mg.concentration..M.	0
Tris.concentration..M.	0
K.concentration..M.	0
dNTP.concentration..M.	0
DMSO.concentration. . . .	0
Formamide.concentration..M.or. . .	10
Self.complementarity	FALSE
Correction.factor	4

Approximative.formula	NA
Nearest.neighbour.model	all97
GU.model	NA
Single.mismatch.model	allsanpey
Tandem.mismatch.model	allsanpey
Single.dangling.end.model	bom00
Double.dangling.end.model	sugdna02
Long.dangling.end.model	sugdna02
Internal.loop.model	san04
Single.bulge.loop.model	tan04
Long.bulge.loop.model	san04
CNG.repeats.model	NA
Inosine.bases.model	san05
Hydroxyadenine.bases.model	sug01
Azobenzenes.model	asa05
Locked.nucleic.acids.model	mct04
Ion.correction.method	NA
Na.equivalence.correction.method	ahs01
DMSO.correction.method	ahs01
Formamide.correction.method	lincorr
Mode	def

Enthalpy..cal.	-123600.00000
Entropy..cal.	-328.30000
Enthalpy..J.	-516648.00000
Entropy..J.	-1372.29400
Melting.temperature..C.	66.40154