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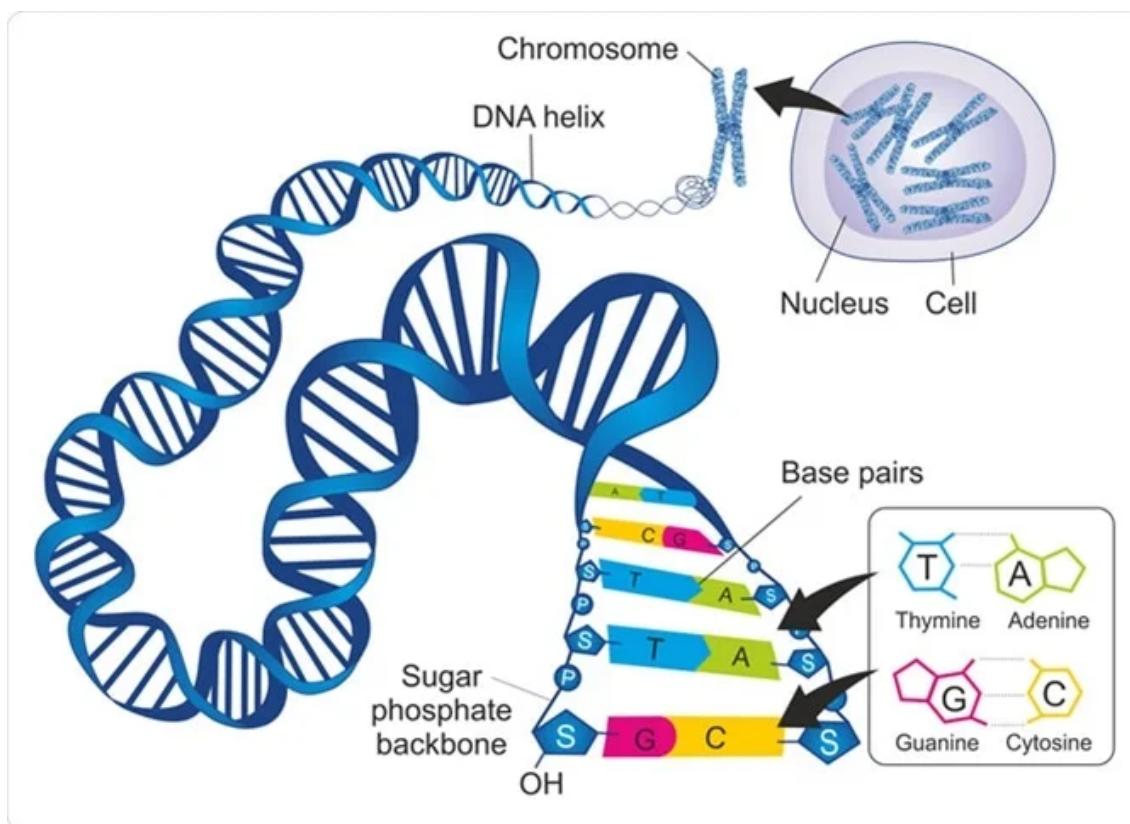








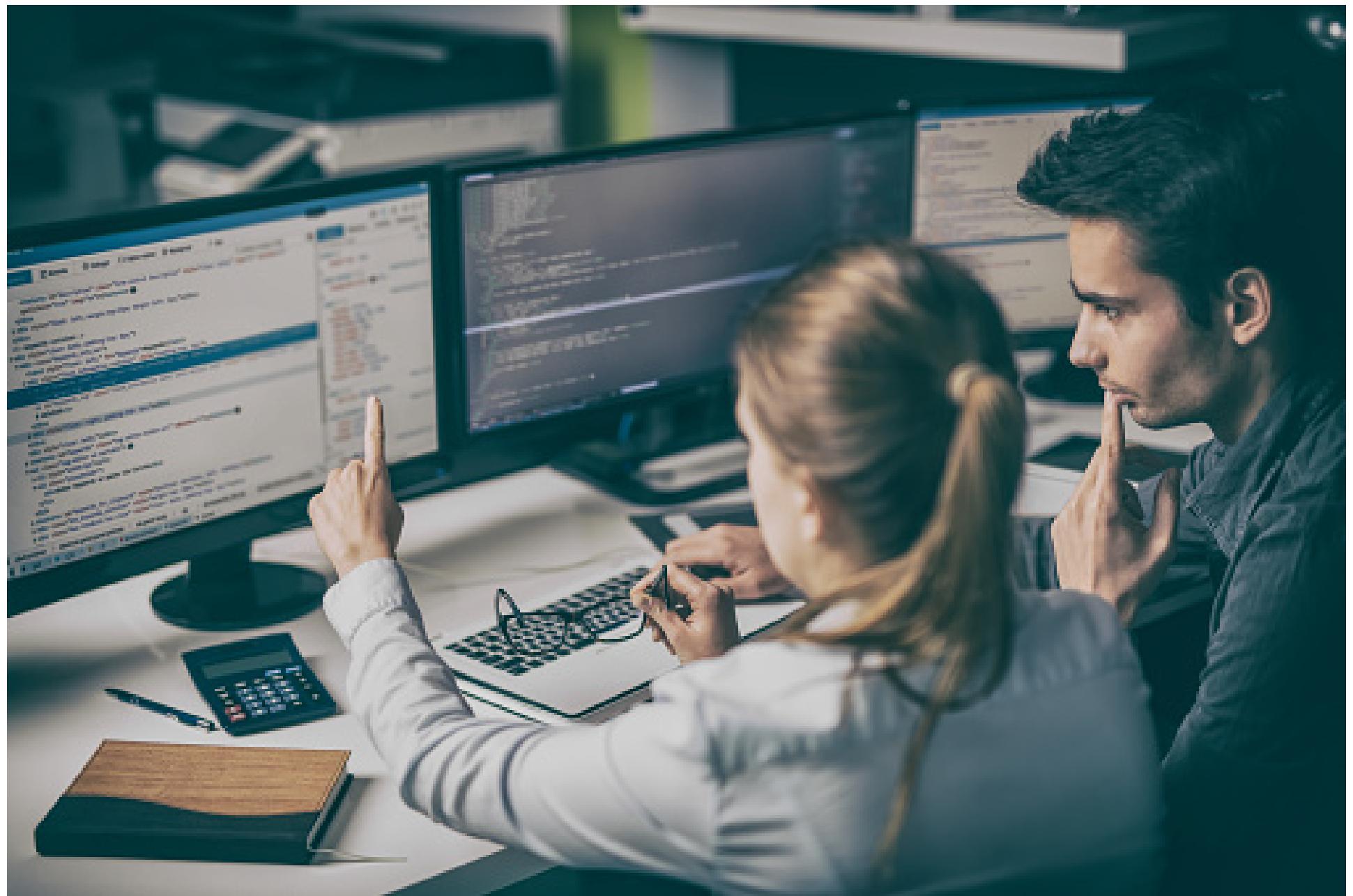
DNA



A C G T

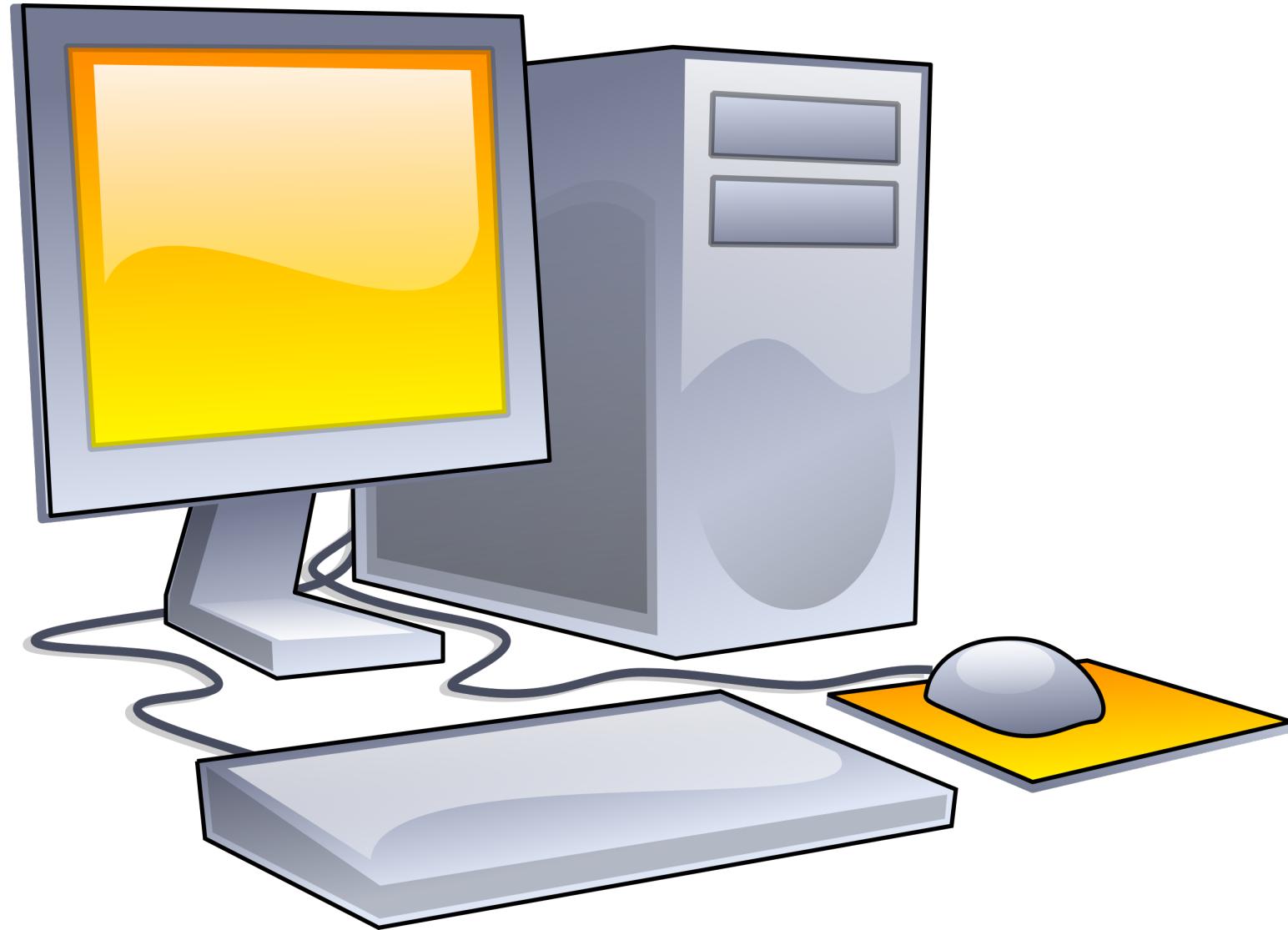
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GACTTCTTAATCTAACTTGGTAAAGTGCTGGTCTTGCCTCGTAGC
TCAGCAGGATAGAGCGGTTGCCTCCTAACGCAGCAGGCCATGCCTCGAAT
CGCATCGAGGACGATTTTGCCTTAACCTCTAAAGTACTAATTGCTT
GTATCTGTGGTTACGTATTTAGCGATATTCTGTTGGTTCTGAAAA
CTAGGTCCAGAAAGAAAATTATGAACCTCCCTCGCGATGCCTTCGCTAC
ATGCATACGATAGCGAGCATCTGCAGGGCCGCACGTTCACGACTATTGG
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ACAACAAAGTTCGCAGTTCAAACCTCGAGACTTCAAAATGCCATT
TTCCATAGCAGCTAAAATGTTTCCCAGTACTTCTGACATGCGATTCC
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GCTGCTGCGTTGAAGAATGATTACAGTGGATGCTGATAAAGACATCCCC
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TTCCTTACTGCCGTGCCTTGATCTTCCCCGTGTCCAGGATCTATAA
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GTAACCGTAAATAATAACTTTGAAGTCTAAGCTCATCATATCTATTCA
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GACTTCTTAATCTAACTTGGTAAAGTGCTGGTCTTGC**GT****C****C****T****C****G****T****A****G**
TC**A****G****C****A****G****G****A****T****A****G****A****G****C****G****G****T****T****G****C****C****T****C****T****A****A****G****C****A****G****C****A****G****G****C****C****A****T****G****C****G****T****T****G****A****A**
C**G****C****A****T****C****G****A****G****G****A****C****G****A****T****T****T****T****G****C****C****T****T****A****A****C****T****C****C****T****A****A****G****T****A****C****T****A****T****T****G****C****T**
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TTCCTTACTGCCGTGCCTTGATCTTCCCCGTGTCCAGGATCTATAA
ATATAACCTCACTGCGTCGTACACGCTGAGGAGGATTGGTGTGAGCA



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File Edit Options Buffers Tools C Help
/* serial_loop():
 *
 * Read the sequence file one window of CM_MAX_RESIDUE_COUNT
 * residues (or one sequence, if seqlen < CM_MAX_RESIDUE_COUNT)
 * at a time. Search the top strand of the window, then revcomp it and
 * search the bottom strand.
 */
static int
serial_loop(WORKER_INFO *info, ESL_SQFILE *dbfp, int64_t *srcL)
{
    int      status;
    int      wstatus;
    int      prv_pli_ntophits; /* number of top hits before each cm_Pipeline() */
    int64_t  seq_idx = 0;
    ESL_SQ   *dbsq   = esl_sq_CreateDigital(info->cm->abc);

    wstatus = esl_sqio_ReadWindow(dbfp, info->pli->maxW, CM_MAX_RESIDUE_COUNT, dbsq);
    seq_idx++;

    while(wstatus == eslEOD) { /* this block is only necessary to chew up zero-length sequences */
        info->pli->nseqs++;
        esl_sq_Reuse(dbsq);
        wstatus = esl_sqio_ReadWindow(dbfp, info->pli->maxW, CM_MAX_RESIDUE_COUNT, dbsq);
        seq_idx++;
    }

    /*printf("SER just read seq %ld (%40s) %10ld..%10ld\n", seq_idx, dbsq->name, dbsq->start, dbsq->end);*/
    while (wstatus == eslOK) {
        /* if this is the first window for this sequence, set dbsq->L */
        if(dbsq->start == 1) dbsq->L = srcL[seq_idx-1];

        cm_pli_NewSeq(info->pli, dbsq, seq_idx-1);

        if (info->pli->do_top) {
            prv_pli_ntophits = info->th->N;
            if((status = cm_Pipeline(info->pli, info->cm->offset, info->om, info->bg, info->p7_evparam, info->msvdata, dbsq, info->th, FALSE, /* FALSE: not in reverse complement */
                NULL, &(info->gm), &(info->rgm), &(info->lgm), &(info->tgm), &(info->cm))) != eslOK cm_Fail("cm_pipeline() failed unexpected with status code %d\n", status, i)
            info->pli->errbuf;
            cm_pipeline_Reuse(info->pli); /* prepare for next search */

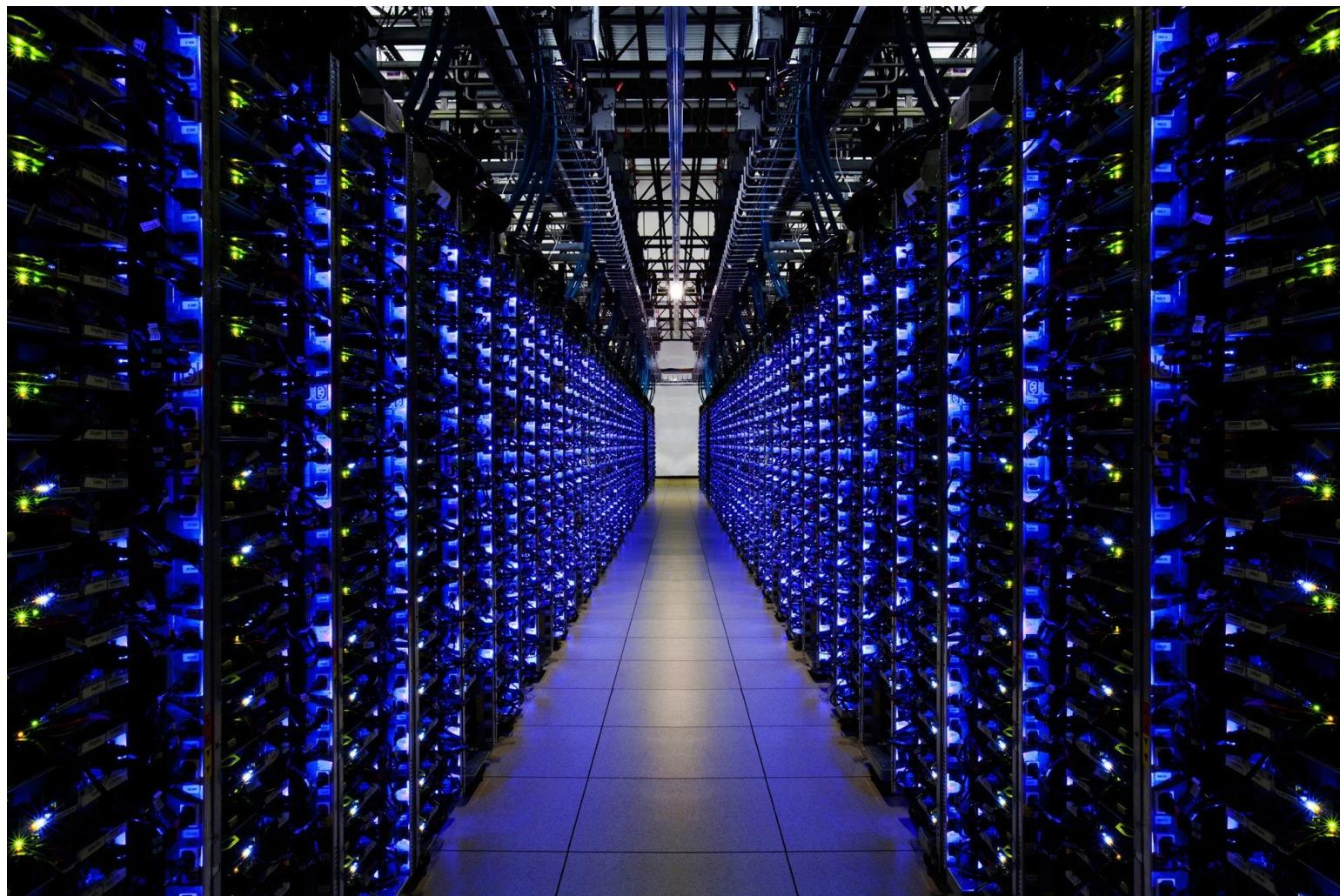
            /* subtract overlapping residues from previous window */
            if(dbsq->C > 0) cm_pli_AdjustResForOverlaps(info->pli, dbsq->C, FALSE); /* 'FALSE': we're not on bottom strand */

            /* modify hit positions to account for the position of the window in the full sequence */
            cm_tophits_UpdateHitPositions(info->th, prv_pli_ntophits, dbsq->start, FALSE);
        }

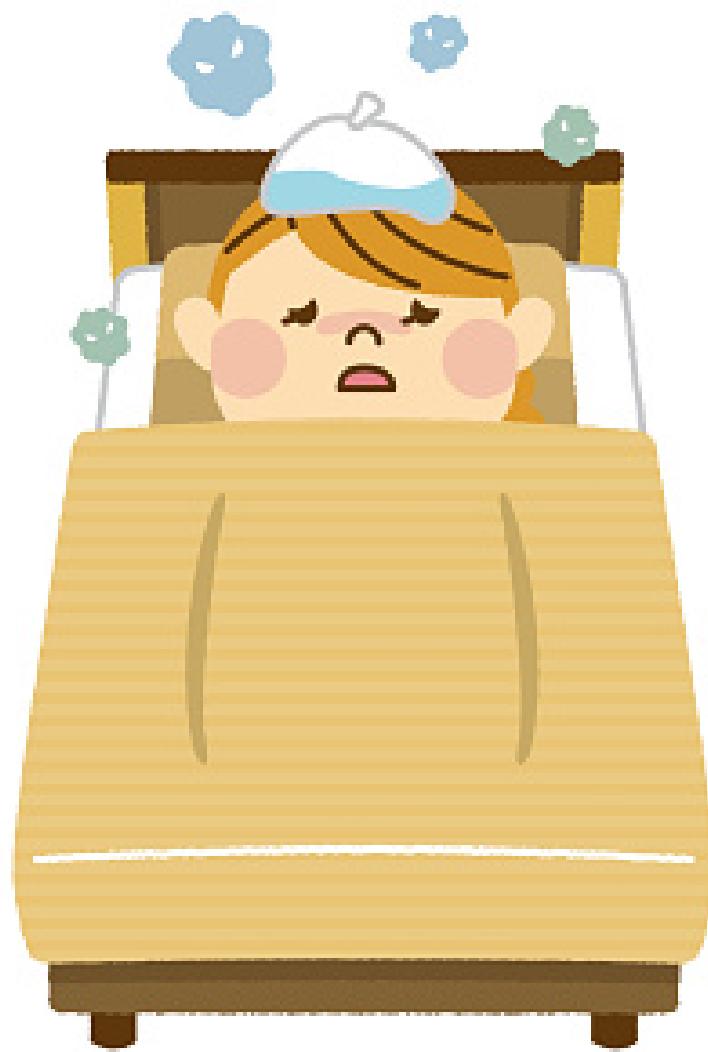
        /* reverse complement */
        if (info->pli->do_bot && dbsq->abc->complement != NULL) {
-UU-:----F1  cmsearch.c<src>  28% (796,0)  ((/*l Abbrev) ----

```













THANK Y^OU

