Output Nucleotide Subsequences with Context

Consider nucleotide sequences which contain the possible base values: `'A'`, `'C'`, `'G'`, `'T'`, and the end-of-sequence value: `'ε'`.

Implement a command-line program that accepts a nucleotide sequence on `stdin`, finds target nucleotide subsequence, and writes each subsequence to `stdout` along with its surrounding context.

More specifically: given a nucleotide sequence *S*, a target subsequence *T*, and two numbers *x* and *y*; for each *T* in *S*: print the *x* preceding nucleotides, the target *T*, and the *y* succeeding nucleotides.

An example command line

```
echo "ACACGTCAε" | matchseq -T:ACGT -x:1 -y:2
```

would yield

```
C ACGT CA
```

where C is the *x*=1 preceding nucleotide, ACGT is the target nucleotide subsequence *T*, and CA is the *y*=2 succeeding nucleotides.

Be aware that:

- *x* may be zero, which indicates that no preceding nucleotides should be printed. Likewise, *y* may be zero, which indicates that no succeeding nucleotides should be printed. However, *T* will not be empty.
- The end-of-sequence value `'ε'` will not appear in *T*.
- If the sequence contains fewer than *x* nucleotides before *T*, or fewer than *y* nucleotides after *T*, print as many as there actually are.
- Targets may overlap in the sequence *S*, and each should be treated as a distinct occurrence with its own preceding/succeeding context.
- `stdin` is a potentially unlimited stream, so be sure to consider the case where the size of *S* exceeds a system's memory.

Example

```
echo "AAGTACGTGCAGTGAGTAGTAGACCTGACGTAGACCGATATAAGTAGCTAε" | \
matchseq -T:AGTA -x:5 -y:7
```

should print the following lines (whose targets we've bolded):

```
A AGTA CGTGCAG
CAGTG AGTA GTAGACC
TGAGT AGTA GACCTGA
ATATA AGTA GCTA
```

Notice that the 2nd and 3rd lines display overlapping targets and that the 1st and 4th show fewer than *x* and *y* elements of context, respectively.